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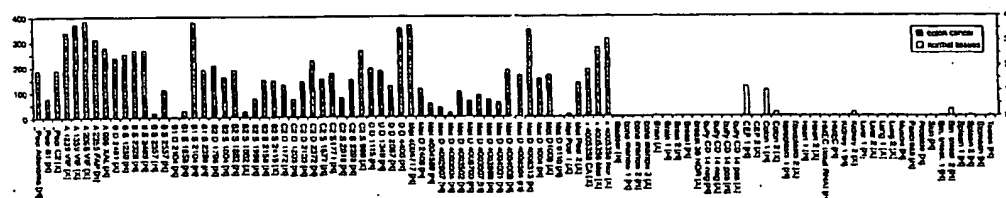
(71) Applicant: EOS BIOTECHNOLOGY, INC. [US/US];
225A Gateway Boulevard, South San Francisco, CA
94080-7019 (US).(72) Inventors: MACK, David; 2076 Monterey Avenue,
Menlo Park, CA 94025 (US). GISH, Kurt, C.; 4302 23rd
Street, San Francisco, CA 94114 (US). WILSON, Keith,
E.; 219 Jeter Street, Redwood City, CA 94062 (US).(74) Agents: BREZNER, David, J. et al.; Flehr Hohbach Test
Albritton & Herbert LLP, Suite 3400, 4 Embarcadero Center,
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(54) Title: METHODS OF SCREENING FOR COLORECTAL CANCER MODULATORS



(57) Abstract: Described herein are methods that can be used for diagnosis and prognosis of colorectal cancer. Also described herein are methods that can be used to screen candidate bioactive agents for the ability to modulate colorectal cancer. Additionally, methods and molecular targets (genes and their products) for therapeutic intervention in colorectal and other cancers are described.

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NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AND METHODS OF SCREENING FOR COLORECTAL CANCER MODULATORS

FIELD OF THE INVENTION

The invention relates to the identification of expression profiles and the nucleic acids involved in colorectal cancer, and to the use of such expression profiles and nucleic acids in diagnosis and prognosis of colorectal cancer. The invention further relates to methods for identifying and using candidate agents and/or targets which modulate colorectal cancer.

BACKGROUND OF THE INVENTION

Colorectal cancer is a significant cancer in Western populations. It develops as the result of a pathologic transformation of normal colon epithelium to an invasive cancer. There have been a number of recently characterized genetic alterations that have been implicated in colorectal cancer, including mutations in two classes of genes, tumor-suppressor genes and proto-oncogenes, with recent work suggesting that mutations in DNA repair genes may also be involved in tumorigenesis. For example, inactivating mutations of both alleles of the adenomatous polyposis coli (APC) gene, a tumor suppressor gene, appears to be one of the earliest events in colorectal cancer, and may even be the initiating event. Other genes implicated in colorectal cancer include the MCC gene, the p53 gene, the DCC (deleted in colorectal carcinoma) gene and other chromosome 18q genes, and genes in the TGF- β signaling pathway. For a review, see Molecular Biology of Colorectal Cancer, pp238-299, in Curr. Probl. Cancer, Sept/Oct 1997.

Imaging of colorectal cancer for diagnosis has been problematic and limited. In addition, dissemination of tumor cells (metastases) to locoregional lymph nodes is an important prognostic factor; five year survival rates drop from 80 percent in patients with no lymph node metastases to 45 to 50 percent in those patients who do have lymph node metastases. A recent report showed that micrometastases can be detected from lymph nodes using reverse transcriptase-PCR methods based on the presence of mRNA for carcinoembryonic antigen, which has previously been shown to be present in the vast

majority of colorectal cancers but not in normal tissues. Liefers et al., New England J. of Med. 339(4):223 (1998).

Thus, methods that can be used for diagnosis and prognosis of colorectal cancer would be desirable. Accordingly, provided herein are methods that can be used in diagnosis and prognosis of colorectal cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate colorectal cancer. Additionally, provided herein are molecular targets for therapeutic intervention in colorectal and other cancers.

SUMMARY OF THE INVENTION

The present invention provides methods for screening for compositions which modulate colorectal cancer. Also provided herein are methods of inhibiting proliferation of cell, preferably a colorectal cancer cell. Methods of treatment of cancer, as well as compositions, are also provided herein.

In one aspect, a method of screening drug candidates comprises providing a cell that expresses an expression profile gene or fragments thereof. Preferred embodiments of the expression profile gene are genes which are differentially expressed in cancer cells, preferably colorectal cancer cells, compared to other cells. Preferred embodiments of expression profile genes used in the methods herein include but are not limited to the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9; fragments of the proteins of this group are also preferred. It is understood that molecules for use in the present invention may be from any figure or any subset of listed molecules. Therefore, for example, any one or more of the genes listed above can be used in the methods herein. In another embodiment, a nucleic acid is selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. The method further includes adding a drug candidate to the cell and determining the effect of the drug candidate on the expression of the expression profile gene.

In one embodiment, the method of screening drug candidates includes comparing the level of expression in the absence of the drug candidate to the level of expression in the presence of the drug candidate, wherein the concentration of the drug candidate can vary when present, and wherein the comparison can occur after addition or removal of the drug candidate. In a preferred embodiment, the cell expresses at least two expression profile genes. The profile genes may show an increase or decrease.

Also provided herein is a method of screening for a bioactive agent capable of binding to a colorectal cancer modulator protein (CCMP), the method comprising combining the CCMP and a candidate bioactive agent, and determining the binding of the candidate agent to the CCMP. Preferably the CCMP is a protein or fragment thereof selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

Further provided herein is a method for screening for a bioactive agent capable of modulating the activity of a CCMP. In one embodiment, the method comprises combining the CCMP and a candidate bioactive agent, and determining the effect of the candidate agent on the bioactivity of the CCMP. Preferably the CCMP is a protein or fragment thereof selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

Also provided is a method of evaluating the effect of a candidate colorectal cancer drug comprising administering the drug to a transgenic animal expressing or over-expressing the CCMP, or an animal lacking the CCMP, for example as a result of a gene knockout.

Additionally, provided herein is a method of evaluating the effect of a candidate colorectal cancer drug comprising administering the drug to a patient and removing a cell sample from the patient. The expression profile of the cell is then determined. This method may further comprise comparing the expression profile to an expression profile of a healthy individual.

Moreover, provided herein is a biochip comprising a nucleic acid segment which encodes a colorectal cancer protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof, wherein the biochip comprises fewer than 1000 nucleic acid probes. Preferably at least two nucleic acid segments are included. In another embodiment, the nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

Furthermore, a method of diagnosing a disorder associated with colorectal cancer is provided. The method comprises determining the expression of a gene which encodes a colorectal cancer protein preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9 or a fragment thereof in a first tissue type of a first individual, and comparing the distribution to the expression of the gene from a second normal tissue type from the first individual or a second unaffected individual. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. A difference in the expression indicates that the first individual has a disorder associated with colorectal cancer.

In another aspect, the present invention provides an antibody which specifically binds to a colorectal cancer protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. In a preferred embodiment, the fragment of CAA9 is selected from CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 and CAA9p5MAPS. Other preferred fragments for the breast cancer proteins are shown in the figures. Preferably the antibody is a monoclonal antibody. The antibody can be a fragment of an antibody such as a single stranded antibody as further described herein, or can be conjugated to another molecule. In one embodiment, the antibody is a humanized antibody.

In one embodiment a method for screening for a bioactive agent capable of interfering with the binding of a colorectal cancer protein (CCMP) or a fragment thereof and an antibody which binds to said CCMP or fragment thereof. In a preferred embodiment, the method comprises combining a CCMP or fragment thereof, a candidate bioactive agent and an antibody which binds to said CCMP or fragment thereof. The method further includes determining the binding of said CCMP or fragment thereof and said antibody. Wherein there is a change in binding, an agent is identified as an interfering agent. The interfering agent can be an agonist or an antagonist. Preferably, the antibody as well as the agent inhibits colorectal cancer.

In a further aspect, a method for inhibiting colorectal cancer is provided. In one embodiment, the method comprises administering to a cell a composition comprising an antibody to a colorectal modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment

thereof. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. The method can be performed in vitro or in vivo, preferably in vivo to an individual. In a preferred embodiment the method of inhibiting colorectal cancer is provided to an individual with cancer. As described herein, methods of inhibiting colorectal cancer can be performed by administering an inhibitor of colorectal cancer protein activity, including antisense molecules, and preferably small molecules.

Also provided herein are methods eliciting an immune response in an individual. In one embodiment a method provided herein comprises administering to an individual a composition comprising a colorectal modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. In another aspect, said composition comprises a nucleic acid comprising a sequence encoding a colorectal cancer modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof. In another embodiment, the nucleic acid is selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

Further provided herein are compositions capable of eliciting an immune response in an individual. In one embodiment, a composition provided herein comprises a colorectal cancer modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. In another embodiment, said composition comprises a nucleic acid comprising a sequence encoding a colorectal cancer modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, the nucleic acid is selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

A method of neutralizing the effect of a colorectal cancer protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

In another aspect of the invention, a method of treating an individual for colorectal cancer is provided. In one embodiment, the method comprises administering to said individual an inhibitor of CJA8. In another embodiment, the method comprises administering to a patient having colorectal cancer an antibody to CJA8 conjugated to a therapeutic moiety. Such a therapeutic moiety can be a cytotoxic agent or a radioisotope.

Also provided herein is a method for determining the prognosis of an individual with colorectal cancer comprising determining the level of CJA8 in a sample, wherein a high level of CJA8 indicates a poor prognosis.

Novel sequences are also provided herein. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

DETAILED DESCRIPTION OF THE FIGURES

Figure 1 provides the Accession numbers for genes, including expression sequence tags, (incorporated in their entirety here and throughout the application where Accession numbers are provided), upregulated in tumor tissue compared to normal colon tissue.

Figure 2 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue.

Figure 3 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue.

Figure 4 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue.

Figure 5 provides the Accession numbers for genes, including expression sequence tags, downregulated in tumor tissue compared to normal colon tissue.

Figure 6 provides the Accession numbers for genes, including expression sequence tags, downregulated in tumor tissue compared to normal colon tissue.

Figure 7 provides the Accession numbers for genes, including expression sequence tags, downregulated in tumor tissue compared to normal colon tissue.

Figure 8 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames in the sequences have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

Figure 9 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames in the sequences have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

Figure 10 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

Figure 11 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

Figure 12 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

Figure 13 provides the Accession numbers for genes or fragments thereof, including descriptions of the gene or encoded protein, upregulated in tumor tissue compared to normal colon tissue.

Figure 14 provides a list of proteins, including Accession numbers for nucleic acid sequences associated with the encoding genes thereof, upregulated in tumor tissue compared to normal colon tissue.

Figure 15 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal protein provided herein, CAA2. The start and stop codon are shaded. The sequence within the two cross marks indicates a preferred novel fragment of CAA2 provided herein, referred to herein as the "CAA2 5' end". Preferred embodiments of CAA2 include at least a portion of the CAA2 5'. The sequence in bold and indicated with a bar at the bottom right beginning with "GGC" and ending with "AAA" can be found in Accession no. AA505133.

Figure 16 shows an embodiment of a nucleic acid encoding CAA2, wherein the start and stop codons are shaded.

Figure 17 shows an embodiment of an amino acid sequence of CAA2. Preferred fragments include at least about 10 amino acids in the N-terminal end. The N-terminus as defined herein includes an embodiment beginning at the first amino acid until about any one of the three amino acids marked with a dot above them. In another embodiment, the N-terminus of CAA2 is defined as the amino acid sequence encoded by the CAA2 5' end.

Figure 18 shows the amino acid sequence of CAA2p1, a preferred CAA2 fragment provided herein.

Figure 19 shows the amino acid sequence of CAA2p2, a preferred CAA2 fragment provided herein.

Figure 20 shows an alignment of the human and mouse CAA2 polypeptides provided herein. The mouse polypeptide contains at least some of the sequence of each of the following Accession numbers: AA386837; A1508773; AA505293; and AA636546.

Figure 21 shows the relative amount of expression of CAA2 in various samples of colon cancer tissue (dark bars) and many normal tissue types (light bars).

Figure 22 shows an embodiment of a colorectal cancer nucleic acid, CAA9 mRNA. The start and stop codons are underlined.

Figure 23 shows the open reading frame of the CAA9 gene wherein the start and stop codons are underlined.

Figure 24 shows an embodiment of the amino acid sequence of a colorectal cancer protein, CAA9, wherein putative transmembrane sequences are underlined. In one embodiment, CAA9 or fragments

of CAA9 are soluble, therefore, the transmembrane domains are deleted, inactivated, and/or the peptide is truncated (with or without re-ligation) to form soluble CAA9.

Figure 25 shows embodiments of colorectal cancer proteins (also termed colorectal cancer modulator proteins). Specifically, Figure 25 shows CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 and CAA9p5MAPS and their respective solubilities.

Figure 26 shows the relative amount of CAA9 expression in several different samples of colon cancer tissue (dark bars) and normal tissues (light bars).

Figure 27 shows the nucleic acid sequence for the gene encoding CGA7. Start (ATG) and stop (TAG) codons are indicated by shaded boxes. In bold is the sequence of Accession No. AA331393. Underlined is the consensus sequence derived from the compilation and alignment of published est sequences.

Figures 28A and 28B show the alignment summary and descriptions, respectively, of the various est's (by accession number) compiled to generate the consensus sequence of figure 1.

Figure 29 shows the amino acid sequence of CGA7.

Figures 30A and 30B show the relative expression of CGA7 in normal tissue and colon cancer tissue, respectively.

Figure 31 shows the nucleic acid sequence for the mRNA encoding CGA8. Start (ATG) and stop (TAG) codons are indicated by shaded boxes. In bold is the sequence of Accession No. AA2786503. Underlined is the consensus sequence derived from the compilation and alignment of published est sequences.

Figures 32A and 32B show the alignment summary and descriptions, respectively, of the various est's (by accession number) compiled to generate the consensus sequence of figure 1.

Figure 33 shows the amino acid sequence of CGA8.

Figure 34 shows the relative expression of CGA8 in breast cancer tissue, colon cancer tissue, normal tissue and fetal tissue.

Figure 35 shows the sequence for the mRNA encoding CJA8. Start (ATG) and stop (TAA) codons are indicated by shaded boxes.

Figure 36 shows the amino acid sequence for CJA8. A putative transmembrane region is designated by shading. A mouse homolog of this human protein is found at Accession Number AAF21308.1.

Figure 37 shows the relative amount of expression of CJA8 in several different samples of colon tissues (dark bars) and normal tissues (light bars).

Figure 38 shows the relative amount of expression of BCN7 in several different samples of colon tissues (dark bars) and normal tissues (light bars), as determined using the sequence of Accession Number N22107 as a probe.

Figure 39 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal cancer protein provided herein, BCN7.

Figure 40 shows the sequence for the mRNA encoding CZA8. Start (ATG) and stop (TGA) codons are indicated by underlining.

Figure 41 shows the sequence for the mRNA encoding BCX2. Start (ATG) and stop (TGA) codons are indicated by underlining.

Figure 42 shows the sequence for the mRNA encoding CBC2. Start (ATG) and stop (TAA) codons are indicated by underlining.

Figure 43 shows the sequence for the mRNA encoding CBC1. Start (ATG) and stop (TGA) codons are indicated by underlining.

Figure 44 shows the sequence for the mRNA encoding CBC3. Start (ATG) and stop (TGA) codons are indicated by underlining.

Figure 45 shows the sequence for the mRNA encoding BCN5. Start (ATG) and stop (TAA) codons are indicated by underlining.

Figure 46 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal cancer protein provided herein, CJA9.

Figure 47 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal cancer protein provided herein, CQA1.

Figure 48 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal cancer protein provided herein, CQA2.

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides novel methods for diagnosis and prognosis evaluation for colorectal cancer (CRC), as well as methods for screening for compositions which modulate CRC. In one aspect, the expression levels of genes are determined in different patient samples for which either diagnosis or prognosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is unique to the state of the cell. That is, normal tissue may be distinguished from CRC tissue, and within CRC tissue, different prognosis states (good or poor long term survival prospects, for example) may be determined. By comparing expression profiles of colon tissue in known different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. The identification of sequences that are differentially expressed in CRC versus normal colon tissue, as well as differential expression resulting in different prognostic outcomes, allows the use of this information in a number of ways. For example, the evaluation of a particular treatment regime may be evaluated: does a chemotherapeutic drug act to improve the long-term prognosis in a particular patient. Similarly, diagnosis may be done or confirmed by comparing patient samples with the known expression profiles. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; for example, screening can be done for drugs that suppress the CRC expression profile or convert a poor prognosis profile to a better prognosis profile. This may be done by making biochips comprising sets of the important CRC genes, which can then be used in these screens. These methods can also be done on the protein basis; that is, protein expression levels of the CRC proteins can be evaluated for diagnostic and prognostic purposes or to screen candidate agents. In addition, the CRC nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the CRC proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in colorectal cancer, CRC, herein termed "CRC sequences". As outlined below, CRC sequences include those that are up-regulated (i.e. expressed at a higher level) in CRC, as well as those that are down-regulated (i.e. expressed at a lower level) in CRC. In a preferred embodiment, the CRC sequences are from humans; however, as will be appreciated by those in the art, CRC sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other CRC sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc). CRC sequences from other organisms may be obtained using the techniques outlined below.

CRC sequences can include both nucleic acid and amino acid sequences. In a preferred embodiment, the CRC sequences are recombinant nucleic acids. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid by polymerases and endonucleases, in a form not normally found in nature. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e. using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

Similarly, a "recombinant protein" is a protein made using recombinant techniques, i.e. through the expression of a recombinant nucleic acid as depicted above. A recombinant protein is distinguished from naturally occurring protein by at least one or more characteristics. For example, the protein may be isolated or purified away from some or all of the proteins and compounds with which it is normally associated in its wild type host, and thus may be substantially pure. For example, an isolated protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, preferably constituting at least about 0.5%, more preferably at least about 5% by weight of the total protein in a given sample. A substantially pure protein comprises at least about 75% by weight of the total protein, with at least about 80% being preferred, and at least about 90% being particularly preferred. The definition includes the production of a CRC protein from one organism in a different organism or host cell. Alternatively, the protein may be made at a significantly higher concentration than is normally seen, through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. Alternatively, the protein may be in a form

not normally found in nature, as in the addition of an epitope tag or amino acid substitutions, insertions and deletions, as discussed below.

In a preferred embodiment, the CRC sequences are nucleic acids. As will be appreciated by those in the art and is more fully outlined below, CRC sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; for example, biochips comprising nucleic acid probes to the CRC sequences can be generated. In the broadest sense, then, by "nucleic acid" or "oligonucleotide" or grammatical equivalents herein means at least two nucleotides covalently linked together. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, as outlined below, nucleic acid analogs are included that may have alternate backbones, comprising, for example, phosphoramidate (Beaucage et al., *Tetrahedron* 49(10):1925 (1993) and references therein; Letsinger, *J. Org. Chem.* 35:3800 (1970); Sprinzl et al., *Eur. J. Biochem.* 81:579 (1977); Letsinger et al., *Nucl. Acids Res.* 14:3487 (1986); Sawai et al., *Chem. Lett.* 805 (1984), Letsinger et al., *J. Am. Chem. Soc.* 110:4470 (1988); and Pauwels et al., *Chemica Scripta* 26:141-9 (1986)), phosphorothioate (Mag et al., *Nucleic Acids Res.* 19:1437 (1991); and U.S. Patent No. 5,644,048), phosphorodithioate (Briu et al., *J. Am. Chem. Soc.* 111:2321 (1989), O-methylphosphoroamidite linkages (see Eckstein, *Oligonucleotides and Analogues: A Practical Approach*, Oxford University Press), and peptide nucleic acid backbones and linkages (see Egholm, *J. Am. Chem. Soc.* 114:1895 (1992); Meier et al., *Chem. Int. Ed. Engl.* 31:1008 (1992); Nielsen, *Nature*, 365:566 (1993); Carlsson et al., *Nature* 380:207 (1996), all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy et al., *Proc. Natl. Acad. Sci. USA* 92:6097 (1995); non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141 and 4,469,863; Kiedrowski et al., *Angew. Chem. Intl. Ed. English* 30:423 (1991); Letsinger et al., *J. Am. Chem. Soc.* 110:4470 (1988); Letsinger et al., *Nucleoside & Nucleotide* 13:1597 (1994); Chapters 2 and 3, *ASC Symposium Series* 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook; Mesmaeker et al., *Bioorganic & Medicinal Chem. Lett.* 4:395 (1994); Jeffs et al., *J. Biomolecular NMR* 34:17 (1994); *Tetrahedron Lett.* 37:743 (1996)) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, *ASC Symposium Series* 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins et al., *Chem. Soc. Rev.* (1995) pp169-176). Several nucleic acid analogs are described in Rawls, *C & E News* June 2, 1997 page 35. All of these references are hereby expressly incorporated by reference. These modifications of the ribose-phosphate backbone may be done for a variety of reasons, for example to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip.

As will be appreciated by those in the art, all of these nucleic acid analogs may find use in the present invention. In addition, mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4°C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9°C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand ("Watson") also defines the sequence of the other strand ("Crick"); thus the sequences described herein also includes the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA or a hybrid, where the nucleic acid contains any combination of deoxyribo- and ribo-nucleotides, and any combination of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus for example the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A CRC sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the CRC sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

The CRC sequences of the invention can be identified as follows. Samples of normal and tumor tissue are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are

commercially available, for example from Affymetrix. Gene expression profiles as described herein are generated, and the data analyzed.

In a preferred embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, including, but not limited to lung, heart, brain, liver, breast, kidney, muscle, prostate, small intestine, large intestine, spleen, bone, and placenta. In a preferred embodiment, those genes identified during the CRC screen that are expressed in any significant amount in other tissues are removed from the profile, although in some embodiments, this is not necessary. That is, when screening for drugs, it is preferable that the target be disease specific, to minimize possible side effects.

In a preferred embodiment, CRC sequences are those that are up-regulated in CRC; that is, the expression of these genes is higher in colorectal carcinoma as compared to normal colon tissue. "Up-regulation" as used herein means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. All accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, DA, et al., Nucleic Acids Research 26:1-7 (1998) and <http://www.ncbi.nlm.nih.gov/>. In addition, these genes were found to be expressed in a limited amount or not at all in heart, brain, lung, liver, breast, kidney, prostate, small intestine and spleen.

In a preferred embodiment, CRC sequences are those that are down-regulated in CRC; that is, the expression of these genes is lower in colorectal carcinoma as compared to normal colon tissue. "Down-regulation" as used herein means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred.

CRC proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In a preferred embodiment the CRC protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, for example, signaling pathways); aberrant expression of such proteins results in unregulated or disregulated cellular processes. For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing intracellular proteins is the presence in the proteins of one or more motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of primary sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate.

In a preferred embodiment, the CRC sequences are transmembrane proteins. Transmembrane proteins are molecules that span the phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Important transmembrane protein receptors include, but are not limited to insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, interleukin receptors, e.g. IL-1 receptor, IL-2 receptor, etc.

Characteristics of transmembrane domains include approximately 20 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid

sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted.

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. For example, cytokine receptors are characterized by a cluster of cysteines and a WSXWS (W= tryptophan, S= serine, X=any amino acid) motif. Immunoglobulin-like domains are highly conserved. Mucin-like domains may be involved in cell adhesion and leucine-rich repeats participate in protein-protein interactions.

Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell for example via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

CRC proteins that are transmembrane are particularly preferred in the present invention as they are good targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, for example through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In a preferred embodiment, the CRC proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; by virtue of their circulating nature, they serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor) or an

endocrine manner (acting on cells at a distance). Thus secreted molecules find use in modulating or altering numerous aspects of physiology. CRC proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, for example for blood tests.

A CRC sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology to the CRC sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

As used herein, a nucleic acid is a "CRC nucleic acid" if the overall homology of the nucleic acid sequence to the nucleic acid sequences encoding the amino acid sequences of the figures is preferably greater than about 75%, more preferably greater than about 80%, even more preferably greater than about 85% and most preferably greater than 90%. In some embodiments the homology will be as high as about 93 to 95 or 98%. Homology in this context means sequence similarity or identity, with identity being preferred. A preferred comparison for homology purposes is to compare the sequence containing sequencing errors to the correct sequence. This homology will be determined using standard techniques known in the art, including, but not limited to, the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *PNAS USA* 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Drive, Madison, WI), the Best Fit sequence program described by Devereux et al., *Nucl. Acid Res.* 12:387-395 (1984), preferably using the default settings, or by inspection.

In a preferred embodiment, the sequences which are used to determine sequence identity or similarity are selected from the sequences set forth in the figures, preferably those represented in Figure 12, more preferably those represented in Figures 13A and 13B, still more preferably those of Figures 14-20, 22-25, 27-29, 31-33, 35-37 and 39-48, and fragments thereof. In one embodiment the sequences utilized herein are those set forth in the figures. In another embodiment, the sequences are naturally occurring allelic variants of the sequences set forth in the figures. In another embodiment, the sequences are sequence variants as further described herein.

One example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments. It can also plot a tree showing the

clustering relationships used to create the alignment. PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle, *J. Mol. Evol.* 35:351-360 (1987); the method is similar to that described by Higgins & Sharp *CABIOS* 5:151-153 (1989). Useful PILEUP parameters including a default gap weight of 3.00, a default gap length weight of 0.10, and weighted end gaps.

Another example of a useful algorithm is the BLAST algorithm, described in Altschul et al., *J. Mol. Biol.* 215, 403-410, (1990) and Karlin et al., *PNAS USA* 90:5873-5787 (1993). A particularly useful BLAST program is the WU-BLAST-2 program which was obtained from Altschul et al., *Methods in Enzymology*, 266: 460-480 (1996); <http://blast.wustl.edu/blast/REACRCE.html>. WU-BLAST-2 uses several search parameters, most of which are set to the default values. The adjustable parameters are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11. The HSP S and HSP S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the sequence of interest is being searched; however, the values may be adjusted to increase sensitivity. A % amino acid sequence identity value is determined by the number of matching identical residues divided by the total number of residues of the "longer" sequence in the aligned region: The "longer" sequence is the one having the most actual residues in the aligned region (gaps introduced by WU-Blast-2 to maximize the alignment score are ignored).

Thus, "percent (%) nucleic acid sequence identity" is defined as the percentage of nucleotide residues in a candidate sequence that are identical with the nucleotide residues of the sequences of the figures. A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively.

The alignment may include the introduction of gaps in the sequences to be aligned. In addition, for sequences which contain either more or fewer nucleosides than those of the figures, it is understood that the percentage of homology will be determined based on the number of homologous nucleosides in relation to the total number of nucleosides. Thus, for example, homology of sequences shorter than those of the sequences identified herein and as discussed below, will be determined using the number of nucleosides in the shorter sequence.

In one embodiment, the nucleic acid homology is determined through hybridization studies. Thus, for example, nucleic acids which hybridize under high stringency to the nucleic acid sequences which encode the peptides identified in the figures, or their complements, are considered a CRC sequence. High stringency conditions are known in the art; see for example Maniatis et al., *Molecular Cloning: A Laboratory Manual*, 2d Edition, 1989, and *Short Protocols in Molecular Biology*, ed. Ausubel, et al.,

both of which are hereby incorporated by reference. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, *Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Acid Probes*, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent conditions are selected to be about 5-10°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g. 10 to 50 nucleotides) and at least about 60°C for long probes (e.g. greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide.

In another embodiment, less stringent hybridization conditions are used; for example, moderate or low stringency conditions may be used, as are known in the art; see Maniatis and Ausubel, *supra*, and Tijssen, *supra*.

In addition, the CRC nucleic acid sequences of the invention are fragments of larger genes, i.e. they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, additional sequences of the CRC genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Maniatis et al., and Ausubel, et al., *supra*, hereby expressly incorporated by reference.

Once the CRC nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire CRC nucleic acid. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant CRC nucleic acid can be further-used as a probe to identify and isolate other CRC nucleic acids, for example additional coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant CRC nucleic acids and proteins.

The CRC nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the CRC nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, for example for gene

therapy and/or antisense applications. Alternatively, the CRC nucleic acids that include coding regions of CRC proteins can be put into expression vectors for the expression of CRC proteins, again either for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to CRC nucleic acids (both the nucleic acid sequences encoding peptides outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the CRC nucleic acids, i.e. the target sequence (either the target sequence of the sample or to other probe sequences, for example in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (i.e. have some sequence in common), or separate.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of either electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent

binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant any material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, TeflonJ, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. A preferred substrate is described in copending application entitled Reusable Low Fluorescent Plastic Biochip, U.S. Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, for example, the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic

acids containing amino groups can be attached to surfaces comprising amino groups, for example using linkers as are known in the art; for example, homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200, incorporated herein by reference). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, the oligonucleotides are synthesized as is known in the art, and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

In an additional embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using well known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affimetrix GeneChip™ technology.

In a preferred embodiment, CRC nucleic acids encoding CRC proteins are used to make a variety of expression vectors to express CRC proteins which can then be used in screening assays, as described below. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the CRC protein. The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the

sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. The transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the CRC protein; for example, transcriptional and translational regulatory nucleic acid sequences from *Bacillus* are preferably used to express the CRC protein in *Bacillus*. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, the transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences encode either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, the expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, for example in mammalian or insect cells for expression and in a procaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The CRC proteins of the present invention are produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a CRC protein, under the appropriate conditions to

induce or cause expression of the CRC protein. The conditions appropriate for CRC protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Drosophila melanogaster* cells, *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, THP1 cell line (a macrophage cell line) and human cells and cell lines.

In a preferred embodiment, the CRC proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral systems. A preferred expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048, both of which are hereby expressly incorporated by reference. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter. Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, CRC proteins are expressed in bacterial systems. Bacterial expression systems are well known in the art. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; for example, the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can

include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the CRC protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others. The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, CRC proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, CRC protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guillermondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The CRC protein may also be made as a fusion protein, using techniques well known in the art. Thus, for example, for the creation of monoclonal antibodies, if the desired epitope is small, the CRC protein may be fused to a carrier protein to form an immunogen. Alternatively, the CRC protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the CRC protein is a CRC peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In one embodiment, the CRC nucleic acids, proteins and antibodies of the invention are labeled. By "labeled" herein is meant that a compound has at least one element, isotope or chemical compound attached to enable the detection of the compound. In general, labels fall into three classes: a) isotopic labels, which may be radioactive or heavy isotopes; b) immune labels, which may be antibodies or

antigens; and c) colored or fluorescent dyes. The labels may be incorporated into the CRC nucleic acids, proteins and antibodies at any position. For example, the label should be capable of producing, either directly or indirectly, a detectable signal. The detectable moiety may be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I , a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter et al., Nature, 144:945 (1962); David et al., Biochemistry, 13:1014 (1974); Pain et al., J. Immunol. Meth., 40:219 (1981); and Nygren, J. Histochem. and Cytochem., 30:407 (1982).

Accordingly, the present invention also provides CRC protein sequences. A CRC protein of the present invention may be identified in several ways. "Protein" in this sense includes proteins, polypeptides, and peptides. As will be appreciated by those in the art, the nucleic acid sequences of the invention can be used to generate protein sequences. There are a variety of ways to do this, including cloning the entire gene and verifying its frame and amino acid sequence, or by comparing it to known sequences to search for homology to provide a frame, assuming the CRC protein has homology to some protein in the database being used. Generally, the nucleic acid sequences are input into a program that will search all three frames for homology. This is done in a preferred embodiment using the following NCBI Advanced BLAST parameters. The program is blastx or blastn. The database is nr. The input data is as "Sequence in FASTA format". The organism list is "none". The "expect" is 10; the filter is default. The "descriptions" is 500, the "alignments" is 500, and the "alignment view" is pairwise. The "Query Genetic Codes" is standard (1). The matrix is BLOSUM62; gap existence cost is 11, per residue gap cost is 1; and the lambda ratio is .85 default. This results in the generation of a putative protein sequence.

Also included within one embodiment of CRC proteins are amino acid variants of the naturally occurring sequences, as determined herein. Preferably, the variants are preferably greater than about 75% homologous to the wild-type sequence, more preferably greater than about 80%, even more preferably greater than about 85% and most preferably greater than 90%. In some embodiments the homology will be as high as about 93 to 95 or 98%. As for nucleic acids, homology in this context means sequence similarity or identity, with identity being preferred. This homology will be determined using standard techniques known in the art as are outlined above for the nucleic acid homologies.

CRC proteins of the present invention may be shorter or longer than the wild type amino acid sequences. Thus, in a preferred embodiment, included within the definition of CRC proteins are portions or fragments of the wild type sequences. herein. In addition, as outlined above, the CRC

nucleic acids of the invention may be used to obtain additional coding regions, and thus additional protein sequence, using techniques known in the art.

In a preferred embodiment, the CRC proteins are derivative or variant CRC proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative CRC peptide will contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at any residue within the CRC peptide.

Also included in an embodiment of CRC proteins of the present invention are amino acid sequence variants. These variants fall into one or more of three classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the CRC protein, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant CRC protein fragments having up to about 100-150 residues may be prepared by *in vitro* synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the CRC protein amino acid sequence. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed CRC variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, for example, M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of CRC protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be tolerated. Deletions range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the

molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the CRC protein are desired, substitutions are generally made in accordance with the following chart:

Original Residue	Chart I Exemplary Substitutions
Ala	Ser
Arg	Lys
Asn	Gln, His
Asp	Glu
Cys	Ser
Gln	Asn
Glu	Asp
Gly	Pro
His	Asn, Gln
Ile	Leu, Val
Leu	Ile, Val
Lys	Arg, Gln, Glu
Met	Leu, Ile
Phe	Met, Leu, Tyr
Ser	Thr
Thr	Ser
Trp	Tyr
Tyr	Trp, Phe
Val	Ile, Leu

Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those shown in Chart I. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, e.g. seryl or threonyl is substituted for (or by) a hydrophobic residue, e.g. leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g. lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g. glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g. phenylalanine, is substituted for (or by) one not having a side chain, e.g. glycine.

The variants typically exhibit the same qualitative biological activity and will elicit the same immune response as the naturally-occurring analogue, although variants also are selected to modify the characteristics of the CRC proteins as needed. Alternatively, the variant may be designed such that the biological activity of the CRC protein is altered. For example, glycosylation sites may be altered or removed.

Covalent modifications of CRC polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a CRC polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a CRC polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking CRC to a water-insoluble support matrix or surface for use in the method for purifying anti-CRC antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxy-succinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propionimide.

Other modifications include deamidation of glutamyl and asparaginy residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl, threonyl or tyrosyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, *Proteins: Structure and Molecular Properties*, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the CRC polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence CRC polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence CRC polypeptide.

Addition of glycosylation sites to CRC polypeptides may be accomplished by altering the amino acid sequence thereof. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence CRC polypeptide (for O-linked glycosylation sites). The CRC amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the CRC polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the CRC polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, *CRC Crit. Rev. Biochem.*, pp. 259-306 (1981).

Removal of carbohydrate moieties present on the CRC polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of CRC comprises linking the CRC polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

CRC polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a CRC polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a CRC polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl-terminus of the CRC polypeptide. The presence of such epitope-tagged forms of a CRC polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the CRC polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a CRC polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)].

Also included with the definition of CRC protein in one embodiment are other CRC proteins of the CRC family, and CRC proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related CRC proteins from humans or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include the unique areas of the CRC nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known in the art.

In addition, as is outlined herein, CRC proteins can be made that are longer than those depicted in the figures, for example, by the elucidation of additional sequences, the addition of epitope or purification tags, the addition of other fusion sequences, etc.

CRC proteins may also be identified as being encoded by CRC nucleic acids. Thus, CRC proteins are encoded by nucleic acids that will hybridize to the sequences of the sequence listings, or their complements, as outlined herein.

In a preferred embodiment, when the CRC protein is to be used to generate antibodies, for example for immunotherapy, the CRC protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller CRC protein will be able to bind to the full length protein. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity. In a preferred embodiment, the epitope is selected from CAA2p1 and CAA2p2. In another preferred embodiment, the epitope is selected from CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA89p5 and CAA9p5MAPS.

In one embodiment, the term "antibody" includes antibody fragments, as are known in the art, including Fab, Fab₂, single chain antibodies (Fv for example), chimeric antibodies, etc., either produced by the modification of whole antibodies or those synthesized de novo using recombinant DNA technologies.

Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the CAA2 or

fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*. The immunizing agent will typically include the CAA2 polypeptide or fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for a CRC protein or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific.

In a preferred embodiment, the antibodies to CRC are capable of reducing or eliminating the biological function of CRC, as is described below. That is, the addition of anti-CRC antibodies (either polyclonal or preferably monoclonal) to CRC (or cells containing CRC) may reduce or eliminate the CRC activity.

Generally, at least a 25% decrease in activity is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the CRC proteins are humanized antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues form a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-329 (1988); and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as import residues, which are typically taken from an import variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeven et al., Science, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol.,

222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, p. 77 (1985) and Boerner et al., J. Immunol., 147(1):86-95 (1991)]. Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks et al., Bio/Technology 10, 779-783 (1992); Lonberg et al., Nature 368 856-859 (1994); Morrison, Nature 368, 812-13 (1994); Fishwild et al., Nature Biotechnology 14, 845-51 (1996); Neuberger, Nature Biotechnology 14, 826 (1996); Lonberg and Huszar, Intern. Rev. Immunol. 13 65-93 (1995).

By immunotherapy is meant treatment of CRC with an antibody raised against CRC proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. As appreciated by one of ordinary skill in the art, the antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen.

In a preferred embodiment the CRC proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted CRC protein.

In another preferred embodiment, the CRC protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment, bind the extracellular domain of the CRC protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane CRC protein. As will be appreciated by one of ordinary skill in the art, the antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the CRC protein. The antibody is also an antagonist of the CRC protein. Further, the antibody prevents activation of the transmembrane CRC protein. In one aspect, when the antibody prevents the binding of other molecules to the CRC protein, the antibody prevents growth of the cell. The antibody also sensitizes

the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity. Thus, CRC is treated by administering to a patient antibodies directed against the transmembrane CRC protein.

In another preferred embodiment, the antibody is conjugated to a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of the CRC protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the CRC protein. The therapeutic moiety may inhibit enzymatic activity such as protease or protein kinase activity associated with CRC.

In a preferred embodiment, the therapeutic moiety may also be a cytotoxic agent. In this method, targeting the cytotoxic agent to tumor tissue or cells, results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with CRC. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against CRC proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane CRC proteins not only serves to increase the local concentration of therapeutic moiety in the CRC afflicted area, but also serves to reduce deleterious side effects that may be associated with the therapeutic moiety.

In another preferred embodiment, the CRC protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the CRC protein can be targeted within a cell, i.e., the nucleus, an antibody thereto contains a signal for that target localization, i.e., a nuclear localization signal.

The CRC antibodies of the invention specifically bind to CRC proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a binding constant in the range of at least 10^{-4} - 10^{-6} M^{-1} , with a preferred range being 10^{-7} - 10^{-9} M^{-1} .

In a preferred embodiment, the CRC protein is purified or isolated after expression. CRC proteins may be isolated or purified in a variety of ways known to those skilled in the art depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the CRC protein may be purified using a standard anti-CRC antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes, R., Protein Purification, Springer-Verlag, NY (1982). The degree of purification necessary will vary depending on the use of the CRC protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the CRC proteins and nucleic acids are useful in a number of applications.

In one aspect, the expression levels of genes are determined for different cellular states in the CRC phenotype; that is, the expression levels of genes in normal colon tissue and in CRC tissue (and in some cases, for varying severities of CRC that relate to prognosis, as outlined below) are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is unique to the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be done or confirmed: does tissue from a particular patient have the gene expression profile of normal or CRC tissue.

"Differential expression," or grammatical equivalents as used herein, refers to both qualitative as well as quantitative differences in the genes' temporal and/or cellular expression patterns within and among the cells. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, for example, normal versus CRC tissue. That is, genes may be turned on or turned off in a particular state, relative to another state. As is apparent to the skilled artisan, any comparison of two or more states can be made. Such a qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques in one such state or cell type, but is not detectable in both. Alternatively, the determination is quantitative in that expression is increased or decreased; that is, the expression of the gene is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard

characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays, Lockhart, Nature Biotechnology, 14:1675-1680 (1996), hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, Northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e. upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably, at least about 200%, with from 300 to at least 1000% being especially preferred.

As will be appreciated by those in the art, this may be done by evaluation at either the gene transcript, or the protein level; that is, the amount of gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, for example through the use of antibodies to the CRC protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Thus, the proteins corresponding to CRC genes, i.e. those identified as being important in a CRC phenotype, can be evaluated in a CRC diagnostic test.

In a preferred embodiment, gene expression monitoring is done and a number of genes, i.e. an expression profile, is monitored simultaneously, although multiple protein expression monitoring can be done as well. Similarly, these assays may be done on an individual basis as well.

In this embodiment, the CRC nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of CRC sequences in a particular cell. The assays are further described below in the example.

In a preferred embodiment nucleic acids encoding the CRC protein are detected. Although DNA or RNA encoding the CRC protein may be detected, of particular interest are methods wherein the mRNA encoding a CRC protein is detected. The presence of mRNA in a sample is an indication that the CRC gene has been transcribed to form the mRNA, and suggests that the protein is expressed. Probes to detect the mRNA can be any nucleotide/deoxynucleotide probe that is complementary to and base pairs with the mRNA and includes but is not limited to oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed *in situ*. In this method permeabilized cells or tissue samples are contacted with a detectably labeled

nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a CRC protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, any of the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The CRC proteins, antibodies, nucleic acids, modified proteins and cells containing CRC sequences are used in diagnostic assays. This can be done on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, CRC proteins, including intracellular, transmembrane or secreted proteins, find use as markers of CRC. Detection of these proteins in putative CRC tissue or patients allows for a determination or diagnosis of CRC. Numerous methods known to those of ordinary skill in the art find use in detecting CRC. In one embodiment, antibodies are used to detect CRC proteins. A preferred method separates proteins from a sample or patient by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be any other type of gel including isoelectric focusing gels and the like). Following separation of proteins, the CRC protein is detected by immunoblotting with antibodies raised against the CRC protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the CRC protein find use in in situ imaging techniques. In this method cells are contacted with from one to many antibodies to the CRC protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label. In another method the primary antibody to the CRC protein(s) contains a detectable label. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of CRC proteins. As will be appreciated by one of ordinary skill in the art, numerous other histological imaging techniques are useful in the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing CRC from blood samples. As previously described, certain CRC proteins are secreted/circulating molecules. Blood samples, therefore, are useful as samples to be probed or tested for the presence of secreted CRC proteins. Antibodies can be used to detect the CRC by any of the previously described immunoassay techniques including ELISA, immunoblotting (Western blotting), immunoprecipitation, BIACORE technology and the like, as will be appreciated by one of ordinary skill in the art.

In a preferred embodiment, in situ hybridization of labeled CRC nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including CRC tissue and/or normal tissue, are made. In situ hybridization as is known in the art can then be done.

It is understood that when comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis as well as a prognosis. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis.

In a preferred embodiment, the CRC proteins, antibodies, nucleic acids, modified proteins and cells containing CRC sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to CRC severity, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. As above, the CRC probes are attached to biochips for the detection and quantification of CRC sequences in a tissue or patient. The assays proceed as outlined for diagnosis.

In a preferred embodiment, any of the three classes of proteins as described herein are used in drug screening assays. The CRC proteins, antibodies, nucleic acids, modified proteins and cells containing CRC sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, Ziolkarnik, et al., Science 279, 84-8 (1998), Heid, 1996 #69.

In a preferred embodiment, the CRC proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified CRC proteins are used in screening assays. That is, the present

invention provides novel methods for screening for compositions which modulate the CRC phenotype. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be executed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in CRC, candidate bioactive agents may be screened to modulate this gene's response; preferably to down regulate the gene, although in some circumstances to up regulate the gene. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tumor tissue, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4 fold increase in tumor compared to normal tissue, a decrease of about four fold is desired; a 10 fold decrease in tumor compared to normal tissue gives a 10 fold increase in expression for a candidate agent is desired.

As will be appreciated by those in the art, this may be done by evaluation at either the gene or the protein level; that is, the amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, for example through the use of antibodies to the CRC protein and standard immunoassays.

In a preferred embodiment, gene expression monitoring is done and a number of genes, i.e. an expression profile, is monitored simultaneously, although multiple protein expression monitoring can be done as well.

In this embodiment, the CRC nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of CRC sequences in a particular cell. The assays are further described below.

Generally, in a preferred embodiment, a candidate bioactive agent is added to the cells prior to analysis. Moreover, screens are provided to identify a candidate bioactive agent which modulates colorectal cancer, modulates CRC proteins, binds to a CRC protein, or interferes between the binding of a CRC protein and an antibody.

The term "candidate bioactive agent" or "drug candidate" or grammatical equivalents as used herein describes any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for bioactive agents that are capable of directly or indirectly altering either the CRC phenotype or the expression of a CRC sequence, including both nucleic acid sequences and protein sequences. In preferred embodiments, the bioactive agents modulate the expression profiles, or expression profile nucleic acids or proteins provided herein. In a particularly preferred embodiment, the candidate agent suppresses a CRC phenotype, for example to a normal colon tissue fingerprint. Similarly, the candidate agent preferably suppresses a severe CRC phenotype. Generally a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

In one aspect, a candidate agent will neutralize the effect of a CRC protein. By "neutralize" is meant that activity of a protein is either inhibited or counter acted against so as to have substantially no effect on a cell.

Candidate agents encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or less than 1500 or less than 1000 or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof. Particularly preferred are peptides.

Candidate agents are obtained from a wide variety of sources including libraries of synthetic or natural compounds. For example, numerous means are available for random and directed synthesis of a wide variety of organic compounds and biomolecules, including expression of randomized oligonucleotides. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available or readily produced. Additionally, natural or synthetically produced libraries and compounds are readily modified through conventional chemical, physical and biochemical means. Known pharmacological agents may be subjected to directed or random

chemical modifications, such as acylation, alkylation, esterification, amidification to produce structural analogs.

In a preferred embodiment, the candidate bioactive agents are proteins. By "protein" herein is meant at least two covalently attached amino acids, which includes proteins, polypeptides, oligopeptides and peptides. The protein may be made up of naturally occurring amino acids and peptide bonds, or synthetic peptidomimetic structures. Thus "amino acid", or "peptide residue", as used herein means both naturally occurring and synthetic amino acids. For example, homo-phenylalanine, citrulline and noreleucine are considered amino acids for the purposes of the invention. "Amino acid" also includes imino acid residues such as proline and hydroxyproline. The side chains may be in either the (R) or the (S) configuration. In the preferred embodiment, the amino acids are in the (S) or L-configuration. If non-naturally occurring side chains are used, non-amino acid substituents may be used, for example to prevent or retard in vivo degradations.

In a preferred embodiment, the candidate bioactive agents are naturally occurring proteins or *fragments of naturally occurring proteins*. Thus, for example, cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of procaryotic and eucaryotic proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred.

In a preferred embodiment, the candidate bioactive agents are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate any nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a

defined class, for example, of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc., or to purines, etc.

In a preferred embodiment, the candidate bioactive agents are nucleic acids, as defined above.

As described above generally for proteins, nucleic acid candidate bioactive agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate bioactive agents are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing the target sequences to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR occurring as needed, as will be appreciated by those in the art. For example, an in vitro transcription with labels covalently attached to the nucleosides is done. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, for example, a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. As known in the art, unbound labeled streptavidin is removed prior to analysis.

As will be appreciated by those in the art, these assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670,

5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways, as will be appreciated by those in the art. Components of the reaction may be added simultaneously, or sequentially, in any order, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents may be included in the assays. These include reagents like salts, buffers, neutral proteins, e.g. albumin, detergents, etc which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used, depending on the sample preparation methods and purity of the target.

Once the assay is run, the data is analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

The screens are done to identify drugs or bioactive agents that modulate the CRC phenotype. Specifically, there are several types of screens that can be run. A preferred embodiment is in the screening of candidate agents that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. That is, candidate agents that can mimic or produce an expression profile in CRC similar to the expression profile of normal colon tissue is expected to result in a suppression of the CRC phenotype. Thus, in this embodiment, mimicking an expression profile, or changing one profile to another, is the goal.

In a preferred embodiment, as for the diagnosis and prognosis applications, having identified the differentially expressed genes important in any one state, screens can be run to alter the expression of the genes individually. That is, screening for modulation of regulation of expression of a single gene can be done; that is, rather than try to mimic all or part of an expression profile, screening for regulation of individual genes can be done. Thus, for example, particularly in the case of target genes whose presence or absence is unique between two states, screening is done for modulators of the target gene expression.

In a preferred embodiment, screening is done to alter the biological function of the expression product of the differentially expressed gene. Again, having identified the importance of a gene in a particular state, screening for agents that bind and/or modulate the biological activity of the gene product can be run as is more fully outlined below.

Thus, screening of candidate agents that modulate the CRC phenotype either at the gene expression level or the protein level can be done.

In addition screens can be done for novel genes that are induced in response to a candidate agent. After identifying a candidate agent based upon its ability to suppress a CRC expression pattern leading to a normal expression pattern, or modulate a single CRC gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated CRC tissue reveals genes that are not expressed in normal tissue or CRC tissue, but are expressed in agent treated tissue. These agent specific sequences can be identified and used by any of the methods described herein for CRC genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated CRC tissue sample.

Thus, in one embodiment, a candidate agent is administered to a population of CRC cells, that thus has an associated CRC expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e. a peptide) may be put into a viral construct such as a retroviral construct and added to the cell, such that expression of the peptide agent is accomplished; see PCT US97/01019, hereby expressly incorporated by reference.

Once the candidate agent has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, for example, CRC tissue may be screened for agents that reduce or suppress the CRC phenotype. A change in at least one gene of the expression profile indicates that the agent has an effect on CRC activity. By defining such a signature for the CRC phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "CRC proteins" or a "CCMP". In preferred embodiments, the CCMP is as depicted in Figures 17-20, 24, 25, 29, 33 and 36, more preferably the protein having the sequence shown in Figures 29 or 36 or encoded by the sequences of Figures 27, 36 and 39-48. The CCMP may be a fragment, or alternatively, be the full length protein to a fragment shown herein. Preferably, the CCMP is a fragment of approximately 14 to 24 amino acids long. More preferably the fragment is a soluble fragment.

In a preferred embodiment, the fragment is from CAA9. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the CAA9 fragment has an N-terminal Cys to aid in solubility. Preferably, the fragment is selected from CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 and CAA9p5MAPS.

In a preferred embodiment, the fragment is charged and from the c-terminus of CAA2. In one embodiment, the c-terminus of the fragment is kept as a free acid and the n-terminus is a free amine to aid in coupling, i.e., to cysteine. In another embodiment, the fragment is an internal peptide overlapping hydrophilic stretch of CAA2. In a preferred embodiment, the termini is blocked. Preferably, the fragment of CAA2 is selected from CAA2p1 or CAA2p2. In another preferred embodiment, the fragment is a novel fragment from the N-terminal. In one embodiment, the fragment excludes sequence outside of the N-terminal, in another embodiment, the fragment includes at least a portion of the N-terminal. "N-terminal" is used interchangeably herein with "N-terminus" which is further described above.

In one embodiment the CRC proteins are conjugated to an immunogenic agent as discussed herein. In one embodiment the CRC protein is conjugated to BSA.

Thus, in a preferred embodiment, screening for modulators of expression of specific genes can be done. This will be done as outlined above, but in general the expression of only one or a few genes are evaluated.

In a preferred embodiment, screens are designed to first find candidate agents that can bind to differentially expressed proteins, and then these agents may be used in assays that evaluate the ability of the candidate agent to modulate differentially expressed activity. Thus, as will be appreciated by those in the art, there are a number of different assays which may be run; binding assays and activity assays.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. In general, this is done as is known in the art. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the CRC proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a CRC protein and a candidate bioactive agent, and determining the binding of the candidate agent to the CRC protein. Preferred embodiments utilize the human CRC protein, although other mammalian proteins may also be used, for example for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative CRC proteins may be used.

Generally, in a preferred embodiment of the methods herein, the CRC protein or the candidate agent is non-diffusably bound to an insoluble support having isolated sample receiving areas (e.g. a microtiter plate, an array, etc.). The insoluble supports may be made of any composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the

composition and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the CRC protein is bound to the support, and a candidate bioactive agent is added to the assay. Alternatively, the candidate agent is bound to the support and the CRC protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the candidate bioactive agent to the CRC protein may be done in a number of ways. In a preferred embodiment, the candidate bioactive agent is labeled, and binding determined directly. For example, this may be done by attaching all or a portion of the CRC protein to a solid support, adding a labeled candidate agent (for example a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as is known in the art.

By "labeled" herein is meant that the compound is either directly or indirectly labeled with a label which provides a detectable signal, e.g. radioisotope, fluorescers, enzyme, antibodies, particles such as magnetic particles, chemilumescers, or specific binding molecules, etc. Specific binding molecules include pairs, such as biotin and streptavidin, digoxin and antidigoxin etc. For the specific binding members, the complementary member would normally be labeled with a molecule which provides for detection, in accordance with known procedures, as outlined above. The label can directly or indirectly provide a detectable signal.

In some embodiments, only one of the components is labeled. For example, the proteins (or proteinaceous candidate agents) may be labeled at tyrosine positions using ^{125}I , or with fluorophores. Alternatively, more than one component may be labeled with different labels; using ^{125}I for the proteins, for example, and a fluorophor for the candidate agents.

In a preferred embodiment, the binding of the candidate bioactive agent is determined through the use of competitive binding assays. In this embodiment, the competitor is a binding moiety known to bind to the target molecule (i.e. CRC), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding as between the bioactive agent and the binding moiety, with the binding moiety displacing the bioactive agent.

In one embodiment, the candidate bioactive agent is labeled. Either the candidate bioactive agent, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at any temperature which facilitates optimal activity, typically between 4 and 40°C. Incubation periods are selected for optimum activity, but may also be optimized to facilitate rapid high through put screening. Typically between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by the candidate bioactive agent. Displacement of the competitor is an indication that the candidate bioactive agent is binding to the CRC protein and thus is capable of binding to, and potentially modulating, the activity of the CRC protein. In this embodiment, either component can be labeled. Thus, for example, if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the candidate bioactive agent is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the candidate bioactive agent is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the bioactive agent is bound to the CRC protein with a higher affinity. Thus, if the candidate bioactive agent is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the candidate agent is capable of binding to the CRC protein.

In a preferred embodiment, the methods comprise differential screening to identify bioactive agents that are capable of modulating the activity of the CRC proteins. In this embodiment, the methods comprise combining a CRC protein and a competitor in a first sample. A second sample comprises a candidate bioactive agent, a CRC protein and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the CRC protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the CRC protein.

Alternatively, a preferred embodiment utilizes differential screening to identify drug candidates that bind to the native CRC protein, but cannot bind to modified CRC proteins. The structure of the CRC protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect CRC bioactivity are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably all control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, all samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g. albumin, detergents, etc which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in any order that provides for the requisite binding.

Screening for agents that modulate the activity of CRC proteins may also be done. In a preferred embodiment, methods for screening for a bioactive agent capable of modulating the activity of CRC proteins comprise the steps of adding a candidate bioactive agent to a sample of CRC proteins, as above, and determining an alteration in the biological activity of CRC proteins. "Modulating the activity of CRC" includes an increase in activity, a decrease in activity, or a change in the type or kind of activity present. Thus, in this embodiment, the candidate agent should both bind to CRC proteins (although this may not be necessary), and alter its biological or biochemical activity as defined herein. The methods include both in vitro screening methods, as are generally outlined above, and in vivo screening of cells for alterations in the presence, distribution, activity or amount of CRC proteins.

Thus, in this embodiment, the methods comprise combining a CRC sample and a candidate bioactive agent, and evaluating the effect on CRC activity. By "CRC activity" or grammatical equivalents herein is meant one of the CRC's biological activities, including, but not limited to, cell division, preferably in colon tissue, cell proliferation, tumor growth, transformation of cells. In one embodiment, CRC activity includes activation of CZA8, BCX2, CBC2, CBC1, CBC3, CJA9, BCN5, CQA1, BCN7, CQA2, CJA8,

CAA2, CAA9, CGA7 and/or CGA8*, preferably one of the CRC proteins listed in Figure 14. An inhibitor of CRC activity is the inhibition of any one or more CRC activities.

In a preferred embodiment, the activity of the CRC protein is increased; in another preferred embodiment, the activity of the CRC protein is decreased. Thus, bioactive agents that are antagonists are preferred in some embodiments, and bioactive agents that are agonists may be preferred in other embodiments.

In a preferred embodiment, the invention provides methods for screening for bioactive agents capable of modulating the activity of a CRC protein. The methods comprise adding a candidate bioactive agent, as defined above, to a cell comprising CRC proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a CRC protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, for example hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (i.e. cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, bioactive agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the CRC protein. In one embodiment, "colorectal cancer protein activity" as used herein includes at least one of the following: colorectal cancer activity, binding to CJA8, activation of CJA8 or activation of substrates of CJA8 by CJA8. In one embodiment, colorectal cancer activity is defined as the unregulated proliferation of colon tissue, or the growth of cancer in colon tissue. In one aspect, colorectal cancer activity as defined herein is related to the activity of CJA8 in the upregulation of CJA8 in colon cancer tissue.

In another embodiment, colorectal cancer protein activity includes at least one of the following: colorectal cancer activity, binding to one of CAA2, CAA9, CGA7 and CGA8, activation of one of CAA2, CAA9, CGA7, and CGA8 or activation of substrates of CAA2, CAA9, CGA7 or CGA8 by CAA2, CAA9, CGA7 or CGA8, respectively. In one preferred embodiment, CAA2 comprises its N-terminal end. In one aspect, colorectal cancer activity as defined herein is related to the activity of CAA2, CAA9, CGA7 and/or CGA8 in the upregulation of CAA2, CAA9, CGA7 and/or CGA8, respectively, in colon cancer tissue.

In one embodiment, a method of inhibiting colon cancer cell division is provided. The method comprises administration of a colorectal cancer inhibitor.

In another embodiment, a method of inhibiting tumor growth is provided. The method comprises administration of a colorectal cancer inhibitor.

In a further embodiment, methods of treating cells or individuals with cancer are provided. The method comprises administration of a colorectal cancer inhibitor.

In one embodiment, a colorectal cancer inhibitor is an antibody as discussed above. In another embodiment, the colorectal cancer inhibitor is an antisense molecule. Antisense molecules as used herein include antisense or sense oligonucleotides comprising a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for colorectal cancer molecules. A preferred antisense molecule is for CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, BCN5, CQA1, BCN7, CQA2, CAA2, CAA9, CGA7 or CGA8, more preferably for the CRC sequences referenced in Figure 14, or for a ligand or activator thereof. A most preferred antisense molecule is for CJA8 or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (Cancer Res. 48:2659, 1988) and van der Krol et al. (BioTechniques 6:958, 1988).

Antisense molecules may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

The compounds having the desired pharmacological activity may be administered in a physiologically acceptable carrier to a host, as previously described. The agents may be administered in a variety of

ways, orally, parenterally e.g., subcutaneously, intraperitoneally, intravascularly, etc.' Depending upon the manner of introduction, the compounds may be formulated in a variety of ways. The concentration of therapeutically active compound in the formulation may vary from about 0.1-100 wt.%. The agents may be administered alone or in combination with other treatments, i.e., radiation.

The pharmaceutical compositions can be prepared in various forms, such as granules, tablets, pills, suppositories, capsules, suspensions, salves, lotions and the like. Pharmaceutical grade organic or inorganic carriers and/or diluents suitable for oral and topical use can be used to make up compositions containing the therapeutically-active compounds. Diluents known to the art include aqueous media, vegetable and animal oils and fats. Stabilizing agents, wetting and emulsifying agents, salts for varying the osmotic pressure or buffers for securing an adequate pH value, and skin penetration enhancers can be used as auxiliary agents.

Without being bound by theory, it appears that the various CRC sequences are important in CRC. Accordingly, disorders based on mutant or variant CRC genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant CRC genes comprising determining all or part of the sequence of at least one endogenous CRC genes in a cell. As will be appreciated by those in the art, this may be done using any number of sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the CRC genotype of an individual comprising determining all or part of the sequence of at least one CRC gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced CRC gene to a known CRC gene, i.e. a wild-type gene.

The sequence of all or part of the CRC gene can then be compared to the sequence of a known CRC gene to determine if any differences exist. This can be done using any number of known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the CRC gene of the patient and the known CRC gene is indicative of a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the CRC genes are used as probes to determine the number of copies of the CRC gene in the genome.

In another preferred embodiment CRC genes are used as probed to determine the chromosomal localization of the CRC genes. Information such as chromosomal localization finds use in providing a

diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in CRC gene loci.

Thus, in one embodiment, methods of modulating CRC in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-CRC antibody that reduces or eliminates the biological activity of an endogenous CRC protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a CRC protein. As will be appreciated by those in the art, this may be accomplished in any number of ways. In a preferred embodiment, for example when the CRC sequence is down-regulated in CRC, the activity of the CRC gene is increased by increasing the amount of CRC in the cell, for example by overexpressing the endogenous CRC or by administering a gene encoding the CRC sequence, using known gene-therapy techniques, for example. In a preferred embodiment, the gene therapy techniques include the incorporation of the endogenous gene using enhanced homologous recombination (EHR), for example as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, for example when the CRC sequence is up-regulated in CRC, the activity of the endogenous CRC gene is decreased, for example by the administration of a CRC antisense nucleic acid.

In one embodiment, the CRC proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to CRC proteins, which are useful as described herein. Similarly, the CRC proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify CRC antibodies. In a preferred embodiment, the antibodies are generated to epitopes unique to a CRC protein; that is, the antibodies show little or no cross-reactivity to other proteins. These antibodies find use in a number of applications. For example, the CRC antibodies may be coupled to standard affinity chromatography columns and used to purify CRC proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the CRC protein.

In one embodiment, a therapeutically effective dose of a CRC or modulator thereof is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces the effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques. As is known in the art, adjustments for CRC degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals, and organisms. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, and in the most preferred embodiment the patient is human.

The administration of the CRC proteins and modulators of the present invention can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, for example, in the treatment of wounds and inflammation, the CRC proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a CRC protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol. Additives are well known in the art, and are used in a variety of formulations.

In a preferred embodiment, CRC proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, CRC genes (including both the full-length

sequence, partial sequences, or regulatory sequences of the CRC coding regions) can be administered in gene therapy applications, as is known in the art. These CRC genes can include antisense applications, either as gene therapy (i.e. for incorporation into the genome) or as antisense compositions, as will be appreciated by those in the art.

In a preferred embodiment, CRC genes are administered as DNA vaccines, either single genes or combinations of CRC genes. Naked DNA vaccines are generally known in the art. Brower, *Nature Biotechnology*, 16:1304-1305 (1998).

In one embodiment, CRC genes of the present invention are used as DNA vaccines. Methods for the use of genes as DNA vaccines are well known to one of ordinary skill in the art, and include placing a CRC gene or portion of a CRC gene under the control of a promoter for expression in a CRC patient. The CRC gene used for DNA vaccines can encode full-length CRC proteins, but more preferably encodes portions of the CRC proteins including peptides derived from the CRC protein. In a preferred embodiment a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a CRC gene. Similarly, it is possible to immunize a patient with a plurality of CRC genes or portions thereof as defined herein. Without being bound by theory, expression of the polypeptide encoded by the DNA vaccine, cytotoxic T-cells, helper T-cells and antibodies are induced which recognize and destroy or eliminate cells expressing CRC proteins.

In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the CRC polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are known to those of ordinary skill in the art and find use in the invention.

In another preferred embodiment CRC genes find use in generating animal models of CRC. As is appreciated by one of ordinary skill in the art, when the CRC gene identified is repressed or diminished in CRC tissue, gene therapy technology wherein antisense RNA directed to the CRC gene will also diminish or repress expression of the gene. An animal generated as such serves as an animal model of CRC that finds use in screening bioactive drug candidates. Similarly, gene knockout technology, for example as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence of the CRC protein. When desired, tissue-specific expression or knockout of the CRC protein may be necessary.

It is also possible that the CRC protein is overexpressed in CRC. As such, transgenic animals can be generated that overexpress the CRC protein. Depending on the desired expression level, promoters

of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods find use as animal models of CRC and are additionally useful in screening for bioactive molecules to treat CRC.

It is understood that the examples described herein in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All references and sequences of accession numbers cited herein are incorporated by reference in their entirety.

EXAMPLES

Example 1

Tissue Preparation, Labeling Chips, and Fingerprints

Purify total RNA from tissue using TRIzol Reagent

Estimate tissue weight. Homogenize tissue samples in 1ml of TRIzol per 50mg of tissue using a Polytron 3100 homogenizer. The generator/probe used depends upon the tissue size. A generator that is too large for the amount of tissue to be homogenized will cause a loss of sample and lower RNA yield. Use the 20mm generator for tissue weighing more than 0.6g. If the working volume is greater than 2ml, then homogenize tissue in a 15ml polypropylene tube (Falcon 2059). Fill tube no greater than 10ml.

HOMOGENIZATION

Before using generator, it should have been cleaned after last usage by running it through soapy H₂O and rinsing thoroughly. Run through with EtOH to sterilize. Keep tissue frozen until ready. Add TRIzol directly to frozen tissue then homogenize.

Following homogenization, remove insoluble material from the homogenate by centrifugation at 7500 x g for 15 min. in a Sorvall superspeed or 12,000 x g for 10 min. in an Eppendorf centrifuge at 4°C. Transfer the cleared homogenate to a new tube(s). The samples may be frozen now at -60 to -70°C (and kept for at least one month) or you may continue with the purification.

PHASE SEPARATION

Incubate the homogenized samples for 5 minutes at room temperature.

Add 0.2ml of chloroform per 1ml of TRIzol reagent used in the original homogenization.

Cap tubes securely and shake tubes vigorously by hand (do not vortex) for 15 seconds.

Incubate samples at room temp. for 2-3 minutes. Centrifuge samples at 6500rpm in a Sorvall superspeed for 30 min. at 4°C. (You may spin at up to 12,000 x g for 10 min. but you risk breaking your tubes in the centrifuge.)

RNA PRECIPITATION

Transfer the aqueous phase to a fresh tube. Save the organic phase if isolation of DNA or protein is desired. Add 0.5ml of isopropyl alcohol per 1ml of TRIzol reagent used in the original homogenization. Cap tubes securely and invert to mix. Incubate samples at room temp. for 10 minutes. Centrifuge samples at 6500rpm in Sorvall for 20min. at 4°C.

RNA WASH

Pour off the supernate. Wash pellet with cold 75% ethanol. Use 1ml of 75% ethanol per 1ml of TRIzol reagent used in the initial homogenization. Cap tubes securely and invert several times to loosen pellet. (Do not vortex). Centrifuge at <8000rpm (<7500 x g) for 5 minutes at 4°C. Pour off the wash. Carefully transfer pellet to an eppendorf tube (let it slide down the tube into the new tube and use a pipet tip to help guide it in if necessary). Depending on the volumes you are working with, you can decide what size tube(s) you want to precipitate the RNA in. When I tried leaving the RNA in the large 15ml tube, it took so long to dry (i.e. it did not dry) that I eventually had to transfer it to a smaller tube. Let pellet dry in hood. Resuspend RNA in an appropriate volume of DEPC H₂O. Try for 2-5ug/ul. Take absorbance readings.

Purify poly A⁺ mRNA from total RNA or clean up total RNA with Qiagen's

RNeasy kit

Purification of poly A⁺ mRNA from total RNA. Heat oligotex suspension to 37°C and mix immediately before adding to RNA. Incubate Elution Buffer at 70°C. Warm up 2 x Binding Buffer at 65°C if there is precipitate in the buffer. Mix total RNA with DEPC-treated water, 2 x Binding Buffer, and Oligotex according to Table 2 on page 16 of the Oligotex Handbook. Incubate for 3 minutes at 65°C. Incubate for 10 minutes at room temperature.

Centrifuge for 2 minutes at 14,000 to 18,000 g. If centrifuge has a "soft setting," then use it. Remove supernatant without disturbing Oligotex pellet. A little bit of solution can be left behind to reduce the loss of Oligotex. Save sup until certain that satisfactory binding and elution of poly A⁺ mRNA has occurred.

Gently resuspend in Wash Buffer OW2 and pipet onto spin column. Centrifuge the spin column at full speed (soft setting if possible) for 1 minute.

Transfer spin column to a new collection tube and gently resuspend in Wash Buffer OW2 and centrifuge as describe herein.

Transfer spin column to a new tube and elute with 20 to 100 ul of preheated (70°C) Elution Buffer. Gently resuspend Oligotex resin by pipetting up and down. Centrifuge as above. Repeat elution with fresh elution buffer or use first eluate to keep the elution volume low.

Read absorbance, using diluted Elution Buffer as the blank.

Before proceeding with cDNA synthesis, the mRNA must be precipitated.

Some component leftover or in the Elution Buffer from the Oligotex purification procedure will inhibit downstream enzymatic reactions of the mRNA.

Ethanol Precipitation

Add 0.4 vol. of 7.5 M NH_4OAc + 2.5 vol. of cold 100% ethanol. Precipitate at -20°C 1 hour to overnight (or 20-30 min. at -70°C). Centrifuge at 14,000-16,000 x g for 30 minutes at 4°C. Wash pellet with 0.5ml of 80% ethanol (-20°C) then centrifuge at 14,000-16,000 x g for 5 minutes at room temperature. Repeat 80% ethanol wash. Dry the last bit of ethanol from the pellet in the hood. (Do not speed vacuum). Suspend pellet in DEPC H_2O at 1ug/ul concentration.

Clean up total RNA using Qiagen's RNeasy kit

Add no more than 100ug to an RNeasy column. Adjust sample to a volume of 100ul with RNase-free water. Add 350ul Buffer RLT then 250ul ethanol (100%) to the sample. Mix by pipetting (do not centrifuge) then apply sample to an RNeasy mini spin column. Centrifuge for 15 sec at >10,000rpm. If concerned about yield, re-apply flowthrough to column and centrifuge again. Transfer column to a new 2-ml collection tube. Add 500ul Buffer RPE and centrifuge for 15 sec at >10,000rpm. Discard flowthrough. Add 500ul Buffer RPE and centrifuge for 15 sec at >10,000rpm. Discard flowthrough then centrifuge for 2 min at maximum speed to dry column membrane. Transfer column to a new 1.5-ml collection tube and apply 30-50ul of RNase-free water directly onto column membrane. Centrifuge 1 min at >10,000rpm. Repeat elution. Take absorbance reading. If necessary, ethanol precipitate with ammonium acetate and 2.5X volume 100% ethanol.

Make cDNA using Gibco's "SuperScript Choice System for cDNA Synthesis" kit

First Strand cDNA Synthesis

Use 5ug of total RNA or 1ug of polyA+ mRNA as starting material. For total RNA, use 2ul of SuperScript RT. For polyA+ mRNA, use 1ul of SuperScript RT. Final volume of first strand synthesis mix is 20ul. RNA must be in a volume no greater than 10ul. Incubate RNA with 1ul of 100pmol T7-T24 oligo for 10 min at 70C. On ice, add 7 ul of: 4ul 5X 1st Strand Buffer, 2ul of 0.1M DTT, and 1 ul of 10mM dNTP mix. Incubate at 37C for 2 min then add SuperScript RT. Incubate at 37C for 1 hour.

Second Strand Synthesis

Place 1st strand reactions on ice.

Add: 91ul DEPC H₂O
30ul 5X 2nd Strand Buffer
3ul 10mM dNTP mix
1ul 10U/ul *E.coli* DNA Ligase
4ul 10U/ul *E.coli* DNA Polymerase
1ul 2U/ul RNase H

Make the above into a mix if there are more than 2 samples. Mix and incubate 2 hours at 16C. Add 2ul T4 DNA Polymerase. Incubate 5 min at 16C. Add 10ul of 0.5M EDTA

Clean up cDNA

Phenol:Chloroform:Isoamyl Alcohol (25:24:1) purification using Phase-Lock gel tubes: Centrifuge PLG tubes for 30 sec at maximum speed. Transfer cDNA mix to PLG tube. Add equal volume of phenol:chloroform:isamyl alcohol and shake vigorously (do not vortex). Centrifuge 5 minutes at maximum speed. Transfer top aqueous solution to a new tube. Ethanol precipitate: add 7.5X 5M NH₄OAc and 2.5X volume of 100% ethanol. Centrifuge immediately at room temp. for 20 min, maximum speed. Remove sup then wash pellet 2X with cold 80% ethanol. Remove as much ethanol wash as possible then let pellet air dry. Resuspend pellet in 3ul RNase-free water.

In vitro Transcription (IVT) and labeling with biotin

Pipet 1.5ul of cDNA into a thin-wall PCR tube.

Make NTP labeling mix:

Combine at room temperature:	2ul	T7 10xATP (75mM) (Ambion)
	2ul	T7 10xGTP (75mM) (Ambion)
	1.5ul	T7 10xCTP (75mM) (Ambion)

1.5ul T7 10xUTP (75mM) (Ambion)
3.75ul 10mM Bio-11-UTP (Boehringer-Mannheim/Roche or
Enzo)
3.75ul 10mM Bio-16-CTP (Enzo)
2ul 10x T7 transcription buffer (Ambion)
2ul 10x T7 enzyme mix (Ambion)

Final volume of total reaction is 20ul. Incubate 6 hours at 37C in a PCR machine.

RNeasy clean-up of IVT product

Follow previous instructions for RNeasy columns or refer to Qiagen's RNeasy protocol handbook.

cRNA will most likely need to be ethanol precipitated. Resuspend in a volume compatible with the fragmentation step.

Fragmentation

15 ug of labeled RNA is usually fragmented. Try to minimize the fragmentation reaction volume; a 10 ul volume is recommended but 20 ul is all right. Do not go higher than 20 ul because the magnesium in the fragmentation buffer contributes to precipitation in the hybridization buffer. Fragment RNA by incubation at 94 C for 35 minutes in 1 x Fragmentation buffer.

5 x Fragmentation buffer:

200 mM Tris-acetate, pH 8.1

500 mM KOAc

150 mM MgOAc

The labeled RNA transcript can be analyzed before and after fragmentation. Samples can be heated to 65C for 15 minutes and electrophoresed on 1% agarose/TBE gels to get an approximate idea of the transcript size range

Hybridization

200 ul (10ug cRNA) of a hybridization mix is put on the chip. If multiple hybridizations are to be done (such as cycling through a 5 chip set), then it is recommended that an initial hybridization mix of 300 ul or more be made.

Hybridization Mix: fragment labeled RNA (50ng/ul final conc.)

50 pM 948-b control oligo

1.5 pM BioB

5 pM BioC

25 pM BioD

100 pM CRE

0.1mg/ml herring sperm DNA

0.5mg/ml acetylated BSA

to 300 ul with 1xMES hyb. buffer

The instruction manuals for the products used herein are incorporated herein in their entirety.

Labeling Protocol Provided Herein

Hybridization reaction:

Start with non-biotinylated IVT (purified by RNeasy columns)

(see example 1 for steps from tissue to IVT)

IVT antisense RNA; 4 µg: µl

Random Hexamers (1 µg/µl): 4 µl

H₂O: µl

14 µl

- Incubate 70°C, 10 min. Put on ice.

Reverse transcription:

5X First Strand (BRL) buffer: 6 µl

0.1 M DTT: 3 µl

50X dNTP mix: 0.6 µl

H₂O: 2.4 µl

Cy3 or Cy5 dUTP (1mM): 3 µl

SS RT II (BRL): 1 µl

16 µl

- Add to hybridization reaction.

- Incubate 30 min., 42°C.

- Add 1 µl SSII and let go for another hour.

Put on ice.

- 50X dNTP mix (25mM of cold dATP, dCTP, and dGTP, 10mM of dTTP: 25 μ l each of 100mM dATP, dCTP, and dGTP; 10 μ l of 100mM dTTP to 15 μ l H₂O. dNTPs from Pharmacia)

RNA degradation:

- Add 1.5 μ l 1M NaOH/ 2mM EDTA, incubate at 65°C, 10 min.

86 μ l H ₂ O
10 μ l 10N NaOH
4 μ l 50mM EDTA

U-Con 30

500 μ l TE/sample spin at 7000g for 10 min, save flow through for purification

Qiagen purification:

-suspend u-con recovered material in 500 μ l buffer PB

-proceed w/ normal Qiagen protocol

DNAse digest:

- Add 1 μ l of 1/100 dil of DNAse/30 μ l Rx and incubate at 37°C for 15 min.

-5 min 95°C to denature enzyme

Sample preparation:

- Add:

Cot-1 DNA: 10 μ l

50X dNTPs: 1 μ l

20X SSC: 2.3 μ l

Na pyro phosphate: 7.5 μ l

10mg/ml Herring sperm DNA 1 μ l of 1/10 dilution

21.8 final vol.

- Dry down in speed vac.

- Resuspend in 15 μ l H₂O.

- Add 0.38 μ l 10% SDS.

- Heat 95°C, 2 min.

- Slow cool at room temp. for 20 min.

Put on slide and hybridize overnight at 64°C.

Washing after the hybridization:

3X SSC/0.03% SDS: 2 min. 37.5 mls 20X SSC+0.75mls 10% SDS in 250mls H₂O

1X SSC: 5 min. 12.5 mls 20X SSC in 250mls H₂O

0.2X SSC: 5 min. 2.5 mls 20X SSC in 250mls H₂O

Dry slides in centrifuge, 1000 RPM, 1min.

Scan at appropriate PMT's and channels.

The results are shown in Figures 1 through 11. The lists of genes come from colorectal tumors from a variety of stages of the disease. The genes that are up regulated in the tumors (overall) were also found to be expressed at a limited amount or not at all in the body map. The body map for the colorectal project consists of ten tissues: Heart, Brain, Lung, Liver, Breast, Kidney, Prostate, Small Intestine, Spleen, and Colon. The down regulated genes in tumors (overall) versus normal colon were not selected for their expression or lack of expression in the body map. As indicated, some of the Accession numbers include expression sequence tags (ESTs). Thus, in one embodiment herein, genes within an expression profile, also termed expression profile genes, include ESTs and are not necessarily full length. Figure 1 shows 51 upregulated genes; Figure 2 shows 194 upregulated genes; Figure 3 shows 1144 upregulated genes and Figure 4 shows 1815 upregulated genes. The genes shown in Figures 1 and 5 are particularly preferred. Figure 5 shows 54 downregulated genes; Figure 6 shows 558 downregulated genes; and Figure 7 shows 1923 downregulated genes; and Figures 8, 9, 10 and 11 provide the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue.

Example 2

Expression studies were performed herein.

As indicated in Figure 21, CAA2 is upregulated in colon cancer tissue. CAA2 is found in chromosome 15, cytoband 15q15-22, interval D15S146-D15S117. CAA2 has N-myristoylation sites and a C-terminal microbody targeting signal. The preferred fragments shown in Figures 18 and 19 have a solubility of 1 mg/ 1 ml H₂O.

As indicated in Figure 26, CAA9 is upregulated in colon cancer tissue. CAA9 is found in chromosome 5, cytoband 5q23.3, interval D5S471-D5S393.

As indicated in Figures 30A and 30B, CGA7 is upregulated in colon cancer tissue. CGA7 is found in chromosome 2.

As indicated in Figure 34, CGA8 is upregulated in colon cancer tissue.

As indicated in Figure 37, CJA8 is upregulated in colon cancer tissue. CJA8 is found in chromosome 11.

As indicated in Figure 38, BCN7 is upregulated in colon cancer tissue. BCN7 is found in chromosome 5, cytoband 5q22, interval D5S471-D5S393.

CLAIMS

We claim:

1. A method of screening drug candidates comprising:
 - a) providing a cell that expresses an expression profile gene which encodes a protein selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7 and CQA2 or a fragment thereof;
 - b) adding a drug candidate to said cell; and
 - c) determining the effect of said drug candidate on the expression of said expression profile gene.
2. A method according to claim 1 wherein said determining comprises comparing the level of expression in the absence of said drug candidate to the level of expression in the presence of said drug candidate, wherein the concentration of said drug candidate can vary when present, and wherein said comparison can occur after addition or removal of the drug candidate.
3. A method according to claim 1 wherein the expression of said profile gene is decreased as a result of the introduction of the drug candidate.
4. A method of screening for a bioactive agent capable of binding to a colorectal cancer modulator protein (CCMP), wherein said CCMP is CJA8 or a fragment thereof, said method comprising combining said CCMP and a candidate bioactive agent, and determining the binding of said candidate agent to said CCMP.
5. A method for screening for a bioactive agent capable of modulating the activity of a colorectal cancer modulator protein (CCMP), wherein said CCMP is CJA8 or a fragment thereof, said method comprising combining said CCMP and a candidate bioactive agent, and determining the effect of said candidate agent on the bioactivity of said CCMP.
6. A method of evaluating the effect of a candidate colorectal cancer drug comprising:
 - a) administering said drug to a patient;
 - b) removing a cell sample from said patient; and
 - c) determining the expression profile of said cell.
7. A method according to claim 6 further comprising comparing said expression profile to an expression profile of a healthy individual.

8. A biochip comprising a nucleic acid segment encoding CJA81 or a fragment thereof, wherein said biochip comprises fewer than 1000 nucleic acid probes.
9. A method of diagnosing colorectal cancer comprising:
 - a) determining the expression of a gene encoding CJA8 or a fragment thereof in a first tissue type of a first individual; and
 - b) comparing said expression of said gene from a second normal tissue type from said first individual or a second unaffected individual;wherein a difference in said expression indicates that the first individual has colorectal cancer.
10. An antibody which specifically binds to CJA8, or a fragment thereof.
11. An antibody which specifically binds to CAA9, or a fragment thereof.
12. The antibody of Claim 11 wherein said fragment is selected from the group CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 and CAA9p5MAPS.
13. The antibody of Claim 10, wherein said antibody is a monoclonal antibody.
14. The antibody of Claim 10, wherein said antibody is a humanized antibody.
15. The antibody of Claim 10, wherein said antibody is an antibody fragment.
16. A method for screening for a bioactive agent capable of interfering with the binding of a colorectal cancer modulator protein (CCMP) or a fragment thereof and an antibody which binds to said CCMP or fragment thereof, said method comprising:
 - a) combining a CCMP or fragment thereof, a candidate bioactive agent and an antibody which binds to said CCMP or fragment thereof; and
 - b) determining the binding of said CCMP or fragment thereof and said antibody.
17. A method for inhibiting colorectal cancer, said method comprising administering to a cell a composition comprising an antibody to CAJ8 or a fragment thereof.
18. The method of Claim 17 wherein said cell is a cell of an individual.
19. The method of Claim 18 wherein said individual has cancer.

20. The method of Claim 17 wherein said antibody is a humanized antibody.
21. The method of Claim 17 wherein said antibody is an antibody fragment.
22. A method for inhibiting colorectal cancer in a cell, wherein said method comprises administering to a cell a composition comprising antisense molecules to CJA8.
23. A peptide consisting essentially of CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 or CAA9p5MAPS.
24. A composition comprising the peptide of Claim 23.
25. A method of eliciting an immune response in an individual, said method comprising administering to said individual a composition comprising CJA8 or a fragment thereof.
26. A method of eliciting an immune response in an individual, said method comprising administering to said individual a composition comprising a nucleic acid comprising a sequence encoding CJA8 or a fragment thereof.
27. A composition capable of eliciting an immune response in an individual, said composition comprising CJA8 or a fragment thereof and a pharmaceutically acceptable carrier.
28. A composition capable of eliciting an immune response in an individual, said composition comprising a nucleic acid comprising a sequence encoding CJA8 or a fragment thereof and a pharmaceutically acceptable carrier.
29. A method of treating an individual for colorectal cancer comprising administering to said individual an inhibitor of CJA8.
30. The method of Claim 29 wherein said inhibitor is an antibody.
31. A method for determining the prognosis of an individual with colorectal cancer comprising determining the level of CJA8 in a sample, wherein a high level of CJA8 indicates a poor prognosis.

32. A method of neutralizing the effect of a CJA8, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization.
33. A method for localizing a therapeutic moiety to colorectal cancer tissue comprising exposing said tissue to an antibody to CJA8 or fragment thereof conjugated to said therapeutic moiety.
34. The method of Claim 33, wherein said therapeutic moiety is a cytotoxic agent.
35. The method of Claim 33, wherein said therapeutic moiety is a radioisotope.
36. A method of treating colorectal cancer comprising administering to an individual having colorectal cancer an antibody to CJA8 or fragment thereof conjugated to a therapeutic moiety.
37. The method of Claim 36, wherein said therapeutic moiety is a cytotoxic agent.
38. The method of Claim 36, wherein said therapeutic moiety is a radioisotope.

PRIMARY KEY	FOLD UPREGULATED IN TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
37677	>10	AA460530	Hs.98384	Homo sapiens orphan G protein-coupled receptor HG38 mRNA complete cds
6449	>10	X89986	Hs.32936	H.sapiens mRNA for NBK apoptotic inducer protein
4178	>10	U30246	Hs.110736	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds
18330	>10	AA216722	Hs.54481	Human mRNA for apolipoprotein E receptor 2 complete cds
5692	>10	X17644	Hs.2707	G1 to S phase transition 1
16810	>10	AA053636	Hs.128849	PBK1
33109	>10	W59961	Hs.22564	Human mRNA for KIAA0389 gene complete cds
37246	>10	AA449311	Hs.98658	Homo sapiens mitotic checkpoint protein kinase (BUB1) mRNA complete cds
2857	>10	M58597	Hs.2173	Fucosyltransferase 4 (alpha (13) fucosyltransferase myeloid-specific)
14338	>10	AA598712	Hs.23723	ESTs Weakly similar to ORF YPL212c [S.cerevisiae]
4676	9.6	U55206	Hs.78619	Homo sapiens human gamma-glutamyl hydrolase (hGH) mRNA complete cds
2192	7.8	L48211	Hs.20954	Homo Sapiens angiotensin II receptor gene complete cds
5793	7.4	X54942	Hs.83758	CDC28 protein kinase 2
18231	6.3	AA199747	Hs.79025	Human mRNA for KIAA0096 gene partial cds
6061	6.1	X68314	Hs.2704	Glutathione peroxidase 2 gastrointestinal
27117	5.0	AA405098	Hs.38178	ESTs Weakly similar to MOESIN/EZRIN/RADIXIN HOMOLOG [D.melanogaster]
12669	5.0	AA417030	Hs.5101	Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds
1106	4.8	HG2981-HT3127		EST - HG2981-HT3127
2157	4.6	L41939	Hs.89403	Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA complete cds

FIG. 1Aa

2 / 454

PRIMARY KEY	FOLD UPREGULATED IN TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
13193	4.4	AA442763	Hs.20483	ESTs Highly similar to G2/MITOTIC-SPECIFIC CYCLIN B2 [Mesocricetus auratus]
5690	4.4	X17620	Hs.118638	NUCLEOSIDE DIPHOSPHATE KINASE A
28050	4.1	AA479139	Hs.75393	Acid phosphatase 1 soluble
4540	3.5	U48807	Hs.2359	Human MAP kinase phosphatase (MKP-2) mRNA complete cds
26105	3.1	AA243133	Hs.48915	Homo sapiens serine/threonine kinase (BTAK) mRNA complete cds
19177	3.1	H10984	Hs.12338	ESTs
5780	3.1	X54489	Hs.789	GRO1 oncogene (melanoma growth stimulating activity alpha)
33620	3.0	W93943	Hs.59509	ESTs
4536	2.9	U48705	Hs.75562	Receptor protein-tyrosine kinase EDDR1
5928	2.8	X62048	Hs.75188	WEE1-LIKE PROTEIN KINASE
28258	2.7	AA505133	Hs.62273	ESTs
21256	2.5	R09195	Hs.151385	Homo sapiens mRNA for KIAA0564 protein partial cds
27748	2.5	AA453159	Hs.41723	Human kinesin-like spindle protein HKSP (HKSP) mRNA complete cds
25310	2.4	AA046745	Hs.110457	ESTs
2640	2.4	M30448		EST - M30448
3834	2.3	U12595	Hs.2204	Human tumor necrosis factor type 1 receptor associated protein (TRAP1) mRNA partial cds
4674	2.3	U54999	Hs.93121	Human LGN protein mRNA complete cds
5769	2.3	X53800	Hs.89643	GRO3 oncogene
25050	2.3	AA011134	Hs.25863	ESTs Weakly similar to renin [H.sapiens]
41935	2.3	T29681	Hs.75761	Human serine kinase mRNA complete cds
26895	2.3	AA292765	Hs.42650	H.sapiens mRNA for M-phase phosphoprotein mpp5
1782	2.1	L12711	Hs.89643	Transketolase (Wernicke-Korsakoff syndrome)

FIG.. 1Ab

3 / 454

PRIMARY KEY	FOLD UPREGULATED IN TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
25593	2.1	AA113149		Homo sapiens IPL (IPL) mRNA complete cds
1487	1.8	J03934		NAD(P)H:menadione oxidoreductase
7656	1.5	AA203428		ESTs Moderately similar to ANKYRIN BRAIN VARIANT 2 [Homo sapiens]
683	1.5	D79997		Human mRNA for KIAA0175 gene complete cds
836	1.5	D87444		Human mRNA for KIAA0255 gene complete cds
3098	1.2	M77836		PYROLINE-5-CARBOXYLATE REDUCTASE
6879	1.1	Z29066		H.sapiens nek2 mRNA for protein kinase
6880	1.0	Z29067		H.sapiens nek3 mRNA for protein kinase
2473	0.7	M21904		Antigen identified by monoclonal antibodies 4F2 TRA1.10 TROP4 and T43
36508	0.7	AA429621		Human 100 kDa coactivator mRNA complete cds

FIG.. 1Ac

4 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
33616	>10	W93726	Hs.55279	Proteas inhibitor 5 (maspin)
34197	>10	AA232315	Hs.12540	Homo sapiens clone 23797 and 23917 mRNA partial cds
19387	>10	H20128	Hs.31656	ESTs
8125	>10	AA330771	Hs.82911	Human protein-tyrosine phosphatase (HU-PP-1) mRNA partial sequence
18362	>10	AA223912	Hs.12013	Ribonuclease L (2'5'-oligoadenylate synthetase-dependent) inhibitor
39995	>10	H62474	Hs.108240	EST
19328	>10	H17808	Hs.22858	ESTs
38590	>10	AA598648	Hs.78202	Human mRNA for transcriptional activator hSNF2b complete cds
38456	>10	AA504343	Hs.101074	ESTs
17559	>10	AA128407	Hs.71190	ESTs
5619	>10	X14850	Hs.2711	HISTONE H2A.X
4029	>10	U21090	Hs.74598	Human DNA polymerase delta small subunit mRNA complete cds
15006	>10	U30246	Hs.110736	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds
3659	>10	U04313	Hs.55279	Proteas inhibitor 5 (maspin)
26916	>10	AA331393	Hs.47378	ESTs
1346	>10	HG4716-HT5158		EST - HG4716-HT5158
37491	10.0	AA455239	Hs.87630	ESTs Highly similar to CHROMOSOME CONDENSATION PROTEIN DPY-27 [Caenorhabditis elegans]
13110	9.8	AA435840	Hs.19114	Homo sapiens mRNA for high mobility group protein HMG2a
4676	9.6	U55206	Hs.78619	Homo sapiens human gamma-glutamyl hydrolase (hGH) mRNA complete cds
21655	8.7	R38239	Hs.25276	EST

FIG..2Aa

5 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
14723	8.3	D59894	Hs.34782	ESTs
5793	7.4	X54942	Hs.83758	CDC28 protein kinase 2
29848	7.1	N22107	Hs.124215	ESTs
9347	7.0	H03686	Hs.112013	ESTs
6078	7.0	X69141	Hs.48876	FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE
9326	6.8	D89377	Hs.89404	Msh (Drosophila) homeo box homolog 2
1566	6.7	J05614	EST - J05614	EST - J05614
25675	6.7	AA129757	Hs.54602	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L22 [Rattus norvegicus]
20126	6.4	N22015	Hs.18457	ESTs
6061	6.1	X68314	Hs.2704	Glutathione peroxidase 2 gastrointestinal
10867	6.1	AA088458	Hs.19322	ESTs Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
18062	6.0	AA179845	Hs.73625	ESTs Moderately similar to rakninin-6 [M.musculus]
4093	5.9	U25182	Hs.83383	Human antioxidant enzyme AOE37-2 mRNA complete cds
18290	5.8	AA211901	Hs.86430	ESTs
5330	5.8	U91327	EST - U91327	EST - U91327
4244	5.7	U33286	Hs.90073	Human chromosome segregation gene homolog CAS mRNA complete cds
6928	5.7	Z46629	Hs.2316	SRP (sex-determining region Y)-box 9 (campomelic dysplasia autosomal sex-reversal)
6160	5.6	X74794	Hs.89699	CDC21 HOMOLOG
31487	5.4	N69507	Hs.129849	ESTs
9470	5.3	H46617	EST - H46617	EST - H46617
33458	5.0	W86835	Hs.14158	Homo sapiens mRNA for KIAA0636 protein complete cds
12669	5.0	AA417030	Hs.5101	Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds

FIG..2Ab

6 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
1106	4.8	HG2981-HT3127		EST - HG2981-HT3127
34367	4.8	AA251758	Hs.40323	Homo sapiens spleen mitotic checkpoint BUB3 (BUB3) mRNA complete cds
11595	4.8	AA242819	Hs.32539	ESTs
17622	4.8	AA131584	Hs.71435	ESTs Weakly similar to SOF1 PROTEIN [Saccharomyces cerevisiae]
34754	4.7	AA287642	Hs.81848	Human mRNA for KIAA0078 gene complete cds
25038	4.7	AA010065	Hs.83758	CDC28 protein kinase 2
5312	4.6	U90716	Hs.79187	Human cell surface protein HCAR mRNA complete cds
8085	4.6	AA314779	Hs.105484	ESTs Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
33656	4.6	W95477	Hs.50582	ESTs
8264	4.5	AA401334	Hs.106941	ESTs
34479	4.5	AA262080	Hs.110736	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds
7898	4.4	AA263032	Hs.81634	ESTs
10716	4.4	AA053319	Hs.9951	ESTs
5690	4.4	X17620	Hs.118638	NUCLEOSIDE DIPHOSPHATE KINASE A
20203	4.3	N26855	Hs.5858	ESTs Moderately similar to !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! [H.sapiens]
10923	4.2	AA116036	Hs.9329	ESTs
28050	4.1	AA479139	Hs.75393	Acid phosphatase 1 soluble
10970	4.1	AA129390	Hs.5285	ESTs
4149	4.1	U28386	Hs.2397	RAG (recombination activating gene) cohort 1
5767	4.1	X53793	Hs.118226	MULTIFUNCTIONAL PROTEIN ADE2
26596	4.0	AA279943	Hs.88671	ESTs
8961	3.9	AFFX-		AFFX-HUMTFRM/M11507_3

FIG.--2Ac

7 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
38604	3.9	AA598803	Hs.111496	ESTs
30560	3.9	N49284	Hs.1334	MYB PHOTO-ONCOGENE PROTEIN
8513	3.8	AA446990	Hs.103135	ESTs
14509	3.8	AA609943	Hs.32793	ESTs
25284	3.8	AA045074	Hs.110146	ESTs Weakly similar to 52-kD SS-A/Ro autoantigen [H.sapiens]
27354	3.8	AA425221	Hs.81688	ESTs
18385	3.8	AA227219	Hs.110826	Homo sapiens CAGF9 mRNA partial cds
25240	3.7	AA039713	Hs.110406	ESTs
16854	3.7	AA055552	Hs.71622	ESTs Weakly similar to KIAA0319 [H.sapiens]
3709	3.7	U07550	Hs.11197	Heat shock 10 kD protein 1 (chaperonin 10)
13606	3.5	AA456437	Hs.20386	ESTs Weakly similar to CLEAVAGE STIMULATION FACTOR 64 KD SUBUNIT [H.sapiens]
8338	3.4	AA417152	Hs.5101	Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds
387	3.4	D28589		EST - D28589
15643	3.4	W58247	Hs.27437	ESTs Highly similar to KINESIN-LIKE PROTEIN KIF4 [Mus musculus]
13838	3.4	AA465342	Hs.34045	ESTs
251	3.4	D14520	Hs.84728	Basic transcription element binding protein 2
3778	3.4	U09848	Hs.363	Zinc finger protein 139 (clone pHZ-37)
5660	3.4	X16396	Hs.37791	NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE
17365	3.4	AA101551	Hs.68900	ESTs
33985	3.3	AA181580	Hs.81690	Homo sapiens importin beta subunit mRNA complete cds
19233	3.3	H12634	Hs.8104	ESTs
13767	3.3	AA463234	Hs.119387	ESTs
4738	3.3	U58766	Hs.75801	Human FX protein mRNA complete cds

FIG..2Ad

8 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
17041	3.3	AA070364		EST - RC_AA070364
15504	3.3	W28362	Hs.44131	ESTs
7401	3.3	AA094800	Hs.55682	Human translation initiation factor eIF3 p66 subunit mRNA complete cds
18683	3.2	F04258	Hs.36454	ESTs Highly similar to INORGANIC PYROPHOSPHATASE [Bos taurus]
23930	3.2	T96690	Hs.125123	ESTs Weakly similar to IIII ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
11288	3.1	AA196512	Hs.25916	ESTs
170	3.1	D00596	Hs.82962	Thymidylate synthase
11659	3.1	AA251909	Hs.36708	Homo sapiens MAD3-like protein kinase mRNA complete cds
14134	3.1	AA489080	Hs.3566	ESTs Highly similar to phosphorylation regulatory protein HP-10 [H.sapiens]
11140	3.1	AA158132	Hs.11817	ESTs Highly similar to YSA1 PROTEIN [Saccharomyces cerevisiae]
17925	3.0	AA164209	Hs.31730	Homo sapiens RRM RNA binding protein Gry-rbp (GRY-R3P) mRNA complete cds
26530	3.0	AA278650	Hs.73291	ESTs
7445	3.0	AA104023	Hs.110048	ESTs
18055	3.0	AA179387	Hs.73596	ESTs
15174	3.0	U82987	Hs.87246	Human Bcl-2 binding component 3 (bbc3) mRNA partial cds
33620	3.0	W93943	Hs.59509	ESTs
1932	3.0	L24804	Hs.75839	Human (p23) mRNA complete cds
39556	3.0	F03738	Hs.3657	ESTs
1605	2.9	L00058	Hs.79070	V-myc avian myelocytomatosis viral oncogene homolog
4536	2.9	U48705	Hs.75562	Receptor protein-tyrosine kinase EDDR1
36200	2.9	AA421164	Hs.107213	ESTs

FIG._2Ae

9 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
12313	2.9	AA397916	Hs.22595	ESTs
19867	2.9	H61476	Hs.15641	ESTs
6081	2.9	X69398	Hs.82685	CD47 antigen (Rh-related antigen integrin-associated signal transducer)
16708	2.8	AA043944	Hs.62663	ESTs
357	2.8	D26156	Hs.78202	Human mRNA for transcriptional activator hSNF2b complete cds
8059	2.8	AA310967	Hs.5080	ESTs Weakly similar to T04A8.11 [C.elegans]
35830	2.8	AA411448	Hs.139386	ESTs
20151	2.8	N22895	Hs.6831	Homo sapiens clone 1400 unknown protein mRNA partial cds
28258	2.8	AA505133	Hs.62273	ESTs
8616	2.8	AA460077	Hs.28555	ESTs
6480	2.8	X91788	Hs.84974	H.sapiens mRNA for Icln protein
14566	2.8	AA621122	Hs.5198	ESTs
14182	2.8	AA490885	Hs.21766	ESTs
35955	2.7	AA412528	Hs.20183	ESTs Weakly similar to ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH [R.norvegicus]
17642	2.7	AA132983	Hs.44155	ESTs Moderately similar to C-1-TETRAHYDROFOLATE SYNTHASE CYTOPLASMIC [H.sapiens]
6131	2.7	X72841	Hs.2758	Human retinoblastoma-binding protein (RbAp46) mRNA complete cds
6444	2.7	X89750	Hs.90077	H.sapiens mRNA for TGIF protein
7701	2.7	AA215333	Hs.97101	ESTs
42534	2.7	W73189	Hs.89403	Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA complete cds
34796	2.7	AA291259	Hs.97101	ESTs

FIG..2A1

10 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
1923	2.7	L23808	Hs.1695	Matrix metalloproteinase 12 (macrophage elastase)
10951	2.6	AA126719	Hs.25282	ESTs
11308	2.6	AA207114	Hs.27842	ESTs
4086	2.6	U24704	Hs.111709	Human antisecretory factor-1 mRNA complete cds
5587	2.6	X13482	Hs.80506	U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A'
19841	2.6	H59617	Hs.5199	ESTs Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD [Drosophila melanogaster]
7614	2.6	AA187579	Hs.102696	ESTs Weakly similar to Yel007c-ap [S.cerevisiae]
11362	2.6	AA227261	Hs.20922	ESTs
13866	2.6	AA476319	Hs.5327	ESTs
2993	2.6	M64929	Hs.75200	Protein phosphatase 2 (formerly 2A) regulatory subunit B (PR 52) alpha isoform
12986	2.6	AA430032	Hs.7487	ESTs Moderately similar to PTTG gene product [R.norvegicus]
5932	2.5	X62153	Hs.82479	Minichromosome maintenance deficient (S. cerevisiae) 3
38434	2.5	AA497013	Hs.142592	ESTs
38185	2.5	AA487508	Hs.9877	Homo sapiens mRNA for KIAA0688 protein complete cds
1424	2.5	J02645	Hs.81613	Eukaryotic translation initiation factor 2A
21876	2.5	R43286		EST - RC_R43286
6485	2.5	X92098	Hs.75914	H.sapiens mRNA for transmembrane protein rnp24
7960	2.4	AA285277	Hs.8932	Homo sapiens brain expressed ring finger protein mRNA complete cds
452	2.4	D38076	Hs.24763	RAN binding protein 1
11701	2.4	AA253031	Hs.31730	Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA complete cds
36390	2.4	AA426291	Hs.108527	ESTs Weakly similar to No definition line found [C.elegans]
14420	2.4	AA600322	Hs.19574	ESTs Highly similar to AAC-RICH MRNA CLONE AAC3 PROTEIN [Dictyostelium discoideum]

FIG. 2Ag

PRIMARY KEY	FOLD UPREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
6387	2.4	X85372	Hs.105465	H.sapiens mRNA for Sm protein F
1497	2.4	J04088	Hs.3378	Topoisomerase (DNA) II alpha (170kD)
27872	2.4	AA459254	Hs.48855	ESTs
8163	2.4	AA357394	Hs.98073	ESTs
23065	2.4	T23539	Hs.7165	ESTs Highly similar to zinc finger protein [M.musculus]
20837	2.4	N69263	Hs.20524	ESTs Highly similar to HEXOKINASE TYPE I [Homo sapiens]
17352	2.3	AA100925	Hs.20990	ESTs
28796	2.3	D51272		EST - RC_D51272_s
26679	2.3	AA281733	Hs.4310	ESTs
24092	2.3	W42845	Hs.14611	Homo sapiens protein tyrosine phosphatase PIR1 mRNA complete cds
5875	2.3	X59405	Hs.83532	Membrane cofactor protein (CD46 trophoblast-lymphocyte cross-reactive antigen)
7404	2.3	AA094989	Hs.7381	Homo sapiens voltage dependent anion channel protein mRNA complete cds
6388	2.3	X85373	Hs.77496	H.sapiens mRNA for Sm protein G
25050	2.3	AA011134	Hs.25863	ESTs Weakly similar to renin [H.sapiens]
41935	2.3	T29681	Hs.75761	Human serine kinase mRNA complete cds
3343	2.3	M97936	Hs.21486	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA
5937	2.2	X62534	Hs.80684	High-mobility group (nonhistone chromosomal) protein 2
7387	2.2	AA093977	Hs.71475	ESTs
20843	2.2	N69352	Hs.5683	Homo sapiens mRNA for ATP-dependent RNA helicase #46 complete cds
28448	2.2	AA621752	Hs.76887	Human 26S proteasome-associated pad1 homolog (POH1) mRNA complete cds
651	2.2	D78129		EST - D78129

11 / 454

FIG.-2Ah

12 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
11688	2.2	AA252672	Hs.103300	Homo sapiens diphthamide biosynthesis protein-2 (DPH2) mRNA, complete cds
11803	2.2	AA257971	Hs.21214	ESTs
4046	2.2	U22376	Hs.1334	MYB PROTO-ONCOGENE PROTEIN
20276	2.2	N32919	Hs.27931	ESTs
34370	2.1	AA251829	Hs.104058	ESTs Weakly similar to HYPOTHETICAL 27.4 KD PROTEIN IN MER2-CPR7 INTERGENIC REGION
14582	2.1	AA621340	Hs.10600	[Saccharomyces cerevisiae] ESTs Weakly similar to HYPOTHETICAL 39.6 KD PROTEIN IN MTD1-NUP133 INTERGENIC REGION
3461	2.1	S75256		[Saccharomyces cerevisiae] EST - S75256
924	2.1	HG1112-HT1112		EST - HG1112-HT1112
24348	2.1	W86469	Hs.77899	Tropomyosin alpha chain (skeletal muscle)
10898	2.1	AA112063	Hs.15313	ESTs Weakly similar to PRE-MRNA SPLICING HELICASE BRR2, [S. cerevisiae]
381	2.1	D28473	Hs.78770	Isolcine-tRNA synthetase
11528	2.1	AA236018	Hs.10724	ESTs Weakly similar to unknown [S. cerevisiae]
25593	2.1	AA113149	Hs.8130	Homo sapiens IPL (IPL) mRNA complete cds
38040	2.1	AA481403	Hs.107213	ESTs
4111	2.1	U26312	Hs.83550	Human heterochromatin protein HP1Hs-gamma mRNA complete cds
61	2.0	AC002115	Hs.83379	Cytochrome c oxidase subunit VIb
9112	2.0	D16611	Hs.89866	Coproporphyrinogen oxidase (coproporphyrin harderoporphyria)
380	2.0	D28423		EST - D28423
377	2.0	D28364		EST - D28364
28379	2.0	AA609710	Hs.42582	ESTs

FIG. 2Ai

13 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
24230	2.0	W72276	Hs.5950	ESTs
40212	2.0	H88535	Hs.9564	Human clone 121711 defective mariner transposon Hsmar2 mRNA sequence
8118	2.0	AA328993	Hs.104558	ESTs

FIG. 2Aj

14 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
33616	>10	W93726	Hs.55279	Protease inhibitor 5 (maspin)
34197	>10	AA232315	Hs.12540	Homo sapiens clone 23797 and 23917 mRNA partial cds
19387	>10	H20128	Hs.31656	ESTs
8125	>10	AA330771	Hs.82911	Human protein-tyrosine phosphatase (HU-PP-1) mRNA partial sequence
18362	>10	AA223912	Hs.12013	Ribonuclease L (2'5'-oligoadenylate synthetase-dependent) inhibitor
39995	>10	H62474	Hs.108240	EST
19328	>10	H17808	Hs.22858	ESTs
38590	>10	AA598648	Hs.78202	Human mRNA for transcriptional activator hSNF2b complete cds
38456	>10	AA504343	Hs.101074	ESTs
17559	>10	AA128407	Hs.71190	ESTs
6106	>10	X70683	Hs.83484	SRY (sex determining region Y)-box 4
8648	>10	AA465016	Hs.69423	Homo sapiens serine protease-like protease (nes1) mRNA complete cds
5619	>10	X14850	Hs.2711	HISTONE H2A.X
5603	>10	X14253	Hs.75561	Teratocarcinoma-derived growth factor 1
37677	>10	AA460530	Hs.98384	Homo sapiens orphan G protein-coupled receptor HG38 mRNA complete cds
11561	>10	AA236533	Hs.19222	Evi-1
39787	>10	H20131	Hs.107561	ESTs
16490	>10	AA026418	Hs.91539	ESTs
32240	>10	R50976	Hs.12013	Ribonuclease L (2'5'-oligoadenylate synthetase-dependent) inhibitor
12480	>10	AA403116	Hs.9880	Homo sapiens U-snRNP-associated cyclophilin (USA-CyP) mRNA complete cds

FIG._3Aa

15 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
2144	>10	L41349	Hs.74014	Phospholipase C beta 4
12143	>10	AA290991	Hs.17296	ESTs
33006	>10	W46286	Hs.107039	ESTs Weakly similar to ZK1058.5 [C.elegans]
39535	>10	F02450	Hs.111980	ESTs Moderately similar to unknown protein [H.sapiens]
41005	>10	N79516	Hs.73287	ESTs
6449	>10	X89986	Hs.32936	H.sapiens mRNA for NBK apoptotic inducer protein
37653	>10	AA460017	Hs.99513	ESTs
4178	>10	U30246	Hs.110736	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds
1863	>10	L19161	Hs.121541	TRANSLATIONAL INITIATION FACTOR 2 GAMMA SUBUNIT
19787	>10	H56679	Hs.37362	ESTs
8092	>10	AA316272	Hs.24550	ESTs
37074	>10	AA446344	Hs.99068	ESTs
39405	>10	D50975	Hs.21281	ESTs
10747	>10	AA055841	Hs.31953	ESTs
5002	>10	U72761	Hs.6990	Human karyopherin beta 3 mRNA complete cds
33791	>10	Z40883	Hs.65588	ESTs
6188	>10	X76029	Hs.2841	NEUFLOMEDIN U-25 PRECURSOR
13136	>10	AA436560	Hs.7327	ESTs
5963	>10	X63629	Hs.2877	Cadherin 3 (P-cadherin)
38179	>10	AA487492	Hs.76272	Human sapiens clone 23592 mRNA sequence
30938	>10	N58561	Hs.84898	Cathepsin B
34692	>10	AA285079	Hs.125873	ESTs
17987	>10	AA169379	Hs.72865	ESTs
23832	>10	T92018	Hs.16961	ESTs
36695	>10	AA433910	Hs.98786	ESTs

FIG.-3Ab

16 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
10233	>10	R71427	Hs.9081	ESTs Highly similar to PHENYLALANYL-TRNA SYNTHETASE ALPHA CHAIN CYTOPLASMIC [Saccharomyces cerevisiae]
38330	>10	AA490882	Hs.112227	ESTs
1349	>10	G4747-HT5195		EST - HG4747-HT5195
36962	>10	AA442082	Hs.131915	ESTs
4975	>10	U71088	Hs.84374	Human MEK5 mRNA complete cds
5510	>10	X05360	Hs.58393	Cell division cycle 2 G1 to S and G2 to M
3021	>10	M68941	Hs.73826	Protein tyrosine phosphatase non-receptor type 4
17734	>10	AA137246	Hs.84980	ESTs
36371	>10	AA426017	Hs.109761	ESTs
459	>10	D38293	Hs.77770	Human mRNA for clathrin-like protein complete cds
17419	>10	AA113349	Hs.69588	EST
14054	>10	AA485223	Hs.34892	ESTs
5021	>10	U73524	Hs.87465	Human putative ATP/GTP-binding protein (HEAB) mRNA complete cds
4994	>10	U72514	Hs.12045	Human C2f mRNA complete cds
26355	>10	AA256379	Hs.99291	ESTs
4455	>10	U43944	Hs.14732	MALATE OXIDOREDUCTASE
10748	>10	AA055892	Hs.14543	ESTs
8111	>10	AA323787	Hs.4770	ESTs
19389	>10	H20165	Hs.31734	EST
32195	>10	R43471	Hs.22355	ESTs Weakly similar to ORF YOR258w [S.cerevisiae]
38970	>10	AA609749	Hs.112759	ESTs
21519	>10	R27975		EST - RC_R27975
34013	>10	AA190888		EST - RC_AA190888
6167	>10	X74987	Hs.12013	Ribonuclease L (2'5'-oligoadenylate synthetase-dependent) inhib for

FIG._3Ac

17 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
41107	>10	R01634	Hs.119878	ESTs
5986	>10	X64810	Hs.78977	Protein convertase subtilisin/kexin type 1
11603	>10	AA243052	Hs.16389	ESTs Highly similar to GONADOTROPIN-RELEASING HORMONE RECEPTOR [Rattus norvegicus]
40498	>10	N26086	Hs.132991	Homo sapiens citrate synthase mRNA complete cds
6315	>10	X81889	Hs.16381	H.sapiens mRNA for p0071 protein
4702	>10	U57341		EST - U57341
18676	>10	F04022	Hs.27885	ESTs
24197	>10	W67277	Hs.17546	ESTs
4713	>10	U57721	Hs.81771	Human L-kynurenine hydrolase mRNA complete cds
38460	>10	AA504462	Hs.105730	ESTs
18330	>10	AA216722	Hs.54481	Human mRNA for apolipoprotein E receptor 2 complete cds
18782	>10	F09739	Hs.12562	ESTs
42766	>10	Z99394	Hs.94432	ESTs Moderately similar to !!! ALU SUBFAMILY SP WARNINGENTRY !!!! [H.sapiens]
34014	>10	AA191348	Hs.96178	ESTs
16835	>10	AA054438	Hs.60753	ESTs
6384	>10	X85137	Hs.41723	Human kinesin-like spindle protein FKSP (HKSP) mRNA complete cds
29893	>10	N23003	Hs.42186	ESTs
38553	>10	AA521471	Hs.102652	ESTs
11160	>10	AA164289	Hs.26006	ESTs
1158	>10	G3344-HT3521		EST - HG3344-HT3521
7325	>10	AA090842	Hs.19736	ESTs Weakly similar to HYPOTHETICAL 36.7 KD PROTEIN C2F7.02C IN CHROMOSOME I [Schizosaccharomyces pombe]
37978	>10	AA479294		EST - RC_AA479294
31136	>10	N63512	Hs.14484	ESTs Weakly similar to M01F1.4 [C.elegans]

FIG..3Ad

18 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
11813	>10	AA258158	Hs.22153	ESTs
10992	>10	AA132523	Hs.22900	Homo sapiens BAC clone RG119C02 from 7p15
5789	>10	X54925	Hs.83169	Matrix metalloproteinase 1 (interstitial collagenase)
16993	>10	AA065300	Hs.75337	Human mRNA for KIAA0035 gene partial cds
17654	>10	AA133250	Hs.62180	ESTs
20057	>10	H98079	Hs.31497	ESTs
39436	>10	D52692	Hs.74574	Human Ca2+-dependent activator protein for secretion mRNA complete cds
19727	>10	H52702	Hs.36690	ESTs
41381	>10	R42278	Hs.31748	H. sapiens mRNA for TRE5
22576	>10	R79111	Hs.29388	ESTs
35769	>10	AA406206	Hs.104746	ESTs
33980	>10	AA180223	Hs.8454	CAMP-DEPENDENT PROTEIN KINASE TYPE II-ALPHA REGULATORY CHAIN
40911	>10	N69114	Hs.21336	H. sapiens mRNA for orphan nuclear hormone receptor
37084	>10	AA446486	Hs.125129	Homo sapiens Ran binding protein 2 (RanBP2alpha) mRNA partial cds
26935	>10	AA347193	Hs.77831	ESTs Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 [Caenorhabditis elegans] EST - L47276
2188	>10	L47276		Bloom syndrome
4362	>10	U39817	Hs.36820	ESTs
42354	>10	W19346	Hs.89319	PHOSPHATIDYLINOSITOL
9127	>10	D30037	Hs.91447	ESTs
20614	>10	N59230	Hs.18937	G1 to S phase transition 1
5692	>10	X17644	Hs.2707	Human tyrosyl-tRNA synthetase mRNA complete cds
4388	>10	U40714	Hs.109631	Glucagon-like peptide-1 receptor
3598	>10	U01157	Hs.165	

FIG.-3Ae

19 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
24545	>10	Z38462	Hs.12403	ESTs
35309	>10	AA398660	Hs.97301	EST
23662	>10	T86674	Hs.16253	ESTs
37456	>10	AA454632	Hs.123157	ESTs
10840	>10	AA084104	Hs.30177	ESTs
25179	>10	AA031268	Hs.113319	H.sapiens mRNA for kinesin-2
21	>10	AB000905	Hs.143080	H.sapiens histone H4 gene
18762	>10	F09458	Hs.12421	ESTs
39221	>10	AA621346	Hs.99234	Homo sapiens protein phosphatase with EF-hands-1 (PPEF-1) mRNA complete cds
39232	>10	AA621409	Hs.112986	ESTs
42602	>10	W86423	Hs.105413	ESTs
22372	>10	R62831	Hs.28366	EST
39110	>10	AA620709	Hs.20563	ESTs Weakly similar to HYPOTHETICAL 90.8 KD PROTEIN T05H10.7 IN CHROMOSOME II [C.elegans]
16810	>10	AA053636	Hs.129849	ESTs
29645	>10	H95840	Hs.42116	ESTs
36405	>10	AA426406	Hs.10801	Homo sapiens mRNA for KIAA0530-protein partial cds
4029	>10	U21090	Hs.74598	Human DNA polymerase delta small subunit mRNA complete cds
15006	>10	U30246	Hs.110736	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds
25282	>10	AA044825	Hs.103446	ESTs
34561	>10	AA280298	Hs.107119	ESTs
40594	>10	N35388	Hs.112227	ESTs
16074	>10	AA001507	Hs.59861	ESTs
27046	>10	AA400670	Hs.79507	Homo sapiens mRNA for KIAA0582 protein partial cds

FIG._3A*f*

20 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
31484	>10	N69466	Hs.49683	ESTs
39504	>10	D80632	Hs.10726	ESTs
20304	>10	N34686	Hs.7749	Homo sapiens clone 23915 mRNA sequence
36395	>10	AA426353	Hs.98394	ESTs
38601	>10	AA598738	Hs.109041	ESTs
40631	>10	N45124	Hs.6809	ESTs
236	>10	D13645	Hs.2471	Human mRNA for KIAA0020 gene complete cds
5623	>10	X14975	Hs.139305	T-CELL SURFACE GLYCOPROTEIN CD1E PRECURSOR
35803	>10	AA410295	Hs.97911	ESTs
5243	>10	U85946	Hs.29494	Human brain secretory protein hSec10p (HSEC10) mRNA complete cds
19591	>10	H40688	Hs.33785	ESTs
38828	>10	AA609177	Hs.109363	ESTs
35798	>10	AA410231	Hs.98069	ESTs
3163	>10	M84424	Hs.1355	Cathepsin E
22400	>10	R64109	Hs.28487	ESTs
20657	>10	N62889	Hs.107242	ESTs
39062	>10	AA620333	Hs.112857	EST
25082	>10	AA017257	Hs.101139	ESTs
40876	>10	N67607	Hs.109450	Human Rho-associated coiled-coil containing protein kinase p160ROCK mRNA complete cds
5857	>10	X58377	Hs.1721	Human mRNA for adipogenesis inhibitory factor
29551	>10	H90134	Hs.141382	ESTs
39529	>10	F02202	Hs.100960	ESTs
6155	>10	X74331	Hs.74519	DNA primase polypeptide 2A (58kD)
5214	>10	U83303	Hs.123029	H.sapiens mRNA for granulocyte chemotactic protein
36958	>10	AA442060	Hs.87507	ESTs

FIG.-3Ag

21 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
40660	>10	N49104	Hs.79108	NUCLEAR FACTOR RIP140
37816	>10	AA469954	Hs.104820	EST
25951	>10	AA234556	Hs.135158	EST
22072	>10	R49406	Hs.28410	ESTs
39832	>10	H26279		EST - RC_H26279
23198	>10	T40530	Hs.8241	ESTs Weakly similar to B0035.14 [C.elegans]
29331	>10	H68116	Hs.39063	ESTs
38316	>10	AA490500	Hs.18747	Homo sapiens ribonuclease P protein subunit p20 (RPP20) mRNA complete cds
37829	>10	AA470084	Hs.98358	ESTs
3870	>10	U14518	Hs.1594	Centromere protein A (17kD)
39176	>10	AA621091	Hs.72087	ESTs
41793	>10	T03887	Hs.7327	ESTs
33666	>10	W95876	Hs.59741	ESTs
35766	>10	AA406169	Hs.16349	Homo sapiens KIAA0431 mRNA partial cds
32277	>10	R61493	Hs.26886	Human mRNA for rod photoreceptor protein complete cds
5558	>10	X07876	Hs.89791	Wingless-type MMTV integration site 2 human homolog
6382	>10	X85133	Hs.85273	H.sapiens RBQ-1 mRNA
41040	>10	N91948	Hs.125034	ESTs
39080	>10	AA620552		EST - RC_AA620552_r
20307	>10	N34830	Hs.37636	ESTs
18260	>10	AA206801	Hs.86277	ESTs
41065	>10	N93618	Hs.28554	ESTs
33109	>10	W59961	Hs.22564	Human mRNA for KIAA0389 gene complete cds
28015	>10	AA477421	Hs.21801	ESTs
30610	>10	N50138	Hs.47032	EST
34015	>10	AA191353	Hs.109884	ESTs

FIG. 3Ah

22 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
40559	>10	N33024	Hs.23450	ESTs
1445	>10	J03027	Hs.73885	MHC class I protein HLA-G
13242	>10	AA445994	Hs.21331	ESTs
37983	>10	AA479348	Hs.52871	H.sapiens mRNA for SYT
42242	>10	T89579	Hs.79353	Homo sapiens E2F-related transcription factor (DP-1) mRNA complete cds
37135	>10	AA447540	Hs.99112	EST
20564	>10	N55443	Hs.23625	ESTs
28141	>10	AA488432	Hs.56407	ESTs
21240	>10	R08613	Hs.20188	ESTs
34382	>10	AA252512	Hs.10069	ESTs
25948	>10	AA234365	Hs.102456	Homo sapiens survival of motor neuron protein interacting protein 1 (SIP1) mRNA complete cds
33953	>10	AA173290	Hs.67397	Human HOXA1 mRNA long transcript and alternatively spliced forms complete cds
40913	>10	N69218	Hs.108232	ESTs
35697	>10	AA405512	Hs.104741	ESTs
34672	>10	AA284372	Hs.111471	ESTs
3659	>10	U04313	Hs.55279	Protease inhibitor 5 (maspin)
17051	>10	AA070801	Hs.51615	ESTs
34372	>10	AA251973	Hs.143853	ESTs
19203	>10	H11593	Hs.28116	ESTs
20791	>10	N68057	Hs.90357	Homo sapiens telomeric repeat binding factor (TRF1) mRNA complete cds
24215	>10	W69425	Hs.15767	ESTs
37246	>10	AA449311	Hs.98658	Homo sapiens mitotic checkpoint protein kinase (BUB1) mRNA complete cds

FIG. 3A1

23 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
6790	>10	Y12394	Hs.3886	Homo sapiens importin-alpha homolog (SRP1gamma) mRNA complete cds
25806	>10	AA149007	Hs.103871	EST
1852	>10	L17328	Hs.103419	Human FEZ2 mRNA partial cds
38871	>10	AA609333	Hs.139867	EST
36307	>10	AA424803	Hs.98474	EST
25047	>10	AA011031	Hs.110182	ESTs
33343	>10	W79834	Hs.58559	ESTs Weakly similar to rho-kin [M.musculus]
5799	>10	X55330	Hs.111661	Aspartylglucosaminidase
23623	>10	T84047	Hs.15428	ESTs
13143	>10	AA436619	Hs.36353	ESTs
29523	>10	H88353	Hs.139312	ESTs Weakly similar to line-1 protein ORF2 [H.sapiens]
26291	>10	AA253422	Hs.142179	ESTs
35801	>10	AA410291	Hs.114121	ESTs
37159	>10	AA447714	EST - RC_AA447714	
40064	>10	H72283	Hs.38483	Human mRNA for KIAA0265 gene partial cds
38867	>10	AA609318	Hs.3144	Human cbl-b mRNA complete cds
29795	>10	N20641	Hs.46230	ESTs Highly similar to HYPOTHETICAL MYELOID CELL LINE PROTEIN 3 [Homo sapiens]
26677	>10	AA281636	Hs.88882	ESTs
5960	>10	X63575	Hs.89512	ATPase Ca++ transporting plasma membrane 2 (NOTE: redefinition of symbol)
37611	>10	AA458996	Hs.32970	Human signaling lymphocytic activation molecule (SLAM) mRNA complete cds
36753	>10	AA435686	Hs.97439	ESTs
26274	>10	AA253011	Hs.88756	ESTs
32789	>10	W02779	Hs.55271	ESTs Moderately similar to kinesin-73 [D.melanogaster]

FIG.-3Aj

24 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
37168	>10	AA477772	Hs.125153	ESTs
39433	>10	D52037	Hs.35650	Human thymidine kinase 2 (TK2) mRNA complete cds
1570	>10	K01383		EST - K01383
30617	>10	N50646	Hs.47083	ESTs
35106	>10	AA371561	Hs.142355	EST Weakly similar to putative p150 [H.sapiens]
30190	>10	N33264	Hs.44463	EST
789	>10	D86971	Hs.78851	Human mRNA for KIAA0217 gene partial cds
4386	>10	U40622	Hs.21523	DNA repair protein XRCC4
31944	>10	N93193	Hs.80310	ESTs
13237	>10	AA443971	Hs.142495	ESTs Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
4157	>10	U28811	Hs.78979	Human cysteine-rich fibroblast growth factor receptor (CFR-1) mRNA complete cds
2070	>10	L37378	Hs.123074	Homo sapiens guanylyl cyclase (RetGC-2) mRNA complete cds
2123	>10	L40396	Hs.26956	Homo sapiens (clone s22i71) mRNA fragment
26926	>10	AA342402	Hs.48729	ESTs
6479	>10	X91653		EST - X91653
11969	>10	AA280670	Hs.24968	ESTs
37601	>10	AA458864	Hs.102946	ESTs
34904	>10	AA321746	Hs.96719	EST
35958	>10	AA412550	Hs.97804	ESTs
28644	>10	D12163	Hs.103262	ESTs
38194	>10	AA487969	Hs.96692	ESTs
42177	>10	T79786	Hs.100582	ESTs
40604	>10	N38893	Hs.28578	Homo sapiens KIAA0428 mRNA complete cds
3913	>10	U16261	Hs.66576	Human MDA-7 (mda-7) mRNA complete cds

FIG. 3Ak

25 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
23759	>10	T90313	Hs.16732	ESTs
21238	>10	R08564	Hs.51919	Plasminogen-like protein
2857	>10	M58597	Hs.2173	Fucosyltransferase 4 (alpha (13) fucosyltransferase myeloid-specific)
34518	>10	AA278721	Hs.103104	ESTs
18008	>10	AA171895	Hs.30057	Homo sapiens clone 24749 and 24750 mRNA sequences
19001	>10	H02890	Hs.29885	ESTs
39488	>10	D60831	Hs.126021	ESTs
23360	>10	T58531	Hs.141905	ESTs
34105	>10	AA207123	Hs.130857	ESTs
38121	>10	AA485724		EST - RC_AA485724
35038	>10	AA350541	Hs.106601	ESTs Moderately similar to URACIL-DNA GLYCOSYLASE 1 PRECURSOR [H.sapiens]
29080	>10	F13655	Hs.65638	ESTs Moderately similar to !!! ALU SUBFAMILY SB1 WARNING ENTRY !!!! [H.sapiens]
3196	>10	M86917	Hs.143065	Oxysterol binding protein
9723	>10	L44542	Hs.126923	ESTs
25215	>10	AA035540	Hs.1255	APOLIPOPROTEIN A1 REGULATORY PROTEIN-1
2627	>10	M29610	Hs.93223	Glycophorin E
39218	>10	AA621330	Hs.114381	ESTs
20088	>10	N20054	Hs.20325	ESTs Weakly similar to putative p150 [H.sapiens]
22557	>10	R76722	Hs.29557	ESTs
30265	>10	N35115	Hs.44698	ESTs
33713	>10	Z39427	Hs.65748	ESTs
41678	>10	R80675	Hs.144133	EST
18392	>10	AA227751	Hs.55896	ESTs

FIG._3A1

26 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
42390	>10	W40150	Hs.24485	Homo sapiens chromosome-associated polypeptide (HCAP) mRNA complete cds
38984	>10	AA609839	Hs.61060	ESTs Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
35693	>10	AA405485	Hs.96854	ESTs Weakly similar to similar to t complex testis-specific protein [C.elegans]
35500	>10	AA400715	Hs.107479	ESTs
1856	>10	L18920	Hs.36980	MELANOMA-ASSOCIATED ANTIGEN 2
36258	>10	AA423962	Hs.108465	ESTs Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
37068	>10	AA446312	Hs.22143	ESTs Weakly similar to !!!! ALU CLASS C WARNING ENTRY !!!! [H.sapiens]
33020	>10	W46891	Hs.55968	ESTs Weakly similar to polypeptide N-acetylgalactosaminyltransferase [H.sapiens]
41719	>10	R89260	Hs.6333	EST - RC_R89260
39725	>10	H11323	Hs.93753	ESTs
27037	>10	AA400198	Hs.48920	ESTs
40827	>10	N64051	Hs.54681	Homo sapiens Werner syndrome gene complete cds
31872	>10	N91109	Hs.80132	EST
25934	>10	AA165355	Hs.37104	Human clone iota unknown protein mRNA complete cds
3406	>10	S66896	Hs.108642	SQUAMOUS CELL CARCINOMA ANTIGEN 1
3375	>10	S50223	Hs.99246	HKR-T1
37310	>10	AA451707	Hs.105223	ESTs
38235	>10	AA489030	Hs.26536	ESTs
22258	>10	R56432	Hs.82292	ESTs
787	>10	D86969	Hs.44841	Human mRNA for KIAA0215 gene complete cds
27787	>10	AA454660		ESTs

FIG.-3Am

27 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
36845	>10	AA436198	Hs.103902	ESTs
6095	>10	X69962	Hs.89764	Fragile X mental retardation 1
28323	>10	AA599639	Hs.50216	ESTs
30207	>10	N33920	Hs.44532	H.sapiens mRNA for diubiquitin
30631	>10	N50807	Hs.47120	EST
6494	>10	X92689	Hs.55823	H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyl transferase
36288	>10	AA424502	Hs.98402	ESTs
37546	>10	AA456641	Hs.99433	ESTs
4193	>10	U31116	Hs.77501	Human beta-sarcoglycan A3b mRNA complete cds
25669	>10	AA128978	Hs.141982	ESTs
37777	>10	AA464860	Hs.115541	Homo sapiens Jak2 kinase mRNA complete cds
38280	>10	AA489791	Hs.79306	EST - RC_AA489791
2343	>10	M15353		Eukaryotic translation initiation factor 4E
976	>10	G2036-HT2090		EST - HG2036-HT2090
39045	>10	AA610077	Hs.102314	ESTs
35495	>10	AA400527	Hs.111914	ESTs
3522	>10	S80267	Hs.74101	Spleen tyrosine kinase
22282	>10	R59197	Hs.21320	ESTs
32740	>10	T92950	Hs.91077	ESTs
5802	>10	X55544	Hs.36908	CYCL C-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-1
37057	>10	AA446131	Hs.124918	ESTs
34107	>10	AA209469	Hs.96297	ESTs
34391	>10	AA252703		EST - RC_AA252703
33301	>10	W73883	Hs.58174	ESTs
30790	>10	N52935	Hs.47580	EST

FIG._3An

28 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
38172	>10	AA487424		EST - RC_AA487424
24915	>10	YEL003w/		EST - YEL003w/
37492	>10	AA455248		EST - RC_AA455248
765	>10	D86096	Hs.495	Prostaglandin E receptor 3 (subtype EP3) {alternative products}
7785	>10	AA243375		EST - AA243375
14708	>10	D59388	Hs.34712	EST
34070	>10	AA196549	Hs.6592	ESTs
6041	>10	X67155	Hs.75530	MITOTIC KINESIN-LIKE PROTEIN-1
33890	>10	HUMTFRR/M11507		AFFX-HUMTFRR/M11507_5
35277	>10	AA398536	Hs.97365	ESTs
26059	>10	AA236685	Hs.58940	ESTs
25801	>10	AA148530		EST - RC_AA148530
32258	>10	R55623	Hs.26434	ESTs
34554	>10	AA280016	Hs.80961	DNA polymerase gamma
32034	>10	N98926	Hs.55209	ESTs Moderately similar to DMR-N9 PROTEIN [H.sapiens]
4787	>10	U61145	Hs.77256	Human enhancer of zeste homolog 2 (EZH2) mRNA complete cds
1684	>10	L07541	Hs.9969	Replication factor C (activator 1) 3 (38kD)
18718	>10	F04915	Hs.22226	ESTs
11121	>10	AA156359	Hs.7786	Human TAR DNA-binding protein-43 mRNA complete cds
38167	>10	AA487207		EST - RC_AA487207
40427	>10	N21147	Hs.121688	ESTs
40444	>10	N22140	Hs.61541	ESTs Highly similar to TUBULIN GAMMA CHAIN [Euplotes octocarinatus]
32635	>10	T61116	Hs.90527	ESTs
21946	>10	R44707	Hs.22687	ESTs
4306	>10	U36798	Hs.777	Homo sapiens platelet cGI-PDE mRNA complete cds

FIG. 3Aa

29 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
38211	>10	AA488687	Hs.142639	ESTs
6438	>10	X89398	Hs.78853	URACIL-DNA GLYCOSYLASE 1 PRECURSOR
38838	>10	AA609215		EST - RC_AA609215
21412	>10	R20670	Hs.21388	ESTs
36981	>10	AA442845	Hs.98985	EST
38580	>10	AA598545	Hs.141444	ESTs
4945	>10	U69108	Hs.29736	Homo sapiens mRNA for TRAF5 complete cds
41654	>10	R76437	Hs.2001	THROMBOXANE-A SYNTHASE
41163	>10	R08176	Hs.20116	ESTs
34400	>10	AA253400	Hs.104326	ESTs
35822	>10	AA411144	Hs.104768	ESTs
40905	>10	N68738	Hs.125026	ESTs
26628	>10	AA280641	Hs.40128	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L39 [Rattus norvegicus]
3799	>10	U10690	Hs.37108	Human MAGE-5a antigen (MAGE5a) gene complete cds
41752	>10	R97063	Hs.102020	ESTs
39302	>10	C14944	Hs.12136	ESTs
4680	>10	U55766	Hs.54485	Human Rev interacting protein Rip-1 mRNA complete cds
36506	>10	AA429610	Hs.98592	ESTs
40204	>10	H88296		EST - RC_H88296
19164	>10	H10395	Hs.30980	EST
36571	>10	AA430726		EST - RC_AA430726
26240	>10	AA252282	Hs.90438	Human mRNA for KIAA0152 gene complete cds
8963	>10	HUMTFRR/M11507		AFFX-HUMTFRR/M11507_M
34575	>10	AA280738	Hs.128679	ESTs
35322	>10	AA398710	Hs.87195	H. sapiens RNA for CLCN3
1210	>10	HG37-HT37		EST - HG37-HT37

FIG.-3Ap

30 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
22793	>10	R96208	Hs.35533	ESTs
36052	>10	AA417027	Hs.104787	EST
26574	>10	AA279504	Hs.88629	ESTs
31818	>10	N89774	Hs.2223	Homo sapiens mRNA for KIAA0292 gene partial cds
35197	>10	AA398120	Hs.97504	ESTs
17600	>10	AA130596	Hs.71331	ESTs
37979	>10	AA479295	Hs.106290	ESTs Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]
4862	>10	U65437	Hs.95838	Human homeodomain-containing protein (HANF) mRNA complete cds
28122	>10	AA485928	Hs.69559	ESTs Weakly similar to LOK [M.musculus]
26700	>10	AA282197	Hs.89002	EST
38182	>10	AA487501	Hs.112329	ESTs
22593	>10	R79777	Hs.29897	EST
35049	>10	AA350857	Hs.22507	ESTs
40083	>10	H73466	Hs.79086	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3
7296	>10	AA085661	Hs.26023	ESTs
37615	>10	AA459101	Hs.79337	Human serine/threonine kinase mRNA partial cds
17541	>10	AA127459	Hs.108788	ESTs
19949	>10	H78263	Hs.124151	ESTs
4477	>10	U45880	Hs.37137	Human IAP-like protein ILP mRNA complete cds
26916	>10	AA331393	Hs.47378	ESTs
34188	>10	AA228030	Hs.120234	ESTs
37453	>10	AA454610	Hs.96538	ESTs
29229	>10	H48459	Hs.36232	Human mRNA for KIAA0186 gene complete cds
40760	>10	N57927	Hs.120777	ESTs Weakly similar to ELL [M.musculus]
5149	>10	U79716	Hs.12246	Human reelin (RELN) mRNA complete cds

FIG.-3Aq

31 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
42773	>10	L019c/MMS21		EST - Y019c/MMS21
32189	>10	R43183	Hs.95044	ESTs
33556	>10	W90705	Hs.431	Murine leukemia viral (bmi-1) oncogene homolog
36739	>10	AA435610		EST - RC_AA435610
31310	>10	N66831	Hs.49268	EST
26545	>10	AA278979	Hs.88547	ESTs
21902	>10	R43822	Hs.22691	EST
25925	>10	AA164494	Hs.29417	ESTs Weakly similar to CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 [H.sapiens]
29344	>10	H68839	Hs.38782	EST
1346	>10	G4716-HT5158		EST - HG4716-HT5158
35874	>10	AA412024	Hs.104732	EST
218	>10	D13540	Hs.22868	PROTEIN-TYROSINE PHOSPHATASE 2C
26100	>10	AA242835	Hs.5917	Human mRNA for KIAA0391 gene complete cds
41593	>10	R64129	Hs.143745	ESTs
42290	>10	T95105	Hs.142670	ESTs
6713	>10	Y08564		EST - Y08564
6478	>10	X91648	Hs.29117	H.sapiens mRNA for pur alpha extended 3'untranslated region
33377	>10	W81219	Hs.42636	ESTs Weakly similar to F46B6.7 [C.elegans]
39329	>10	C20797	Hs.95481	EST
31619	>10	N73449	Hs.50273	ESTs
26718	10.0	AA282576	Hs.49407	ESTs
21558	10.0	R33112	Hs.100469	Human AF-6 mRNA complete cds
40113	10.0	H78003	Hs.15266	ESTs
10801	10.0	AA069285	Hs.9922	ESTs Weakly similar to PROBABLE UBIQUITIN CARBOXYL- TERMINAL HYDROLASE R10E11.3 [C.elegans]

FIG._3Ar

32 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
37491	10.0	AA455239	Hs.87630	ESTs Highly similar to CHROMOSOME CONDENSATION PROTEIN DPY-27 [Caenorhabditis elegans]
23900	9.9	T95789	Hs.17669	ESTs
254	9.9	D14657	Hs.81892	Human mRNA for KIAA0101 gene complete cds
6885	9.9	Z29331	Hs.28505	Ubiquitin-conjugating enzyme E2H (homologous to yeast UBC8)
29693	9.9	H97819	Hs.42453	ESTs
26482	9.9	AA262491	Hs.47222	ESTs
23123	9.9	T25306	Hs.13595	EST
26525	9.8	AA278392	Hs.43881	ESTs
13110	9.8	AA435840	Hs.19114	Homo sapiens mRNA for high mobility group protein HMG2a
34863	9.7	AA299784	Hs.96641	EST
39432	9.7	D51691	Hs.82285	Phosphoribosylglycinamide formyltransferase phosphoribosylglycinamide synthetase phosphoribosylaminoimidazole synthetase
31312	9.7	N66845	Hs.136910	ESTs Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]
21112	9.6	R01179	Hs.112536	ESTs
31572	9.6	N71294	Hs.110524	ESTs
17903	9.6	AA160259	Hs.72354	EST
20747	9.6	N66842	Hs.16395	ESTs
4676	9.6	U55206	Hs.78619	Homo sapiens human gamma-glutamyl hydrolase (hGH) mRNA complete cds
34363	9.6	AA251587	Hs.10801	Homo sapiens mRNA for KIAA0530 protein partial cds
39094	9.5	AA620636	Hs.112264	ESTs
3888	9.5	U15128	Hs.36573	Human beta-12-N-acetylglucosaminyltransferase II (MGAT2) gene complete cds

FIG. 3As

33 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
39386	9.5	D12184	Hs.3350	ESTs
7674	9.4	AA203742	Hs.38057	ESTs
4192	9.4	U31099	Hs.121479	Human DP prostanoid receptor (PTGDR) mRNA partial cds
4507	9.4	U47050	Hs.24852	Human putative calcium influx channel (htrp3) mRNA complete cds
35606	9.4	AA402227	Hs.97345	ESTs Moderately similar to N-tropomodulin [R.norvegicus]
4970	9.4	U70862	Hs.23442	Human nuclear factor I-B2 (NFIB2) mRNA complete cds
19829	9.3	H58813	Hs.37629	EST
14837	9.3	T40145	Hs.21921	ESTs
17336	9.3	AA099585	Hs.41175	ESTs
40541	9.3	N30160	Hs.101459	ESTs
29496	9.2	H85434	Hs.40672	EST
29943	9.2	N24786	Hs.42993	ESTs Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
17997	9.2	AA169633	Hs.72835	EST
21320	9.1	R11673	Hs.18957	ESTs
13883	9.1	AA476917	Hs.34627	ESTs Weakly similar to No definition line found [C.elegans]
30539	9.1	N49072	Hs.93968	ESTs
32778	9.1	W02063	Hs.55231	EST
26380	9.1	AA257012	Hs.88054	EST
15888	9.1	X95632	Hs.86870	Human Abl interactor 2 (Abi-2) mRNA complete cds
40812	9.0	N63419	Hs.83389	ESTs
903	9.0	D90070	Hs.96	ATL-derived PMA-responsive (APR) peptide
22674	9.0	R87160	Hs.33665	ESTs
40807	9.0	N62995	Hs.58593	TRANSCRIPTION INITIATION FACTOR IIF BETA SUBUNIT
15244	8.9	W00904	Hs.8037	ESTs
32296	8.9	R67075	Hs.2074	Zinc finger protein X-linked

FIG._3A

34 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
18269	8.9	AA209467	Hs.92489	ESTs
19662	8.9	H47391	Hs.33947	ESTs
41607	8.8	R67868	Hs.82767	CLEAVAGE SIGNAL-1 PROTEIN
2548	8.8	M25897	Hs.81564	Platelet factor 4
7736	8.8	AA232121	Hs.109631	Human tyrosyl-tRNA synthetase mRNA complete cds
34490	8.8	AA262354	Hs.111395	ESTs
38658	8.8	AA599477	Hs.103345	ESTs
7528	8.8	AA149543	Hs.5316	ESTs
39939	8.8	H53454	EST - FC_H53454	
25111	8.7	AA020787	Hs.110291	ESTs
21655	8.7	R38239	Hs.25276	EST
39663	8.7	H04756	Hs.109646	ESTs Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE B17 SUBUNIT [Bos taurus]
1042	8.7	G2510-HT2606	EST - HG2510-HT2606	
32330	8.6	R77776	Hs.18103	ESTs
25382	8.6	AA059007	Hs.61126	ESTs
27074	8.6	AA401475	Hs.39733	ESTs Weakly similar to C36B1.3 [C.elegans]
3955	8.5	U18259	Hs.3076	MHC class II transactivator
4959	8.5	U70322	Hs.82925	Human transportin (TRN) mRNA complete cds
2315	8.5	M14123	EST - M14123_xpt1	
37253	8.5	AA449357	Hs.17731	ESTs
39624	8.5	F10836	Hs.101234	ESTs
23213	8.5	T40891	Hs.8330	ESTs
2798	8.5	M54995	Hs.2164	Connective tissue activation peptide III
41154	8.4	R07499	Hs.141384	ESTs
32479	8.4	T16282	Hs.75188	WEE1-LIKE PROTEIN KINASE
41251	8.4	R28279	Hs.71848	Human clone 23548 mRNA sequence

FIG. 3Au

35 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
19081	8.4	H06701	Hs.27948	ESTs Weakly similar to RHOMBOTIN-1 [H.sapiens]
21098	8.3	R00545	Hs.18930	ESTs
14723	8.3	D59894	Hs.34782	ESTs
37154	8.3	AA447666	Hs.77204	Human CENP-F kinetochore protein mRNA complete cds
8068	8.3	AA313387	Hs.133101	ESTs Highly similar to HYPOTHETICAL 84.7 KD PROTEIN ZK1093.1 IN CHROMOSOME III [Caenorhabditis elegans]
7485	8.3	AA129547	Hs.81688	ESTs
16501	8.3	AA026969	Hs.61423	ESTs
34527	8.2	AA279091	Hs.104420	ESTs
6700	8.2	Y07867	Hs.38842	H.sapiens mRNA for Pirin isolate 1
2852	8.2	M58460	Hs.91728	Human 75-kD autoantigen (PM-Sc1) mRNA complete cds
11188	8.2	AA172372	Hs.20608	ESTs
42293	8.2	T95333	Hs.122730	ESTs Weakly similar to coded for by C. elegans cDNA yk110g8.3 [C.elegans]
5443	8.2	X02530	Hs.2248	Interferon (gamma)-induced cell line protein 10 from
40937	8.2	N70607	Hs.142460	ESTs
23371	8.1	T59505	EST - RC_T59505	EST - RC_T59505
26272	8.1	AA252981	Hs.87699	ESTs Weakly similar to K07C11.10 gene product [C.elegans]
17306	8.1	AA086201	Hs.92702	ESTs
18497	8.1	AA233795	Hs.65828	ESTs
235	8.1	D13644	Hs.140933	Human mRNA for KIAA0019 gene complete cds
24525	8.1	Z38347	Hs.118338	ESTs
7826	8.1	AA248884	EST - AA248884	EST - AA248884
32142	8.1	R38715	Hs.123918	Homo sapiens clone 24540 mRNA sequence
39067	8.1	AA620405	Hs.112860	ESTs
6235	8.0	X78416	Hs.3155	Casein alpha S1
29517	8.0	H88261	Hs.41116	ESTs

FIG.-3Av

36 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
28570	8.0	C21104	Hs.110776	Homo sapiens STAT-induced STAT inhibitor-2 mRNA
39344	7.9	C21034	Hs.76822	complete cds ESTs Moderately similar to initiation factor eIF-2B gamma subunit [R.norvegicus]
18951	7.9	H00580	Hs.29889	ESTs
18953	7.9	H00615	Hs.24227	ESTs
18376	7.9	AA226925	Hs.88057	ESTs
19830	7.8	H58911	Hs.26645	ESTs
36023	7.8	AA416881	Hs.97383	ESTs
13347	7.8	AA449238	Hs.26838	ESTs
36614	7.8	AA431466	Hs.107319	ESTs
2192	7.8	L48211	Hs.20954	Homo sapiens angiotensin II receptor gene complete cds
33016	7.8	W46577	Hs.41716	H.sapiens mRNA for ESM-1 protein
17215	7.8	AA083044	Hs.144225	ESTs
34894	7.8	AA311881	Hs.96700	EST
40614	7.7	N39257	Hs.99291	ESTs
36295	7.7	AA424534	Hs.98415	ESTs
19564	7.7	H38833	Hs.32838	ESTs
16914	7.7	AA058665	Hs.23744	ESTs
35967	7.6	AA412694	Hs.6891	Human splicing factor SRp55-2 (SRp55) mRNA complete cds
21672	7.6	R38635	Hs.12328	ESTs
19918	7.6	H69787	Hs.14699	ESTs
10511	7.6	AA024482	Hs.9029	ESTs Highly similar to KERATIN TYPE I CYTOSKELETAL 14 [Homo sapiens]
17721	7.6	AA136590	Hs.71711	ESTs
42302	7.6	T96130	Hs.137551	EST
26134	7.6	AA243763	Hs.87694	ESTs

FIG._3AW

37 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
18766	7.6	F09497	Hs.12755	ESTs
34492	7.5	AA262439	Hs.96	ATL-derived PMA-responsive (APR) peptide
270	7.5	D14822		EST - D14822
35975	7.4	AA412738	Hs.3688	ESTs
29842	7.4	N21688	Hs.43050	ESTs
35389	7.4	AA399555	Hs.97558	ESTs
19979	7.4	H88477	Hs.124237	ESTs
5793	7.4	X54942	Hs.83758	CDC28 protein kinase 2
19978	7.4	H87770		EST - RC_H87770
1280	7.4	G4126-HT4396		EST - HG4126-HT4396
31571	7.4	N71250	Hs.50004	ESTs
23765	7.4	T90443	Hs.15053	ESTs Weakly similar to KIAA0376 [H.sapiens]
35123	7.3	AA380927	Hs.97113	EST
38252	7.3	AA489247	Hs.105234	ESTs
38216	7.3	AA488861	Hs.134943	ESTs
29418	7.2	H77915		EST - RC_H77915
4834	7.2	U63541	Hs.20225	Human mRNA expressed in HC/HCC livers and MolT-4 proliferating cells partial sequence
42504	7.2	W69803	Hs.103159	ESTs
6111	7.2	X71125	Hs.79033	H.sapiens mRNA for glutamine cyclotransferase
41773	7.2	T03024	Hs.29170	ESTs Weakly similar to ribosomal protein L7 [H.sapiens]
9951	7.1	N71513	Hs.39328	ESTs
28109	7.1	AA485212	Hs.9591	ESTs
988	7.1	G2160-HT2230		EST - HG2160-HT2230
29848	7.1	N22107	Hs.124215	ESTs
30628	7.1	N50744	Hs.124025	ESTs
22567	7.0	R77771	Hs.129445	ESTs

FIG..3Ax

38 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
9347	7.0	H03686	Hs.112013	ESTs
11696	7.0	AA252894	Hs.20474	ESTs
40584	7.0	N34870	Hs.102520	EST
193	7.0	D10923	Hs.137555	PROBABLE G PROTEIN-COUPLED RECEPTOR HM74
18305	7.0	AA214048	Hs.259	Collagen type IV alpha 4
6078	7.0	X69141	Hs.48876	FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE
26741	6.9	AA283198	Hs.89113	ESTs
35069	6.9	AA358397	Hs.97007	EST
23504	6.9	T71042	Hs.12066	ESTs
299	6.9	D16815	Hs.37288	Homo sapiens orphan nuclear hormone receptor BD73 mRNA 3' end
40583	6.9	N34855	Hs.109099	ESTs
31428	6.9	N68594	Hs.125029	ESTs
6169	6.9	X75091	Hs.75055	SET PROTEIN
39524	6.9	F01905	Hs.14732	MALATE OXIDOREDUCTASE
34578	6.8	AA280837	Hs.111429	ESTs
38678	6.8	AA599920	Hs.141503	Small inducible cytokine A5 (RANTES)
23936	6.8	T96930	Hs.15553	ESTs
9326	6.8	D89377	Hs.89404	Msh (Drosophila) homeo box homolog 2
19188	6.8	H11255	Hs.12887	ESTs Highly similar to ACTIN-LIKE PROTEIN [Bos taurus]
18185	6.8	AA194983	Hs.81791	Homo sapiens mRNA for osteoclastogenesis inhibitory factor (OCIF) complete cds
27028	6.8	AA399630	Hs.94396	ESTs Weakly similar to KIAA0371 [H.sapiens]
41289	6.8	R37265	Hs.106266	EST
34511	6.7	AA278298		EST - HC_AA278298
1566	6.7	J05614		EST - J05614

FIG.-3Ay

39 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
25675	6.7	AA129757	Hs.54602	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L22 [Rattus norvegicus]
5814	6.7	X56088	Hs.1644	CYTOKROME P450 VII
13861	6.6	AA470145	Hs.25130	ESTs
29794	6.6	N20598	Hs.94288	ESTs
39333	6.6	C20910	Hs.23960	Cyclin 31
3770	6.6	U09609	Hs.73090	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)
31831	6.6	N89894	Hs.91454	ESTs
33063	6.6	W53000	Hs.56155	Homo sapiens clone 24431 mRNA sequence
20326	6.6	N35583	Hs.8768	ESTs Weakly similar to PROBABLE E5 PROTEIN [Human papillomavirus type 58]
34384	6.6	AA252537	Hs.96499	ESTs
25599	6.5	AA114091	Hs.44898	Human (clone 8B1) Br-cadherin mRNA complete cds
39749	6.5	H14988	Hs.107375	ESTs
42596	6.5	W85900	Hs.109333	ESTs
39606	6.5	F10243	Hs.140873	ESTs Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]
14617	6.5	C14983	Hs.37380	ESTs
27831	6.5	AA456044	Hs.40367	ESTs
34896	6.4	AA312551	Hs.96703	EST
27360	6.4	AA425356	Hs.89306	ESTs
20126	6.4	N22015	Hs.18457	ESTs
6663	6.4	Y00291	Hs.82783	RETINOIC ACID RECEPTOR BETA-2
30692	6.4	N51563	Hs.47044	ESTs
36472	6.4	AA428633	Hs.98604	EST
9578	6.4	H87652	Hs.24912	Homo sapiens bicaudal-D (BICD) mRNA complete cds

FIG. 3Az

40 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
39670	6.4	H05626	Hs.6921	ESTs
22697	6.4	R89218	Hs.34256	ESTs
37308	6.4	AA451694	Hs.99244	EST
16101	6.4	AA002147	Hs.59952	EST
20629	6.3	N59798	Hs.18917	ESTs
36100	6.3	AA417740	Hs.96345	ESTs
15488	6.3	W28097	Hs.101664	Homo sapiens clone 23711 unknown mRNA partial cds
36667	6.3	AA432136	Hs.98682	ESTs
30766	6.3	N52627	EST - FIC_N52627	
32882	6.3	W37683	Hs.55080	ESTs
18072	6.3	AA180448	Hs.144300	EST
18231	6.3	AA199747	Hs.79025	Human mRNA for KIAA0096 gene partial cds
38282	6.3	AA489814	Hs.105299	EST
28125	6.3	AA486073	Hs.57362	ESTs
37464	6.2	AA454747	Hs.14934	ESTs
36618	6.2	AA431478	Hs.98739	ESTs
5082	6.2	U78524	Hs.75251	Human Gu binding protein mRNA partial cds
1441	6.2	J02963	Hs.785	Integrin alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex antigen CD41B)
42105	6.1	T67710	Hs.105780	ESTs
6061	6.1	X68314	Hs.2704	Glutathione peroxidase 2 gastrointestinal
32570	6.1	T30222	Hs.4220	ESTs Weakly similar to tetracycline transporter-like protein [M.musculus]
32504	6.1	T17063	Hs.65721	EST
23335	6.1	T56804	Hs.10104	EST
10867	6.1	AA088458	Hs.19322	ESTs Weakly similar to !!!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]

FIG.-3Ba

41 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
30883	6.1	N56923	Hs.48000	EST
14528	6.1	AA620295	Hs.99821	ESTs
29454	6.1	H81308	Hs.40253	EST
6798	6.1	Y13153	Hs.28526	Human sapiens mRNA for kynurenine 3-monooxygenase
21248	6.1	R08871	Hs.14880	ESTs
21940	6.0	R44538	Hs.140889	ESTs
29066	6.0	F10927	Hs.66163	Human sapiens clone 23636 mRNA sequence
18774	6.0	F09609	Hs.12867	ESTs
36722	6.0	AA435512	Hs.96856	ESTs
18062	6.0	AA179845	Hs.73625	ESTs Moderately similar to rabkinesin-6 [M.musculus]
22989	6.0	T16305	Hs.49349	ESTs
41745	6.0	R95895	Hs.142677	ESTs
8787	6.0	AA504307	Hs.96264	X-LINKED HELICASE II
20550	6.0	N55013	Hs.35100	ESTs
26470	5.9	AA262179	Hs.108470	ESTs
16574	5.9	AA031926	Hs.138960	EST
693	5.9	D80007	Hs.45028	Human mRNA for KIAA0185 gene partial cds
4093	5.9	U25182	Hs.83383	Human antioxidant enzyme AOE37-2 mRNA complete cds
1192	5.9	G3546-HT3744		EST ..HG3546-HT3744
22956	5.9	T10248	Hs.4280	ESTs
36723	5.9	AA435524	Hs.97483	EST
2114	5.9	L40384		EST ..L40384
26872	5.9	AA291137	Hs.109270	ESTs
6602	5.9	X98266		EST ..X98266_cds2
42701	5.9	Z38612	Hs.144000	ESTs
28573	5.8	C21118	Hs.84541	ESTs
18290	5.8	AA211901	Hs.86430	ESTs

FIG. 3Bb

42 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
732	5.8	D83781	Hs.22559	Human mRNA for KIAA0197 gene partial cds
5330	5.8	U91327	EST - U91327	EST - U91327
33503	5.8	W88720	Hs.59196	EST
2553	5.8	M26167	Hs.72933	Human platelet factor 4 variation 1 (PF4var1) gene complete cds
34705	5.8	AA286907	Hs.99692	ESTs Weakly similar to putative p150 [H.sapiens]
42665	5.8	W93659	Hs.106932	ESTs
38180	5.8	AA487495	EST - RC_AA487495	EST - RC_AA487495
4244	5.7	U33286	Hs.90073	Human chromosome segregation gene homolog CAS mRNA complete cds
32822	5.7	W16834	Hs.55378	ESTs
3977	5.7	U18991	Hs.2133	Retinal pigment epithelium-specific protein (65kD)
24673	5.7	Z39301	Hs.7859	ESTs
6928	5.7	Z46629	Hs.2316	SRY (sex-determining region Y)-box 9 (campomelic dysplasia autosomal sex-reversal)
38726	5.7	AA608733	Hs.138663	ESTs
39290	5.7	C14573	Hs.75383	Human mRNA for KIAA0029 gene partial cds
11405	5.7	AA232231	Hs.24596	ESTs
22538	5.7	R73567	Hs.8850	Human sapiens meltrin-L precursor (ADAM12) mRNA complete cds
40747	5.7	N56872	Hs.11175	Human sapiens clone 22 mRNA alternative splice variant alpha-1 complete cds
31596	5.7	N72094	Hs.43234	ESTs
6329	5.6	X82279	EST - X82279	EST - X82279
31578	5.6	N71361	Hs.50019	ESTs
33207	5.6	W70051	Hs.86178	H.sapiens mRNA for M-phase phosphoprotein mpp9
2545	5.6	M25753	Hs.23960	Cyclin B1

FIG. 3Bc

43 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
22580	5.6	R79156	Hs.29613	ESTs
33592	5.6	W93127	Hs.59422	ESTs
28843	5.6	D60252	Hs.113619	ESTs
6160	5.6	X74794	Hs.89699	CDC21 HOMOLOG
37987	5.6	AA479666	Hs.105576	ESTs
42515	5.5	W72116	Hs.106333	Human sapiens clone 23622 mRNA sequence
4732	5.5	U58522	Hs.84713	Human huntingtin interacting protein (HIP2) mRNA complete cds
3299	5.5	M95623	Hs.82609	Hydroxymethylbilane synthase
28320	5.5	AA599574	Hs.65370	ESTs
746	5.5	D84454	Hs.21899	Human mRNA for UDP-galactose translocator complete cds
39373	5.5	C21517	Hs.83313	ESTs
3117	5.4	M81182	Hs.76781	Peroxisomal membrane protein 1 (70kD Zellweger syndrome)
21257	5.4	R09196	Hs.20321	ESTs: Moderately similar to M-phase phosphoprotein 11 [H.sapiens]
31487	5.4	N69507	Hs.129849	ESTs
28954	5.4	F03153	Hs.90383	ESTs
38928	5.4	AA609595	Hs.109960	ESTs
29903	5.4	N23366	Hs.93664	EST
30925	5.3	N58295	Hs.144393	ESTs: Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]
19091	5.3	H07864	Hs.21734	ESTs
28209	5.3	AA491250	Hs.54990	ESTs
9470	5.3	H46617		EST - H46617
9435	5.3	H30201		EST - H30201
28552	5.3	C20914	Hs.84497	ESTs
27411	5.3	AA428137	Hs.86434	ESTs

FIG..3Bd

44 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
30615	5.3	N50556	Hs.47076	ESTs
28313	5.3	AA599309	Hs.60886	ESTs
39321	5.3	C20632	Hs.7972	ESTs
29934	5.3	N24194	Hs.43531	ESTs
1094	5.2	G2846-HT2983		EST - HG2846-HT2983
39578	5.2	F08925	Hs.48610	ESTs
11232	5.2	AA186804	Hs.25740	ESTs Weakly similar to unknown [S.cerevisiae]
2466	5.2	M21539	Hs.2421	Human small proline rich protein (sprl) mRNA clone 1292
26843	5.2	AA287450	Hs.93842	ESTs
40331	5.2	H97562	Hs.4206	ESTs Weakly similar to SPERMATID-SPECIFIC PROTEIN T2 [Sepia officinalis]
8035	5.2	AA305116		EST - AA305116
29793	5.2	N20593	Hs.128781	ESTs Weakly similar to weak similarity to procollagen alpha chain 1(V) chain [C.elegans]
34109	5.1	AA210722	Hs.104158	EST
26408	5.1	AA258177	Hs.38399	ESTs Weakly similar to ROSA26AS [M.musculus]
19263	5.1	H15054	Hs.22184	ESTs
24596	5.1	Z38810	Hs.27194	ESTs
28589	5.1	C21245	Hs.11171	H.sapiens mRNA for apoptosis specific protein
5684	5.1	X17098	Hs.108938	Pregnancy-specific beta-1 glycoprotein 6
30710	5.1	N51761	Hs.47338	EST
35765	5.1	AA406167	Hs.98028	EST
26360	5.1	AA256460	Hs.44610	ESTs
2351	5.1	M15796	Hs.78996	Proliferating cell nuclear antigen
30262	5.1	N35065	Hs.44690	Human sapiens clone 24739 mRNA sequence
41792	5.1	T03886	Hs.100265	ESTs
36710	5.1	AA434411	Hs.98806	ESTs

FIG._3Be

45 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
39090	5.1	AA620628	Hs.112358	ESTs
42185	5.1	T79951	Hs.111805	ESTs
18745	5.0	F09134	Hs.12839	ESTs
35746	5.0	AA406063	Hs.98003	ESTs
35356	5.0	AA399053	Hs.97529	EST
36769	5.0	AA435750	Hs.98830	EST
36900	5.0	AA436866	Hs.86178	H.sapiens mRNA for M-phase phosphoprotein mpp9
27595	5.0	AA443328	Hs.12544	ESTs
16290	5.0	AA016145	Hs.42979	ESTs
27117	5.0	AA405098	Hs.38178	ESTs Weakly similar to MOESIN/EZRIN/RADIXIN HOMOLOG [D.melanogaster]
4304	5.0	U36764	Hs.89996	Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit
33458	5.0	W86835	Hs.14158	Human sapiens mRNA for KIAA0636 protein complete cds
26693	5.0	AA282120	Hs.88975	EST
12669	5.0	AA417030	Hs.5101	Human sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds
29701	5.0	H97970	Hs.42476	EST
20480	5.0	N52168	Hs.22970	ESTs
8720	4.9	AA481218	EST - AA481218	
34828	4.9	AA292436	Hs.27621	Human sapiens semaphorin F homolog mRNA complete cds
14985	4.9	U15128	Hs.36573	Human beta-12-N-acetylglucosaminyltransferase II (MGAT2) gene complete cds
16115	4.9	AA004420	Hs.49360	ESTs
42506	4.9	W70074	Hs.103163	EST
34761	4.9	AA287833	Hs.99668	ESTs
11870	4.9	AA262587	Hs.20137	ESTs
23211	4.9	T40889	Hs.8329	ESTs

FIG. 3Bf

46 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
40611	4.9	N39138	Hs.106794	Homo sapiens mRNA for KIAA0584 protein partial cds
42611	4.9	W87006	Hs.79440	Homo sapiens putative RNA binding protein KOC (koc) mRNA complete cds
39652	4.9	H03099	Hs.101619	ESTs
17581	4.9	AA129395	Hs.71139	EST
37239	4.9	AA449121	Hs.99210	ESTs
18712	4.9	F04677	Hs.12381	ESTs
30709	4.9	N51752	Hs.47334	ESTs Weakly similar to synapse-associated protein sap47-1 [D.melanogaster]
34179	4.9	AA227903	Hs.41127	ESTs Highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluorescens]
21433	4.8	R22183	Hs.144123	EST
39731	4.8	H11760	Hs.23606	ESTs
31295	4.8	N66653	Hs.94181	ESTs
24647	4.8	Z39108	Hs.27285	EST
31292	4.8	N66615	Hs.49232	ESTs
1285	4.8	G4157-HT4427	EST - HG4157-HT4427	
1106	4.8	G2981-HT3127	EST - HG2981-HT3127	
18212	4.8	AA196506	Hs.86076	ESTs
34367	4.8	AA251758	Hs.40323	Homo sapiens spleen mitotic checkpoint BUB3 (BUB3) mRNA complete cds
34802	4.8	AA291468	Hs.98504	ESTs
34762	4.8	AA287834	Hs.109909	ESTs
11595	4.8	AA242819	Hs.32539	ESTs
8295	4.8	AA405082	Hs.125014	ESTs
17622	4.8	AA131584	Hs.71435	ESTs Weakly similar to SOF1 PROTEIN [Saccharomyces cerevisiae]

FIG. 3Bg

47 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
35781	4.8	AA406335	Hs.95187	ESTs
34754	4.7	AA287642	Hs.81848	Human mRNA for KIAA0078 gene complete cds
23237	4.7	T47291	Hs.8610	EST
37667	4.7	AA460318	Hs.110165	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L26 [Rattus norvegicus]
11568	4.7	AA236786	Hs.26076	ESTs
38622	4.7	AA598967	Hs.141982	ESTs
5137	4.7	U79296	Hs.74642	Dihydroipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)
25038	4.7	AA010065	Hs.83758	CTC28 protein kinase 2
19288	4.7	H16567	Hs.21253	ESTs
32503	4.7	T17045	Hs.90283	Collagen type I alpha-2
3278	4.7	M94055	Hs.54499	SODIUM CHANNEL PROTEIN BRAIN II ALPHA SUBUNIT
9696	4.7	L38961	Hs.89650	Integral transmembrane protein 1
35400	4.7	AA399591	Hs.97681	Homo sapiens putative DNA methyltransferase (DNMT2) mRNA complete cds
35246	4.7	AA398367	Hs.97617	EST Weakly similar to HSP60 protein [M.musculus]
36387	4.7	AA426270	Hs.98498	ESTs
21509	4.7	R27314	Hs.23820	ESTs
31381	4.7	N67889	Hs.49397	ESTs
26723	4.7	AA282781	Hs.95321	ESTs Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP28 [Saccharomyces cerevisiae]
36326	4.7	AA425151	Hs.79310	Human GAP SH3 binding protein mRNA complete cds
17409	4.7	AA113136		EST - RC_AA113136
4908	4.7	U67156	Hs.84149	Human mitogen-activated kinase kinase kinase 5 (MAPKKK5) mRNA complete cds
30594	4.6	N49967	Hs.46624	ESTs

FIG..3Bh

48 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
38286	4.6	AA489847	Hs.112019	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOIOG [Nycticebus coucang]
13073	4.6	AA433950	Hs.22530	ESTs
40435	4.6	N21614	Hs.100358	Homo sapiens basic-leucine zipper transcription factor MafG (MAFG) mRNA complete cds
14474	4.6	AA609427	Hs.24164	ESTs Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]
38213	4.6	AA488847	Hs.111380	ESTs Weakly similar to putative p150 [H.sapiens]
5312	4.6	U90716	Hs.79187	Human cell surface protein HCAR mRNA complete cds
24225	4.6	W70326	Hs.16506	ESTs
35588	4.6	AA401750	Hs.97343	EST
29739	4.6	H99626	Hs.42710	EST
7203	4.6	AA053096	EST - AA053096	
2157	4.6	L41939	Hs.89403	Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA complete cds
32086	4.6	R11510	Hs.52054	ESTs
8085	4.6	AA314779	Hs.105484	ESTs Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
224	4.6	D13633	Hs.77695	Human mRNA for KIAA0008 gene complete cds
34006	4.6	AA188761	Hs.80961	DNA polymerase gamma
33656	4.6	W95477	Hs.50582	ESTs
34065	4.6	AA195517	Hs.111160	ESTs Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
6028	4.5	X66503	Hs.90011	Adenylosuccinate synthase
4166	4.5	U29463	Hs.108102	Cytochrome B561
40262	4.5	H93562	Hs.100624	ESTs
22687	4.5	R88209	Hs.34161	ESTs

FIG. 3Bi

49 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
41069	4.5	N93969	Hs.91107	H. sapiens mRNA for hFat protein
8264	4.5	AA401334	Hs.106941	ESTs
27588	4.5	AA443187	Hs.41181	ESTs
35882	4.5	AA412047	Hs.122578	ESTs
34479	4.5	AA262080	Hs.110736	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1)
15921	4.5	Y12065	Hs.5092	mRNA complete cds
11279	4.4	AA195399	Hs.24641	Homio sapiens mRNA for nucleolar protein hNop56
39222	4.4	AA621348	Hs.110042	ESTs
34428	4.4	AA256526	Hs.121002	ESTs Highly similar to DOLICHYL-PHOSPHATE BETA-GLUCOSYLTRANSFERASE [Saccharomyces cerevisiae]
8771	4.4	AA491188	Hs.62273	ESTs
22193	4.4	R53891	Hs.108805	Homio sapiens mRNA from chromosome 5q21-22
7898	4.4	AA263032	Hs.81634	clone A3-A
19902	4.4	H66736	Hs.34180	ESTs
9276	4.4	D82374	Hs.131854	ESTs
10716	4.4	AA053319	Hs.9951	ESTs
13193	4.4	AA442763	Hs.20483	ESTs Highly similar to G2/MITOTIC-SPECIFIC CYCLIN B2 [Mesocricetus auratus]
5690	4.4	X17620	Hs.118638	NUCLEOSIDE DIPHOSPHATE KINASE A
35102	4.4	AA371509		EST - RC_AA371509
17983	4.4	AA169226	Hs.72782	ESTs
24962	4.3	HUMTFRR/M11507		AFFX-HUMTFRR/M11507_5
31680	4.3	N74438	Hs.50492	ESTs
27168	4.3	AA410258	Hs.85908	ESTs
28731	4.3	D20981	Hs.92453	EST

FIG.-3Bj

50 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
28348	4.3	AA608752	Hs.71969	ESTs
16335	4.3	AA018587	Hs.40515	ESTs Weakly similar to !!!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]
33036	4.3	W48580	Hs.39972	ESTs Weakly similar to transposon LRE2 reverse transcriptase homolog [H.sapiens]
30180	4.3	N33144	Hs.44441	ESTs
35591	4.3	AA401758	Hs.78041	ESTs Weakly similar to !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]
25340	4.3	AA054554	Hs.95313	EST
28106	4.3	AA485084	Hs.110462	ESTs
38690	4.3	AA600121	Hs.111467	ESTs
20203	4.3	N26855	Hs.5858	ESTs Moderately similar to !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]
10251	4.3	R76185	Hs.18171	ESTs Weakly similar to C01H6.7 [C.elegans]
12684	4.3	AA417558	Hs.25206	ESTs
31636	4.3	N73680	Hs.57435	Natural resistance-associated macrophage protein 2
20769	4.2	N67277	Hs.9403	ESTs
1572	4.2	K01884	EST - K01884	EST - K01884
10923	4.2	AA116036	Hs.9329	ESTs
34380	4.2	AA252414	Hs.104300	ESTs
10132	4.2	R35733	EST - R35733	EST - R35733
16629	4.2	AA036811	Hs.61859	ESTs
25146	4.2	AA026356	Hs.108106	ESTs
28730	4.2	D20959	Hs.5858	ESTs Moderately similar to !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]
10200	4.2	R64521	Hs.77361	ESTs
38695	4.2	AA600176	Hs.112345	ESTs

FIG. 3Bk

51 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
31365	4.2	N67550	Hs.48907	ESTs
42379	4.1	W37999	Hs.103018	ESTs
28050	4.1	AA479139	Hs.75393	Acid phosphatase 1 soluble
2620	4.1	M29474	Hs.73958	Human recombination activating protein (RAG-1) gene complete cds
8927	4.1	AF008442	Hs.5409	Human sapiens RNA polymerase I subunit hRPA39 mRNA complete cds
13379	4.1	AA449741	Hs.4029	ESTs Weakly similar to AF-9 PROTEIN [H.sapiens]
5134	4.1	U79293	Hs.90802	Human clone 23948 mRNA sequence
2626	4.1	M29581	Hs.2077	Zinc finger protein 8 (clone HF.18)
38005	4.1	AA479969	Hs.105624	ESTs
36575	4.1	AA431085	Hs.98706	EST
18296	4.1	AA213620	Hs.48301	ESTs Weakly similar to putative p150 [H.sapiens]
29531	4.1	H88953	EST · RC_H88953	EST · RC_H88953
143	4.1	HUMTFRR/M11507	AFFX-HUMTFRR/M11507_5	AFFX-HUMTFRR/M11507_5
10970	4.1	AA129390	Hs.5285	ESTs
25836	4.1	AA152305	Hs.2248	Interferon (gamma)-induced cell line protein 10 from
19735	4.1	H53038	Hs.36710	EST
40711	4.1	N53564	Hs.108159	ESTs
4149	4.1	U28386	Hs.2397	RAG (recombination activating gene) cohort 1
5767	4.1	X53793	Hs.118226	MULTIFUNCTIONAL PROTEIN ADE2
5503	4.1	X05232	Hs.83326	Stronielysin
20310	4.1	N34893	Hs.6153	ESTs Highly similar to HYPOTHETICAL 47.8 KD PROTEIN B0283.9 IN CHROMOSOME III [Caenorhabditis elegans]
456	4.1	D38145	Hs.61333	Prostaglandin I2 (prostacyclin) synthase
7814	4.1	AA248406	Hs.19347	ESTs
40230	4.0	H90161	Hs.64592	ESTs

FIG. 3BI

52 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
33651	4.0	W95409	Hs.59704	ESTs
16777	4.0	AA046968	Hs.62823	EST
19110	4.0	H08778	Hs.133521	ESTs
34442	4.0	AA258093	Hs.108642	HKR-T1
5099	4.0	U79247	Hs.90796	Human clone 23599 mRNA sequence
8209	4.0	AA384220	Hs.86605	ESTs
24408	4.0	W90146	Hs.35962	ESTs
26596	4.0	AA279943	Hs.88671	ESTs
16485	4.0	AA026269	Hs.89843	Spleen focus forming virus (SFFV) proviral integration oncoj gene spi1
32969	4.0	W42451	Hs.92260	ESTs
27006	4.0	AA398695	Hs.56159	ESTs Weakly similar to E04F6.2 gene product [C.elegans]
29809	4.0	N21043	Hs.42932	EST
9596	3.9	H91564	Hs.13540	ESTs
29024	3.9	F09315	Hs.76982	Homo sapiens mRNA for KIAA0583 protein partial cds
21694	3.9	R39317	Hs.89403	Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA complete cds
13207	3.9	AA443321	Hs.101810	ESTs
37865	3.9	AA476623	Hs.99819	ESTs Highly similar to PUTATIVE UBIQUITIN CARBOXYL- TERMINAL HYDROLASE C13A11.04C [Schizosaccharomyces pombe]
36201	3.9	AA421164	Hs.107213	ESTs
8961	3.9	HUMTFRR/M11507	AFFX-HUMTFRR/M11507_3	
17444	3.9	AA115933	Hs.42323	ESTs
25869	3.9	AA157267	Hs.144332	ESTs Highly similar to HYPOTHETICAL 37.7 KD PROTEIN ZK686.3 IN CHROMOSOME III [Caenorhabditis elegans]

FIG.-3Bm

53 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
24862	3.9	Z41415	Hs.6823	ESTs Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]
26685	3.9	AA281950	Hs.79656	ESTs
42300	3.9	T95850	Hs.100703	ESTs
6495	3.9	X92715	Hs.3057	Zinc finger protein 74 (Cos52)
38604	3.9	AA598803	Hs.111496	ESTs
36358	3.9	AA425756	Hs.98445	ESTs
30560	3.9	N49284	Hs.1334	MYB PROTO-ONCOGENE PROTEIN
14413	3.9	AA600150	Hs.14366	ESTs
23823	3.9	T91805	Hs.38084	Homo sapiens mRNA for ST1C2 complete cds
38158	3.9	AA487021	Hs.105703	EST
2572	3.9	M27281	Hs.73793	Vascular endothelial growth factor
40100	3.8	H75933	Hs.75901	Laminin receptor (2H5 epitope)
40258	3.8	H93340	Hs.125010	ESTs
20944	3.8	N74443	Hs.16247	ESTs
20411	3.8	N48963	Hs.21992	Homo sapiens mRNA for KIAA0689 protein partial cds
10345	3.8	AA001663	Hs.7959	ESTs
31261	3.8	N66248	Hs.141609	EST
8513	3.8	AA446990	Hs.103135	ESTs
13877	3.8	AA476604	Hs.7114	ESTs
40748	3.8	N56879	Hs.102633	EST
14509	3.8	AA609943	Hs.32793	ESTs
10281	3.8	R80333	Hs.21182	ESTs
25284	3.8	AA045074	Hs.110146	ESTs Weakly similar to 52-kD SS-A/Ro autoantigen [H.sapiens]
6730	3.8	Y09305	Hs.17154	H.sapiens mRNA for protein kinase Dyrk4 partial
16033	3.8	UMISGF3A/M97935		AFFX-HUMISGF3A/M97935_MB
39242	3.8	AA621523	Hs.110832	ESTs

FIG. 3Bn

54 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
27354	3.8	AA425221	Hs.81688	ESTs
4552	3.8	U49188	Hs.76329	Human placenta (Diff33) mRNA complete cds
18385	3.8	AA227219	Hs.110826	Homo sapiens CAGF9 mRNA partial cds
16754	3.8	AA046067		EST - RC_AA046067
12752	3.8	AA421250	Hs.4310	ESTs
42463	3.8	W60180	Hs.103135	ESTs
10614	3.8	AA037357	Hs.18045	ESTs
867	3.7	D87716	Hs.90315	Human mRNA for KIAA0007 gene partial cds
7608	3.7	AA180967	Hs.85432	ESTs
31795	3.7	N80703	Hs.50473	ESTs
35377	3.7	AA399453		EST - RC_AA399453
22828	3.7	R98192	Hs.35828	ESTs
25240	3.7	AA039713	Hs.110406	ESTs
11008	3.7	AA134289	Hs.15423	ESTs Weakly similar to ASH1 [D.melanogaster]
4341	3.7	U38545	Hs.82587	Human ARF-activated phosphatidylcholine-specific phospholipase D1a (hPLD1) mRNA complete cds
28833	3.7	D59787		EST - RC_D59787_f
3750	3.7	U09279	Hs.89457	Collagen type XIX alpha 1
17483	3.7	AA122147	Hs.64691	ESTs
16854	3.7	AA055552	Hs.71622	ESTs Weakly similar to KIAA0319 [H.sapiens]
3709	3.7	U07550	Hs.11197	Heat shock 10 kD protein 1 (chaperonin 10)
1608	3.7	L00205	Hs.111758	KERATIN TYPE II CYTOSKELETAL 6D
24577	3.7	Z38727	Hs.43107	Homo sapiens mRNA for KIAA0555 protein complete cds
31032	3.7	N62508	Hs.91625	ESTs
4951	3.7	U69546	Hs.82321	Human RNA binding protein Etr-3 mRNA complete cds
37660	3.7	AA460225	Hs.99519	ESTs
20418	3.6	N49209	Hs.32170	ESTs

FIG. 3Bo

55 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
27995	3.6	AA470155	Hs.75887	Homo sapiens coatomer protein (COPA) mRNA complete cds
7971	3.6	AA287423	Hs.126389	ESTs
27606	3.6	AA443793	Hs.94761	ESTs
24677	3.6	Z39338	Hs.21201	ESTs Highly similar to POLIOVIRUS RECEPTOR HOMOLOG PRECURSOR [Mus musculus]
11070	3.6	AA148521	Hs.6759	ESTs Weakly similar to putative p150 [H.sapiens]
9328	3.6	D89618	Hs.3886	Homo sapiens importin-alpha homolog (SRP1gamma) mRNA complete cds
36826	3.6	AA435996	Hs.98857	ESTs
17678	3.6	AA134275	Hs.134510	Human HIV1 tata element modulatory factor mRNA sequence from chromosome 3
36209	3.6	AA421266	Hs.13889	ESTs Weakly similar to LIS-1 protein [H.sapiens]
34120	3.6	AA211615	Hs.104173	EST
38152	3.6	AA486737	Hs.105465	H.sapiens mRNA for Sm protein F
38463	3.6	AA504491	Hs.30154	ESTs Weakly similar to contains similarity to C3HC4-class zinc finger [C.elegans]
20064	3.6	H98653	Hs.16056	ESTs
31256	3.6	N66152	Hs.49132	EST
9713	3.6	L44338	Hs.78494	Homo sapiens mRNA for KIAA0525 protein partial cds
28622	3.6	D11837	Hs.29846	ESTs
38057	3.6	AA481549	EST	EST RC_AA481549
28763	3.6	D45568	Hs.65557	EST
16996	3.6	AA069038	EST	EST RC_AA069038
28628	3.6	D11888	Hs.62386	ESTs Moderately similar to PROHIBITIN [H.sapiens]
25804	3.5	AA148885	Hs.111710	ESTs
2492	3.5	M22898	Hs.1846	Tumcr protein p53 (Li-Fraumeni syndrome)
14904	3.5	T83389	Hs.107147	ESTs Highly similar to GEPHYRIN [Rattus norvegicus]

FIG..3Bp

56 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
25265	3.5	AA043765	Hs.54649	H.sapiens RY-1 mRNA for putative nucleic acid binding protein
13606	3.5	AA456437	Hs.20386	ESTs Weakly similar to CLEAVAGE STIMULATION FACTOR 64 KD SUBUNIT [H.sapiens]
42307	3.5	T96595		EST - RC_T96595
1544	3.5	J05068	Hs.2012	TRANSCOBALAMIN I PRECURSOR
42339	3.5	W02072	Hs.26706	ESTs Weakly similar to No definition line found [C.elegans]
42311	3.5	T97257	Hs.94560	ESTs
2023	3.5	L34600	Hs.3823	INITIATION FACTOR IF-2 MITOCHONDRIAL PRECURSOR
4540	3.5	U48807	Hs.2359	Human MAP kinase phosphatase (MKP-2) mRNA complete cds
33707	3.5	Z39297	Hs.3281	Neuronal pentraxin II
17220	3.5	AA083070		EST - RC_AA083070_s
24332	3.5	W85782	Hs.18529	ESTs
35887	3.5	AA412067	Hs.98117	ESTs
20158	3.5	N23638	Hs.16464	ESTs Weakly similar to coded for by C. elegans cDNA yk52e10.5 [C.elegans]
8338	3.4	AA417152	Hs.5101	Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds
387	3.4	D28589		EST - D28589
12319	3.4	AA398109	Hs.20890	ESTs
38276	3.4	AA489711	Hs.105250	ESTs
15643	3.4	W58247	Hs.27437	ESTs highly similar to KINESIN-LIKE PROTEIN KIF4 [Mus musculus]
11218	3.4	AA180488	Hs.33746	ESTs
16539	3.4	AA029328	Hs.1191	Human mRNA for KIAA0073 gene partial cds
29203	3.4	H28581	Hs.92711	ESTs
13838	3.4	AA465342	Hs.34045	ESTs

FIG..3Bq

57 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
25585	3.4	AA112389	Hs.107932	H4(D10S170)
34018	3.4	AA191488	Hs.73614	Human high-affinity copper uptake protein (hCTR1) mRNA complete cds
251	3.4	D14520	Hs.84728	Basic transcription element binding protein 2
3778	3.4	U09848	Hs.363	Zinc finger protein 139 (clone pHZ-37)
24535	3.4	Z38409	Hs.8053	ESTs
16858	3.4	AA055759	Hs.90998	Human mRNA for KIAA0128 gene partial cds
16127	3.4	AA004669	Hs.39441	ESTs
36683	3.4	AA432268	Hs.104910	ESTs
26149	3.4	AA250824	Hs.60478	ESTs Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]
4011	3.4	U20536	Hs.3280	Human cysteine protease Mch2 isoform alpha (Mch2) mRNA complete cds
41001	3.4	N78844	Hs.3749	ESTs
5660	3.4	X16396	Hs.37791	NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE
19204	3.4	H11629	Hs.26790	ESTs
42323	3.4	T98152	Hs.79432	Fibrillin 2
26928	3.4	AA342580	Hs.47232	ESTs
20497	3.4	N52565	Hs.36055	ESTs
19226	3.4	H12455	Hs.13026	ESTs
36267	3.4	AA424046	Hs.98385	ESTs
32257	3.4	R54726	Hs.98493	DNA-REPAIR PROTEIN XRCC1
17365	3.4	AA101551	Hs.68900	ESTs
15296	3.3	W16684	Hs.74284	ESTs Moderately similar to Similar to S.cerevisiae hypothetical protein L3111 [H.sapiens]
17675	3.3	AA134064	Hs.44045	ESTs
40332	3.3	H97565	Hs.108805	Homo sapiens mRNA from chromosome 5q21-22 clone:A3-A

FIG. 3Br

58 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
7219	3.3	AA056319	Hs.79326	Homo sapiens protein phosphatase 2A B56-epsilon (PP2A) mRNA complete cds
10006	3.3	N81193	Hs.43133	Homo sapiens mRNA for KIAA0628 protein complete cds
33985	3.3	AA181580	Hs.81690	Homo sapiens importin beta subunit mRNA complete cds
9570	3.3	H85169	Hs.24837	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene complete cds
37551	3.3	AA456679	Hs.7256	ESTs
886	3.3	D88613	Hs.28346	Human mRNA for hGCMa complete cds
23650	3.3	T86293	Hs.16144	ESTs
18367	3.3	AA224180	Hs.93332	ESTs Moderately similar to ovarian-specific protein [R.norvegicus]
42494	3.3	W69385	Hs.100002	H.sapiens NuMA gene (Clone T33)
14310	3.3	AA598412	Hs.8739	ESTs Highly similar to HYPOTHETICAL TRP-ASP REPEATSCONTAINING PROTEIN IN PMT6-PCT1 INTERGENIC REGION [Saccharomyces cerevisiae]
19233	3.3	H12634	Hs.8104	ESTs
42283	3.3	T94343	Hs.31016	Homo sapiens M962 protein spliced isoform 2 mRNA complete cds
12809	3.3	AA424406	Hs.31839	ESTs
36285	3.3	AA424469	Hs.97849	ESTs
21555	3.3	R33073	Hs.24595	EST
13767	3.3	AA463234	Hs.119387	ESTs
4738	3.3	U58766	Hs.75801	Human FX protein mRNA complete cds
7258	3.3	AA075427	Hs.17296	ESTs
17041	3.3	AA070364		EST - RC_AA070364
15504	3.3	W28362	Hs.44131	ESTs
23793	3.3	T90971		EST - RC_T90971

FIG..3Bs

59 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
18214	3.3	AA196635	Hs.86081	ESTs
7401	3.3	AA094800	Hs.55682	Human translation initiation factor eIF3 p66 subunit mRNA complete cds
18912	3.3	F10913	Hs.12475	Homc sapiens clone 23617 unknown mRNA partial cds
36317	3.3	AA425089	Hs.50722	Human mRNA for KIAA0334 gene complete cds
9410	3.3	H20443	Hs.31748	H.sapiens mRNA for TRE5
2146	3.2	L41390	EST - L41390	EST - L41390
18683	3.2	F04258	Hs.36454	ESTs Highly similar to INORGANIC PYROPHOSPHATASE [Bos taurus]
33891	3.2	HUMTFRR/M11507		AFFX-HUMTFRR/M11507_M
14435	3.2	AA608730	Hs.4192	ESTs Weakly similar to ELONGATION FACTOR 1-ALPHA [Giarcia intestinalis]
9584	3.2	H88128	Hs.41127	ESTs Highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluorescens]
22061	3.2	R49216	Hs.24984	ESTs
35796	3.2	AA410223	EST - RC_AA410223	EST - RC_AA410223
37403	3.2	AA453613	Hs.128708	ESTs
15796	3.2	X16889	Hs.69089	ALPHA-GALACTOSIDASE A PRECURSOR
15840	3.2	X70944	Hs.91379	PTB-ASSOCIATED SPLICING FACTOR
7518	3.2	AA147144	EST - AA147144	EST - AA147144
32335	3.2	R78248	Hs.109156	ESTs
3256	3.2	M92439	Hs.87157	130 KD LEUCINE-RICH PROTEIN
4400	3.2	U41387	Hs.5122	Human Gu protein mRNA partial cds
7681	3.2	AA206983	Hs.104135	Homc sapiens mRNA for DRIM protein
15676	3.2	W68649	Hs.9656	ESTs
39590	3.2	F09281	Hs.106981	ESTs
26883	3.2	AA291921	Hs.44107	ESTs Weakly similar to putative p150 [H.sapiens]

FIG._3Bt

60 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
9808	3.2	M80627	Hs.21704	Transcription factor 12 (HTF4 helix-loop-helix transcription factors 4)
27755	3.2	AA453444	Hs.6809	ESTs
29983	3.2	N26011	Hs.53810	ESTs
21350	3.2	R15846	Hs.21738	ESTs
11981	3.2	AA280928	Hs.24287	ESTs
23930	3.2	T96690	Hs.125123	ESTs Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY!!!! [H.sapiens]
30399	3.2	N45226	Hs.46495	EST
22286	3.2	R59312	Hs.26641	ESTs
13494	3.2	AA453431	Hs.21043	ESTs
12908	3.2	AA427579	Hs.9347	ESTs
22319	3.1	R60567	Hs.26787	ESTs
31309	3.1	N66818	Hs.42179	ESTs
31192	3.1	N64406	Hs.54174	ESTs
11288	3.1	AA196512	Hs.25916	ESTs
170	3.1	D00596	Hs.82962	Thymidylate synthase
5307	3.1	U90549	Hs.63272	Human non-histone chromosomal protein (NHC) mRNA complete cds
26105	3.1	AA243133	Hs.48915	Homo sapiens serine/threonine kinase (BTAK) mRNA complete cds
11659	3.1	AA251909	Hs.36708	Homo sapiens MAD3-like protein kinase mRNA complete cds
19177	3.1	H10984	Hs.12338	ESTs
8389	3.1	AA425230	Hs.112013	ESTs
34087	3.1	AA205125	Hs.1087	Protein: serine/threonine kinase stk2
25001	3.1	AA004718	Hs.138349	ESTs Weakly similar to BAP31 protein [H.sapiens]
14149	3.1	AA489665	Hs.25245	ESTs

FIG..3Bu

61 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
10167	3.1	R55076	Hs.106645	ESTs
17380	3.1	AA102566	Hs.69149	ESTs
42397	3.1	W42928	Hs.103046	ESTs
14935	3.1	T94828	Hs.63220	ESTs Weakly similar to GA BINDING PROTEIN BETA-2 CHAIN [H.sapiens]
41673	3.1	R78618	Hs.101571	ESTs Weakly similar to GTP-binding protein rab10 [R.no vegicus]
2750	3.1	M35999	Hs.87149	Integin beta 3 (platelet glycoprotein IIa antigen CD61)
3190	3.1	M86808	Hs.131361	PYRUVATE DEHYDROGENASE E1 COMPONENT ALPHA SUBUNIT TESTIS-SPECIFIC FORM PRECURSOR
17406	3.1	AA112979	Hs.48269	Homc sapiens mRNA for VRK1 complete cds
598	3.1	D59253	Hs.3709	Homc sapiens mRNA for low molecular mass ubiquinone-binding protein complete cds
29348	3.1	H69021	Hs.62394	ESTs
14130	3.1	AA489041	Hs.15140	ESTs
14134	3.1	AA489080	Hs.3566	ESTs Highly similar to phosphorylation regulatory protein HP-10 [H.sapiens]
42421	3.1	W45491	Hs.106835	ESTs Weakly similar to T23G11.7 [C.elegans]
15723	3.1	W79060	Hs.5337	ESTs Highly similar to ribosome-binding protein p34 [R.no vegicus]
11140	3.1	AA158132	Hs.11817	ESTs Highly similar to YSA1 PROTEIN [Saccharomyces cerevisiae]
28531	3.1	C20679	Hs.32753	ESTs
2021	3.1	L34409	Hs.94799	Homc Sapiens (clone B3B3E13) chromosome 4p16.3 DNA fragment

FIG. 3Bv

62 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
14522	3.1	AA610108	Hs.27693	ESTs Highly similar to PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C21E11.05C [Schizosaccharomyces pombe]
29853	3.1	N22162	Hs.43100	ESTs
15962	3.1	Z21420	Hs.30819	ESTs
6541	3.1	X95632	Hs.86870	Human Abl interactor 2 (Abi-2) mRNA complete cds
13229	3.0	AA443811	Hs.23363	ESTs
27315	3.0	AA424038	Hs.58197	ESTs
13621	3.0	AA456821	Hs.6823	ESTs Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]
35929	3.0	AA412429	Hs.48642	ESTs
17925	3.0	AA164209	Hs.31730	Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA complete cds
5053	3.0	U76992	Hs.71134	Human Tat-SF1 mRNA complete cds
15060	3.0	U54999	Hs.93121	Human LGN protein mRNA complete cds
17757	3.0	AA147224	Hs.71814	EST
19050	3.0	H05509	Hs.24639	ESTs
26530	3.0	AA278650	Hs.73291	ESTs
16806	3.0	AA053258	Hs.31921	Homo sapiens mRNA for KIAA0648 protein partial cds
29088	3.0	F13700	Hs.115823	Homo sapiens ribonuclease P protein subunit p40 (RPP40) gene complete cds
22960	3.0	T10272	Hs.4287	ESTs
33585	3.0	W93000	Hs.59389	ESTs
220	3.0	D13627	Hs.84021	Human mRNA for KIAA0002 gene complete cds
4298	3.0	U36448	Hs.74574	Human Ca2+-dependent activator protein for secretion mRNA complete cds
7445	3.0	AA104023	Hs.110048	ESTs

FIG. 3Bw

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
40903	3.0	N68670	Hs.103808	ESTs
18055	3.0	AA179387	Hs.73596	ESTs
7282	3.0	AA083339	Hs.126781	ESTs
9348	3.0	H03686	Hs.112013	ESTs
806	3.0	D87009	Hs.43834	Human (lambda) DNA for immunoglobulin light chain
38447	3.0	AA504255	Hs.54404	Human protein kinase ATR mRNA complete cds
41464	3.0	R46837	Hs.107450	ESTs
9662	3.0	L19161	Hs.121541	TRANSLATIONAL INITIATION FACTOR 2 GAMMA SUBUNIT
16976	3.0	AA063625	Hs.66696	EST
37426	3.0	AA454016	Hs.99306	ESTs
2588	3.0	M27878	Hs.9450	Zinc finger protein 84 (HPF2)
15174	3.0	U82987	Hs.87246	Human Bcl-2 binding component 3 (bbc3) mRNA partial cds
33620	3.0	W93943	Hs.59509	ESTs
6784	3.0	Y11681	Hs.9964	Homc sapiens ribosomal protein S12 gene nuclear gene encoding mitochondrial protein complete cds
41077	3.0	N95028	Hs.125031	ESTs
1932	3.0	L24804	Hs.75839	Human (p23) mRNA complete cds-
39556	3.0	F03738	Hs.3657	ESTs
16108	3.0	AA002258	Hs.59939	ESTs
32156	3.0	R40381	Hs.142852	ESTs
13617	3.0	AA456646	Hs.28661	ESTs
11989	3.0	AA281251	Hs.35696	ESTs Weakly similar to trithorax protein trxII [D.melanogaster]
6056	2.9	X68194	Hs.80919	Pantophysin [human keratinocyte line HaCaT mRNA 2106 nt]
15446	2.9	W27374	Hs.5300	Homc sapiens 10kD protein (BC10) mRNA complete cds
38086	2.9	AA482557	Hs.105139	EST
13878	2.9	AA476604	Hs.7114	ESTs
6209	2.9	X76770	Hs.49007	H.sapiens PAP mRNA

FIG._3Bx

64 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
388	2.9	D28791	Hs.51	Phosphatidylinositol glycan class A (paroxysmal nocturnal hemoglobinuria)
1351	2.9	G4755-HT5203		EST - HG4755-HT5203
42624	2.9	W87804	Hs.110122	ESTs
34895	2.9	AA311972	Hs.96702	ESTs
20157	2.9	N23393	Hs.20509	ESTs
29248	2.9	H52918	Hs.39188	ESTs
4893	2.9	U66615	Hs.85813	Human SWI/SNF complex 155 KDa subunit (BAF155) mRNA complete cds
10104	2.9	R23855	Hs.107968	ESTs
15039	2.9	U46116	Hs.89627	Protein tyrosine phosphatase receptor type gamma polypeptide
1605	2.9	L00058	Hs.79070	V-myc; avian myelocytomatosis viral oncogene homolog
4536	2.9	U48705	Hs.75562	Receptor protein-tyrosine kinase EDDR1
10173	2.9	R56678	Hs.102963	ESTs Weakly similar to cell division control protein CDC21 [H.sapiens]
26555	2.9	AA279071	Hs.94845	ESTs Weakly similar to T08A11.2 [C.elegans]
4401	2.9	U41515	Hs.85215	Human deleted in split hand/split foot 1 (DSS1) mRNA complete cds
21009	2.9	N90401	Hs.28928	ESTs
3602	2.9	U01317	Hs.117848	HEMOGLOBIN EPSILON CHAIN
4833	2.9	U63455	Hs.54470	Sulfonylurea receptor (hyperinsulinemia)
36200	2.9	AA421164	Hs.107213	ESTs
26645	2.9	AA281076	Hs.109221	ESTs
35299	2.9	AA398622	Hs.75133	Transcription factor 6-like 1 (mitochondrial transcription factor 1-like)
9804	2.9	M74558	Hs.142965	Human SIL mRNA complete cds
5216	2.9	U83410	Hs.82919	Human CUL-2 (cul-2) mRNA complete cds

FIG.-3By

65 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
12313	2.9	AA397916	Hs.22595	ESTs
5928	2.9	X62048	Hs.75188	WEE1-LIKE PROTEIN KINASE
39586	2.9	F09155	Hs.77822	ESTs
34758	2.9	AA287680	Hs.99676	EST
18199	2.9	AA195318	Hs.63311	ESTs
19867	2.9	H61476	Hs.15641	ESTs
6081	2.9	X69398	Hs.82685	CD47 antigen (Rh-related antigen integrin-associated signal transducer)
5254	2.9	U86782	Hs.76887	Human 26S proteasome-associated-pad1 homolog (POH1) mRNA complete cds
13579	2.9	AA455967	Hs.106705	Human neuronal PAS2 (NPAS2) mRNA complete cds
1117	2.9	HG3075-HT3236		EST - HG3075-HT3236
20533	2.9	N54407	Hs.34570	ESTs
38495	2.9	AA505118	Hs.112255	Human nucleoporin 98 (NUP98) mRNA complete cds
33729	2.9	Z39654	Hs.65789	EST
2028	2.9	L35035	Hs.79886	RIBOSE 5-PHOSPHATE ISOMERASE
27374	2.9	AA425816	Hs.64641	ESTs Weakly similar to Y53C12A.3 [C.elegans]
19404	2.9	H20568	Hs.27182	ESTs
26108	2.9	AA243189	Hs.53652	ESTs
4189	2.8	U30930	Hs.57700	UDP glycosyltransferase 8 (UDP-galactose ceramide galactosyltransferase)
16708	2.8	AA043944	Hs.62663	ESTs
357	2.8	D26156	Hs.78202	Human mRNA for transcriptional activator hSNF2b complete cds
26045	2.8	AA236276	Hs.87287	ESTs
17796	2.8	AA150435	Hs.72063	ESTs
8059	2.8	AA310967	Hs.5080	ESTs Weakly similar to T04A8.11 [C.elegans]

FIG.-3Bz

66 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
40914	2.8	N69220	Hs.41381	ESTs
27169	2.8	AA410287	Hs.90304	H.sapiens mRNA for basic transcription factor 2 34 kD subunit
21358	2.8	R16079	Hs.14775	ESTs
3572	2.8	S87759	Hs.57764	Protein phosphatase 2C alpha [human teratocarcinoma mRNA 2346 nt]
11877	2.8	AA262727	Hs.9591	ESTs
1653	2.8	L05424	Hs.57649	CD44 antigen (cell adhesion molecule)
24645	2.8	Z39106	Hs.92414	ESTs
35830	2.8	AA411448	Hs.139386	ESTs
4433	2.8	U43279	EST - U43279	
20151	2.8	N22895	Hs.6831	Homo sapiens clone 1400 unknown protein mRNA partial cds
38648	2.8	AA599267	EST - RC_AA599267	
7777	2.8	AA236820	Hs.118236	ESTs
32845	2.8	W31566	Hs.55459	EST
28258	2.8	AA505133	Hs.62273	ESTs
6853	2.8	Z22951	Hs.75569	TRANSCRIPTION FACTOR P65
35944	2.8	AA412488	Hs.98150	ESTs
30648	2.8	N50971	Hs.42116	ESTs
18965	2.8	H01411	Hs.24382	ESTs
8616	2.8	AA460077	Hs.28555	ESTs
14945	2.8	T99606	Hs.11085	ESTs Weakly similar to F35G2.2 [C.elegans]
8375	2.8	AA422160	Hs.103144	H.sapiens NAP (nucleosome assembly protein) mRNA complete cds
34929	2.8	AA342084	EST - RC_AA342084	
326	2.8	D21262	Hs.75337	Human mRNA for KIAA0035 gene partial cds
27057	2.8	AA400998	Hs.49559	ESTs
36292	2.8	AA424513	EST - RC_AA424513	

FIG.-3Ca

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
6480	2.8	X91788	Hs.84974	H.sapiens mRNA for Icin protein
15424	2.8	W27054	Hs.1255	APOLIPOPROTEIN AI REGULATORY PROTEIN-1
11602	2.8	AA243007	Hs.16420	ESTs
18175	2.8	AA194730	Hs.85916	ESTs
25202	2.8	AA034527	Hs.95182	EST
1681	2.8	L07493	Hs.1608	Replication protein A (E coli RecA homolog RAD51 homolog)
14566	2.8	AA621122	Hs.5198	ESTs
25614	2.8	AA115769	Hs.142290	ESTs
14182	2.8	AA490885	Hs.21766	ESTs
31599	2.8	N72196	Hs.50199	EST
18253	2.7	AA206370	Hs.86248	ESTs
6193	2.7	X76092	Hs.38841	Regulatory factor (trans-acting) 3
22911	2.7	T03865	Hs.27047	ESTs
35549	2.7	AA401274	Hs.31730	Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA complete cds
35955	2.7	AA412528	Hs.20183	ESTs 'Weakly similar to ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH [R.norvegicus]
17642	2.7	AA132983	Hs.44155	ESTs Moderately similar to C-1-TETRAHYDROFOLATE SYNT-HASE CYTOPLASMIC [H.sapiens]
6131	2.7	X72841	Hs.2758	Human retinoblastoma-binding protein (RbAp46) mRNA complete cds
41429	2.7	R44994	Hs.108182	ESTs
17052	2.7	AA070815	EST - RC_AA070815	
34243	2.7	AA235050	Hs.142190	ESTs
22937	2.7	T10065	Hs.4214	Homo sapiens TLS-associated protein TASR-2 mRNA complete cds

FIG..3Cb

68 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
5183	2.7	U82130	Hs.118910	Human tumor susceptibility protein (TSG101) mRNA complete cds
30837	2.7	N54416	Hs.47820	ESTs
16243	2.7	AA012902	Hs.60556	ESTs
19954	2.7	H80100	Hs.33977	ESTs
6444	2.7	X89750	Hs.90077	H.sapiens mRNA for TGIF protein
5916	2.7	X61072	Hs.99996	Human mRNA for T cell receptor clone IGRA17
6240	2.7	X78627	Hs.75066	H.sapiens mRNA for translin
42116	2.7	T69924		EST - RC_T69924
7701	2.7	AA215333	Hs.97101	ESTs
17568	2.7	AA128905	Hs.22587	ESTs
42534	2.7	W73189	Hs.89403	Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA complete cds
29813	2.7	N21111	Hs.42946	ESTs
38898	2.7	AA609458	Hs.98265	ESTs
10316	2.7	R88880	Hs.107823	ESTs Moderately similar to zinc finger protein [M.musculus]
14769	2.7	S54641	Hs.73103	HZF-16
32961	2.7	W38366	Hs.77493	Human mRNA for KIAA0005 gene complete cds
35273	2.7	AA398507	Hs.97361	ESTs
10180	2.7	R60100	Hs.25986	ESTs
32563	2.7	T27697	Hs.21603	Human mRNA for KIAA0036 gene complete cds
34502	2.7	AA262768	Hs.7523	ESTs
13223	2.7	AA443720	Hs.7551	ESTs
8494	2.7	AA443460	Hs.3430	ESTs
7776	2.7	AA236771	Hs.101368	ESTs
10400	2.7	AA007234	Hs.30098	ESTs
1130	2.7	G3132-HT3308		EST - HG3132-HT3308

FIG._3Cc

69 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
2379	2.7	M16937	Hs.819	Human homeo box c1 protein mRNA complete cds
18906	2.7	F10868	Hs.46571	Human SH3 domain-containing protein SH3P18 mRNA complete cds
34796	2.7	AA291259	Hs.97101	ESTs
41955	2.7	T33311	Hs.3281	Neuronal pentraxin II
2009	2.7	L33881	Hs.1904	Protein kinase C iota
33688	2.7	Z38501	Hs.8768	ESTs Weakly similar to PROBABLE E5 PROTEIN [Human papillomavirus type 58]
1385	2.7	G884-HT884		EST - HG884-HT884
24758	2.7	Z40075	Hs.27596	ESTs
7620	2.7	AA192484	Hs.62669	ESTs Weakly similar to MITOCHONDRIAL INNER MEMBRANE PROTEASE SUBUNIT 2 [S.cerevisiae]
30733	2.7	N52078	Hs.13604	Homo sapiens mRNA for KIAA0637 protein complete cds
21256	2.7	R09195	Hs.86013	Homo sapiens mRNA for KIAA0564 protein partial cds
40528	2.7	N29325	Hs.107914	ESTs Highly similar to 47 KD PROTEIN [Pseudomonas chlororaphis]
25285	2.7	AA045083	Hs.77719	VITAMIN K-DEPENDENT GAMMA-CARBOXYLASE
9296	2.7	D82775	Hs.10724	ESTs Weakly similar to unknown [S.cerevisiae]
12174	2.7	AA292128	Hs.26750	ESTs
38357	2.7	AA491265	Hs.105285	EST
3154	2.7	M83712	Hs.1614	Cholinergic receptor nicotinic alpha polypeptide 5
7383	2.7	AA093834	Hs.109822	ESTs Weakly similar to HYPOTHETICAL 16.8 KD PROTEIN IN SMY2-RPS101 INTERGENIC REGION [S.cerevisiae]
1923	2.7	L23808	Hs.1695	Matrix metalloproteinase 12 (macrophage elastase)
24906	2.7	Z41840	Hs.8817	ESTs
30407	2.6	N45983	Hs.46572	ESTs
34726	2.6	AA287278	Hs.97721	ESTs

FIG.-3Cd

70 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
20408	2.6	N48787	Hs.28378	ESTs Moderately similar to !!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!! [H.sapiens]
7158	2.6	AA037206	Hs.72071	ESTs
26286	2.6	AA253351	Hs.44439	ESTs
19822	2.6	H58684	Hs.37573	ESTs
12379	2.6	AA399418	Hs.23170	Homo sapiens mRNA for JM23 protein complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc1101133Q7 (RZPD Berlin))
22698	2.6	R89287	Hs.29406	ESTs
24161	2.6	W58015	Hs.34820	ESTs
9558	2.6	H81497	Hs.12063	ESTs
18104	2.6	AA188801	Hs.85634	ESTs
24882	2.6	Z41563	Hs.26975	ESTs
40038	2.6	H69485	Hs.8236	ESTs
8865	2.6	AB002359	Hs.105478	Human mRNA for KIAA0361 gene KIAA0361 protein
22148	2.6	R51831	Hs.25829	ESTs
4627	2.6	U51990	Hs.94178	Human hPrp18 mRNA complete cds
8394	2.6	AA426156	Hs.42714	ESTs
20422	2.6	N49300	Hs.24908	ESTs
41602	2.6	R67258	Hs.58215	ESTs Moderately similar to rhotekin [M.musculus]
612	2.6	D63480	Hs.74670	Human mRNA for KIAA0146 gene partial cds
4821	2.6	U62801	Hs.79361	Human protease M mRNA complete cds
16807	2.6	AA053296	Hs.63136	ESTs
15288	2.6	W07562	Hs.26198	ESTs Moderately similar to rA8 [R.norvegicus]
38023	2.6	AA481066	Hs.105153	ESTs

FIG.-3Ce

71 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
23822	2.6	T91715	Hs.14574	ESTs Highly similar to HYPOTHETICAL 103.6 KD PROTEIN IN COX5B-PFK26 INTERGENIC REGION [Saccharomyces cerevisiae]
10951	2.6	AA126719	Hs.25282	ESTs
6150	2.6	X74262	Hs.81058	RETINOBLASTOMA BINDING PROTEIN P48
39336	2.6	C20945	Hs.108117	ESTs Highly similar to HYPOTHETICAL 54.2 KD PROTEIN IN CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae]
17793	2.6	AA150242	Hs.71587	ESTs Highly similar to modulator recognition factor 2 [H.sapiens]
26891	2.6	AA292659	Hs.93667	ESTs
2175	2.6	L42621	Hs.83062	Homo sapiens Ly-9 mRNA complete cds
10642	2.6	AA040149	Hs.110103	Humani Chromosome 16 BAC clone CIT987SK-A-270G1
15026	2.6	U41816	Hs.91161	Humani C-1 mRNA complete cds
7699	2.6	AA215299	Hs.70830	Homo sapiens chromosome 19 cosmid R30783
6543	2.6	X95654	Hs.112743	Homo sapiens mRNA for SCP-1 complete cds
20636	2.6	N62122	Hs.83313	ESTs
11308	2.6	AA207114	Hs.27842	ESTs
4086	2.6	U24704	Hs.111709	Humani antiserotory factor-1 mRNA complete cds
38615	2.6	AA598938		EST - IRC_AA598938
11819	2.6	AA258189	Hs.32471	ESTs
37433	2.6	AA454103	Hs.110031	ESTs
28270	2.6	AA521186	Hs.94217	ESTs
5587	2.6	X13482	Hs.80506	U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A'
19841	2.6	H59617	Hs.5199	ESTs Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD [Drosophila melanogaster]
10655	2.6	AA040882	Hs.10290	ESTs

FIG.-3Cf

72 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
14053	2.6	AA485147	Hs.12263	ESTs Highly similar to HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III [Caenorhabditis elegans]
31574	2.6	N71303	Hs.50015	EST
7614	2.6	AA187579	Hs.102696	ESTs Weakly similar to Yel007c-ap [S.cerevisiae]
37971	2.6	AA479195	Hs.105620	EST
7090	2.6	AA009913	Hs.103300	Homo sapiens diphthamide biosynthesis protein-2 (DPH2) mRNA complete cds
17852	2.6	AA156360	Hs.54823	ESTs
24219	2.6	W69960	Hs.19416	ESTs
19070	2.6	H05970	Hs.133828	Human clone 23960 mRNA sequence
17719	2.6	AA136569	Hs.144295	EST
38669	2.6	AA599694	Hs.57730	Human mRNA for KIAA0133 gene complete cds
20982	2.6	N79565	Hs.29894	ESTs
9158	2.6	D31446	Hs.10488	Homo sapiens breakpoint cluster region protein 1 (BCRG1) mRNA complete cds
11362	2.6	AA227261	Hs.20922	ESTs
8613	2.6	AA459555	Hs.31921	Homo sapiens mRNA for KIAA0648 protein partial cds
13866	2.6	AA476319	Hs.5327	ESTs
10303	2.6	R86178	Hs.51187	Ataxia telangiectasia mutated (includes complementation groups A C and D)
22299	2.6	R59601	Hs.26679	EST
18257	2.6	AA206591		EST - FIC_AA206591
20555	2.6	N55168	Hs.19466	ESTs
39552	2.6	F03605	Hs.75574	PUTATIVE 60S RIBOSOMAL PROTEIN
27530	2.6	AA435999	Hs.134132	ESTs
1795	2.6	L13434	Hs.84162	Human chromosome 3p21.1 gene sequence complete cds
14746	2.6	D60354	Hs.90315	Human mRNA for KIAA0007 gene partial cds

FIG._3Cg

73 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
2993	2.6	M64929	Hs.75200	Protein phosphatase 2 (formerly 2A) regulatory subunit B (PR 52) alpha isoform
19191	2.6	H11297	Hs.31050	ESTs
12986	2.6	AA430032	Hs.7487	ESTs Moderately similar to PTTG gene product [R.norvegicus]
15452	2.5	W27451	Hs.12064	Human Cdc5-related protein (PCDC5RP) mRNA complete cds
18003	2.5	AA171692	Hs.70980	ESTs
24198	2.5	W67524	Hs.82911	Human protein-tyrosine phosphatase (HU-PP-1) mRNA partial sequence
42653	2.5	W92703	Hs.103239	ESTs
26446	2.5	AA258796	Hs.142200	EST Weakly similar to putative p150 [H.sapiens]
30438	2.5	N47204	Hs.46680	ESTs Weakly similar to C50F4.12 [C.elegans]
36365	2.5	AA425893	Hs.26676	ESTs Weakly similar to probable CBP3 protein homolog [C.elegans]
26135	2.5	AA243765	Hs.76977	ESTs
41885	2.5	T23449	Hs.110218	ESTs Moderately similar to ZNF127-Xp [H.sapiens]
15457	2.5	W27560	Hs.90789	ESTs
27748	2.5	AA453159	Hs.41723	Human kinesin-like spindle protein HKSP (HKSP) mRNA complete cds
32315	2.5	R69840	Hs.70189	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Nycticebus coucang]
25310	2.5	AA046745	Hs.110457	ESTs
42720	2.5	Z39436	Hs.102720	ESTs
12939	2.5	AA428204	Hs.22630	ESTs
30746	2.5	N52243	Hs.47435	ESTs
2222	2.5	L76703	Hs.79326	Homo sapiens protein phosphatase 2A B56-epsilon (PP2A) mRNA complete cds
11609	2.5	AA243303	Hs.21187	ESTs

FIG..3Ch

74 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
9658	2.5	L16991	Hs.79006	Deoxythymidylate kinase
12210	2.5	AA293774	Hs.21261	ESTs Weakly similar to PROBABLE TRYPTOPHANYL-TRNA SYNTHETASE MITOCHONDRIAL [C.elegans]
3563	2.5	S83364		EST - S83364
42407	2.5	W44768	Hs.75474	Homo sapiens nephrocystin (NPHP1) mRNA partial cds
32826	2.5	W20391	Hs.20830	Human mRNA for kinesin-related protein partial cds
9692	2.5	L37747	Hs.89497	LAMIN B1
27862	2.5	AA458908	Hs.50883	ESTs
33691	2.5	Z38630	Hs.56901	EST
17288	2.5	AA085178	Hs.24382	ESTs
9888	2.5	N35449	Hs.111449	ESTs Highly similar to HYPOTHETICAL 30.3 KD PROTEIN IN APE1/LAP4-CWP1 INTERGENIC REGION [Saccharomyces cerevisiae]
5932	2.5	X62153	Hs.82479	Minichromosome maintenance deficient (S. cerevisiae) 3
15885	2.5	X95073	Hs.96247	H.sapiens mRNA for translin associated protein X
17952	2.5	AA165677	Hs.65757	ESTs Weakly similar to F16A11.1 [C.elegans]
12197	2.5	AA293206	Hs.10852	ESTs
6210	2.5	X76942	Hs.77335	Homo sapiens golgin-245 mRNA complete cds
34047	2.5	AA194166	Hs.106928	ESTs Weakly similar to G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG [H.sapiens]
16929	2.5	AA058952	Hs.62590	ESTs
26834	2.5	AA287138	Hs.59346	ESTs Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus]
5157	2.5	U80034	Hs.68583	Human mitochondrial intermediate peptidase precursor (MIPEP) mRNA mitochondrial gene encoding mitochondrial protein complete cds
38434	2.5	AA497013	Hs.142592	ESTs

FIG. 3Ci

75 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
33269	2.5	W72967	Hs.58257	ESTs
26991	2.5	AA398284	Hs.48050	ESTs
7590	2.5	AA173505	Hs.35353	ESTs Weakly similar to HYPOTHETICAL 46.1 KD PROTEIN IN PHC2-POL3 INTERGENIC REGION [S.cerevisiae]
14960	2.5	U05237	Hs.99872	Human fetal Alz-50-reactive clone 1 (FAC1) mRNA complete cds
13585	2.5	AA455999	Hs.22151	ESTs Highly similar to NEUROLYSIN PRECURSOR [Sus scrofa]
35901	2.5	AA412151	Hs.108974	ESTs
38185	2.5	AA487508	Hs.9877	Homo sapiens mRNA for KIAA0688 protein complete cds
34678	2.5	AA284744	Hs.75510	Annexin XI (56kD autoantigen)
1424	2.5	J02645	Hs.81613	Eukaryotic translation initiation factor 2A
16778	2.5	AA047008	Hs.62800	ESTs
21876	2.5	R43286	Hs.55405	EST - HIC_R43286
17779	2.5	AA149641	Hs.7988	ESTs
24559	2.5	Z38588	Hs.40637	Homo sapiens proline-rich Gla protein 1 (PRGP1) mRNA complete cds
7781	2.5	AA242904	Hs.5400	ESTs Weakly similar to No definition line found [C.elegans]
7474	2.5	AA126592	Hs.111314	ESTs
34290	2.5	AA236866	Hs.79385	Human clone 23574 mRNA sequence
5316	2.5	U90905	Hs.86347	ESTs Highly similar to HYPOTHETICAL 44.2 KD PROTEIN IN SCC2-MRF1 INTERGENIC REGION [Saccharomyces cerevisiae]
10218	2.5	R68884	Hs.58169	Homo sapiens retinoblastoma-associated protein HEC mRNA complete cds
18109	2.5	AA188981	Hs.75914	H.sapiens mRNA for transmembrane protein rnp24
6485	2.5	X92098		

FIG.-3Cj

76 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
34954	2.5	AA342959		EST - RC_AA342959
42558	2.5	W74751	Hs.110041	ESTs
27444	2.5	AA430160	Hs.42785	ESTs Weakly similar to F25H9.7 [C.elegans]
21284	2.5	R10301	Hs.20584	EST
8920	2.5	AF006265	Hs.9222	Homo sapiens cancer associated surface antigen (RCAS1) mRNA complete cds
30037	2.5	N27439	Hs.51652	ESTs
27602	2.5	AA443702	Hs.29835	ESTs Weakly similar to W02B12.7 [C.elegans]
3390	2.5	S59184	Hs.79350	RYK receptor-like tyrosine kinase
25040	2.5	AA010188	Hs.103305	ESTs
37713	2.4	AA461317	Hs.34950	ESTs
40477	2.4	N24006	Hs.99348	Homo sapiens BAC clone RG300E22 from 7q21-q31.1
29382	2.4	H72914	Hs.103318	ESTs
35521	2.4	AA400831	Hs.111916	ESTs
20324	2.4	N35406	Hs.74014	Phospholipase C beta 4
18620	2.4	F02506	Hs.9417	ESTs
21087	2.4	R00186	Hs.18866	EST
9950	2.4	N71503	Hs.43087	ESTs
31965	2.4	N93629	Hs.93391	ESTs
15120	2.4	U73524	Hs.87465	Human putative ATP/GTP-binding protein (HEAB) mRNA complete cds
28813	2.4	D59257	Hs.91161	Human C-1 mRNA complete cds
38082	2.4	AA482284	Hs.110493	ESTs
34723	2.4	AA287115	Hs.99697	ESTs
7960	2.4	AA285277	Hs.8932	Homo sapiens brain expressed ring finger protein mRNA complete cds
18073	2.4	AA180453	Hs.73643	EST

FIG..3Ck

77 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
36755	2.4	AA435698		EST - RC_AA435698
18927	2.4	F11087	Hs.12544	ESTs
3457	2.4	S74728	Hs.74294	Antiquitin
38606	2.4	AA598844	Hs.112492	ESTs
20967	2.4	N76086	Hs.35464	ESTs
24752	2.4	Z40012	Hs.21862	Homo sapiens mRNA for KIAA0587 protein complete cds
28443	2.4	AA621611	Hs.70877	ESTs
452	2.4	D38076	Hs.24763	RAN binding protein 1
11701	2.4	AA253031	Hs.31730	Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA complete cds
13655	2.4	AA458919	Hs.30212	ESTs Weakly similar to 26S proteasome subunit p44.5 [H.sapiens]
24822	2.4	Z40956	Hs.111541	ESTs
12672	2.4	AA417067	Hs.13055	ESTs
4836	2.4	U63717	Hs.95821	Human osteoclast stimulating factor mRNA complete cds
42200	2.4	T83729		EST - RC_T83729
10987	2.4	AA132239	Hs.11810	ESTs Highly similar to HYPOTHETICAL 47.4 KD PROTEIN IN SHF-1-SEC17 INTERGENIC REGION [Saccharomyces cerevisiae]
35672	2.4	AA404995		EST - RC_AA404995
6224	2.4	X77748	Hs.3786	Glutamate receptor metabotropic 3
28395	2.4	AA610064	Hs.73602	ESTs
36390	2.4	AA426291	Hs.108527	ESTs Weakly similar to No definition line found [C.elegans]
21045	2.4	N93403	Hs.109441	ESTs
4558	2.4	U49379	Hs.54506	Human diacylglycerol kinase epsilon DGK mRNA complete cds
12916	2.4	AA427745	Hs.37747	ESTs

FIG..3CI

78 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
20850	2.4	N69514	Hs.28877	ESTs Weakly similar to oxidoreductase [H.sapiens]
29759	2.4	H99972	Hs.42771	ESTs
36786	2.4	AA435815	Hs.77965	Human Clk-associated RS cyclophilin CARS-Cyp mRNA complete cds
31942	2.4	N93185	Hs.54911	ESTs
7097	2.4	AA011452	Hs.21840	ESTs
39462	2.4	D60063	Hs.9012	ESTs
14420	2.4	AA600322	Hs.19574	ESTs Highly similar to AAC-RICH MRNA CLONE AAC3 PROTEIN [Dictyostelium discoideum]
34629	2.4	AA282527		EST - FIC_AA282527
27431	2.4	AA429038	Hs.40541	ESTs
6387	2.4	X85372	Hs.105465	H.sapiens mRNA for Sm protein F
11342	2.4	AA223874	Hs.14843	Homo sapiens mRNA for KIAA0704 protein partial cds
1497	2.4	J04088	Hs.3378	Topoisomerase (DNA) II alpha (170kD)
9841	2.4	M95724	Hs.95723	Centromere autoantigen C
11454	2.4	AA233854	Hs.23348	ESTs
29950	2.4	N24902	Hs.88245	Homo sapiens mRNA for E1B-55kDa-associated protein
8396	2.4	AA426176	Hs.104613	ESTs Weakly similar to Similar to S.cerevisiae hypothetical protein L3111 [H.sapiens]
32978	2.4	W42788	Hs.1098	Human terminal transferase mRNA complete cds
27872	2.4	AA459254	Hs.48855	ESTs
11623	2.4	AA243617	Hs.31082	ESTs
26582	2.4	AA279768	Hs.88663	ESTs
22142	2.4	R51382	Hs.124275	Homo sapiens mRNA for KIAA0659 protein partial cds
13533	2.4	AA454607	Hs.38114	ESTs Highly similar to HYPOTHETICAL 40.2 KD PROTEIN K12H4.3 IN CHROMOSOME III [Caenorhabditis elegans]
11534	2.4	AA236223	Hs.6145	ESTs

FIG..3Cm

79 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
5976	2.4	X64229	Hs.110713	DEK PROTEIN
6231	2.4	X78121	Hs.2010	Choroideremia
2382	2.4	M16967	Hs.30054	Coagulation factor V
22887	2.4	T03314	Hs.25402	ESTs
24371	2.4	W87415	Hs.16918	ESTs Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
25286	2.4	AA045261	Hs.108259	ESTs
9054	2.4	C02472	Hs.5151	ESTs Weakly similar to EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1 PRECURSOR [Homo sapiens]
8163	2.4	AA357394	Hs.98073	ESTs
12233	2.4	AA343513	Hs.28813	ESTs Weakly similar to LINE/lg H-chain fusion protein [M.musculus]
22924	2.4	T08195	Hs.3772	ESTs
14371	2.4	AA599219	Hs.30272	ESTs Moderately similar to ALR [H.sapiens]
12401	2.4	AA400229	Hs.30503	ESTs
26169	2.4	AA251089	Hs.94576	ESTs Weakly similar to ORF YOR281c [S.cerevisiae]
23065	2.4	T23539	Hs.7165	ESTs Highly similar to zinc finger protein [M.musculus]
20524	2.4	N53965	Hs.15741	ESTs
20837	2.4	N69263	Hs.20524	ESTs Highly similar to HEXOKINASE TYPE I [Homo sapiens]
18201	2.4	AA195398	Hs.144550	Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1 the ADORA2BP adenosine A2b receptor LIKE pseudogene the IRF6
7813	2.4	AA248297	Hs.72805	ESTs
21195	2.4	R07210	Hs.19913	ESTs
13377	2.4	AA449720	Hs.20201	Homo sapiens clone 24706 mRNA sequence
9714	2.3	L44367	Hs.86523	ESTs

FIG._3Cn

80 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
41537	2.3	R55673	Hs.106627	ESTs
17352	2.3	AA100925	Hs.20990	ESTs
11914	2.3	AA278907	Hs.24549	ESTs
24890	2.3	Z41634	Hs.26037	ESTs
28796	2.3	D51272	EST - RC_D51272_s	
36798	2.3	AA435870	Hs.97574	ESTs Weakly similar to B0564.1 [C.elegans]
22491	2.3	R70012	Hs.29055	EST
4798	2.3	U61538	Hs.85301	Human calcium-binding protein chp mRNA complete cds
40847	2.3	N66354	Hs.109437	ESTs
15657	2.3	W63627	Hs.141503	Small inducible cytokine A5 (RANTES)
24482	2.3	Z38137	Hs.15386	ESTs
42022	2.3	T53138	Hs.19582	Homo sapiens mRNA for hTCF-4
38233	2.3	AA489023	Hs.99807	ESTs
41221	2.3	R21531	Hs.78973	ESTs Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY' !!!! [H.sapiens]
8053	2.3	AA309880	Hs.109957	ESTs
363	2.3	D26528	Hs.123058	Human mRNA for RNA helicase complete cds
26679	2.3	AA281733	Hs.4310	ESTs
13407	2.3	AA450200	Hs.7919	ESTs
17955	2.3	AA166703	Hs.93589	ESTs
31858	2.3	N90680	Hs.54642	EST
24092	2.3	W42845	Hs.14611	Homo sapiens protein tyrosine phosphatase PIR1 mRNA complete cds
16759	2.3	AA046294	Hs.40814	ESTs
7861	2.3	AA252436	Hs.12540	Homo sapiens clone 23797 and 23917 mRNA partial cds
41176	2.3	R09379	Hs.57435	Natural resistance-associated macrophage protein 2

FIG.-3Co

81 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
3860	2.3	U13913	Hs.89463	Homolog of Drosophila slowpoke (potassium channel calcium-activated)
40886	2.3	N68149	Hs.5151	ESTs Weakly similar to EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1 PRECURSOR [Homo sapiens]
19428	2.3	H22949	Hs.31942	EST
36080	2.3	AA417282		EST - FIC_AA417282
27264	2.3	AA418389	Hs.42219	ESTs
13600	2.3	AA456286	Hs.30794	ESTs
13552	2.3	AA454943	Hs.29911	ESTs
15664	2.3	W67456	Hs.56936	ESTs Moderately similar to YY1-associated factor 2 [H.sapiens]
26583	2.3	AA279774	Hs.142497	ESTs
37434	2.3	AA454149	Hs.99357	EST
7833	2.3	AA249300	Hs.7048	ESTs
3674	2.3	U05237	Hs.99872	Human fetal Alz-50-reactive clone 1 (FAC1) mRNA complete cds
33694	2.3	Z38770	Hs.71623	ESTs
11178	2.3	AA167436	Hs.20848	ESTs
16977	2.3	AA064616	Hs.66983	ESTs
19799	2.3	H57330	Hs.37430	EST
5948	2.3	X63337		EST - X63337
42097	2.3	T66318	Hs.78770	Isoleucine-tRNA synthetase
24247	2.3	W73010	Hs.108761	Ribosomal protein L37
40879	2.3	N67816	Hs.53263	ESTs Moderately similar to IIII ALU SUBFAMILY SX WARNING ENTRY IIII [H.sapiens]
5875	2.3	X59405	Hs.83532	Membrane cofactor protein (CD46 trophoblast-lymphocyte cross-reactive antigen)
22325	2.3	R60777	Hs.8358	ESTs

FIG._3Cp

82 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
9621	2.3	J05032	Hs.80758	ASPARTYL-TRNA SYNTHETASE
9239	2.3	D79100	Hs.83196	ESTs
41997	2.3	T47788	Hs.109628	ESTs
31105	2.3	N63207	Hs.48735	EST
39565	2.3	F04320	Hs.35120	Replication factor C 37-kD subunit
7404	2.3	AA094989	Hs.7381	Homo sapiens voltage dependent anion channel protein mRNA complete cds
6388	2.3	X85373	Hs.77496	H.sapiens mRNA for Sm protein G
20263	2.3	N31952	Hs.103747	ESTs Moderately similar to HYPOTHETICAL 66.5 KD PROTEIN F02A9.5 IN CHROMOSOME III [Caenorhabditis elegans]
14529	2.3	AA620307	Hs.27379	ESTs
21197	2.3	R07320	Hs.19936	ESTs
28203	2.3	AA490969	Hs.59838	ESTs
38320	2.3	AA490611	Hs.99838	ESTs
41625	2.3	R69333	Hs.10490	ESTs
4674	2.3	U54999	Hs.93121	Human LGN protein mRNA complete cds
28861	2.3	D80037	Hs.45129	EST Weakly similar to C50B8.3 [C.elegans]
31062	2.3	N62827	Hs.48645	ESTs
26756	2.3	AA283832	Hs.86619	ESTs
11567	2.3	AA236747	Hs.30327	Homo sapiens mitogen activated protein kinase activated protein kinase gene complete cds
25050	2.3	AA011134	Hs.25863	ESTs Weakly similar to renin [H.sapiens]
41935	2.3	T29681	Hs.75761	Human serine kinase mRNA complete cds
26895	2.3	AA292765	Hs.42650	H.sapiens mRNA for M-phase phosphoprotein mpp5
40585	2.3	N34891	Hs.104929	Homo sapiens mRNA for KIAA0595 protein partial cds

FIG._3Cq

83 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
3343	2.3	M97936	Hs.21486	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA
42435	2.3	W46994	Hs.109903	ESTs
5937	2.2	X62534	Hs.80684	High-mobility group (nonhistone chromosomal) protein 2
21241	2.2	R08617	Hs.20190	ESTs
25756	2.2	AA135868	Hs.95783	ESTs
34184	2.2	AA227959	Hs.3280	Human cysteine protease Mch2 isoform alpha (Mch2) mRNA complete cds
8672	2.2	AA477046	Hs.59838	ESTs
7387	2.2	AA093977	Hs.71475	ESTs
28822	2.2	D59352	Hs.80624	ESTs
18016	2.2	AA173223	Hs.44426	ESTs
20843	2.2	N69352	Hs.5683	Homo sapiens mRNA for ATP-dependent RNA helicase #46 complete cds
10054	2.2	R10266	Hs.120997	ESTs Highly similar to HYPOTHETICAL GTP-BINDING PROTEIN IN PMI40-PAC2 INTERGENIC REGION [Saccharomyces cerevisiae]
34094	2.2	AA206088	Hs.104139	ESTs
41246	2.2	R27296	Hs.23240	ESTs
22634	2.2	R82837	Hs.103329	ESTs
19686	2.2	H48502	Hs.28212	ESTs
34568	2.2	AA280609	Hs.111288	ESTs Weakly similar to K02B2.3 gene product [C.elegans]
28448	2.2	AA621752	Hs.76887	Human 26S proteasome-associated pad1 homolog (POH1) mRNA complete cds
20909	2.2	N71704	Hs.4310	ESTs
651	2.2	D78129	EST - L78129	
40409	2.2	H99877	Hs.85951	Homo sapiens exportin t mRNA complete cds

FIG._3Cr

84 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
20340	2.2	N38825	Hs.36958	ESTs
20002	2.2	H93005	EST - FIC_H93005	
37321	2.2	AA451898	Hs.99260	ESTs
8274	2.2	AA402095	Hs.63131	ESTs
20221	2.2	N29345	Hs.28917	ESTs
5792	2.2	X54941	Hs.77550	CDC28 protein kinase 1
4034	2.2	U21858	Hs.60679	Human transcription initiation factor TFIID subunit TAFII31 mRNA complete cds
36222	2.2	AA421481	Hs.98134	ESTs
16567	2.2	AA031591	Hs.82920	ESTs
4721	2.2	U58046	Hs.82131	Human mRNA for KIAA0139 gene complete cds
28656	2.2	D19708	Hs.5122	Human Gu protein mRNA partial cds
20723	2.2	N66093	Hs.21964	ESTs
6714	2.2	Y08612	Hs.90734	H.sapiens mRNA for Nup88 protein
19240	2.2	H13265	Hs.31196	ESTs
36447	2.2	AA428188	Hs.26006	ESTs
11688	2.2	AA252672	Hs.103300	Homo sapiens diphthamide biosynthesis protein-2 (DPH2) mRNA complete cds
21650	2.2	R37938	Hs.11911	Homo sapiens KIAA0440 mRNA partial cds
14152	2.2	AA489790	Hs.4976	Homo sapiens Ran-GTP binding protein mRNA partial cds
42657	2.2	W92771	Hs.77631	GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR
4642	2.2	U52427	Hs.14839	Human RNA polymerase II subunit hsrPB7 mRNA complete cds
32779	2.2	W02102	Hs.53565	ESTs
38341	2.2	AA490967	Hs.105276	ESTs
11803	2.2	AA257971	Hs.21214	ESTs
34835	2.2	AA292677	Hs.80624	ESTs

FIG. 3Cs

85 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
39085	2.2	AA620599	Hs.24766	ESTs
4046	2.2	U22376	Hs.1334	MYB PROTO-ONCOGENE PROTEIN
11600	2.2	AA242868	Hs.7395	ESTs Weakly similar to house-keeping protein [M.musculus]
5051	2.2	U76638	Hs.54089	Human BRCA1-associated RING domain protein (BARD1) mRNA complete cds
33917	2.2	AA167323	Hs.111046	ESTs
20674	2.2	N63392	Hs.128003	ESTs
41031	2.2	N91246	Hs.102897	ESTs
25114	2.2	AA020923	Hs.103353	EST
24711	2.2	Z39645	Hs.21470	ESTs
4733	2.2	U58658	Hs.57689	Human unknown protein mRNA within the p53 intron 1 complete cds
4871	2.2	U66033	Hs.76828	Human glypican-5 (GPC5) mRNA complete cds
29733	2.2	H99398	Hs.42680	EST
23155	2.2	T30550	Hs.22615	ESTs
34638	2.2	AA282987	Hs.104473	EST
35541	2.2	AA400986	Hs.99955	Prothymosin alpha
1889	2.2	L20591	Hs.1378	Annexin III (lipocortin III)
15106	2.2	U68111	Hs.91585	PROTEIN PHOSPHATASE INHIBITOR 2
40131	2.2	H79779	Hs.6975	Homo sapiens histone deacetylase 3 (HDAC3) mRNA complete cds
19516	2.2	H29207	Hs.32459	EST
4136	2.2	U28014	Hs.74122	ICH-2 PROTEASE PRECURSOR
20276	2.2	N32919	Hs.27931	ESTs
13292	2.2	AA447621	Hs.31257	ESTs Highly similar to 40 KD PROTEIN [Borna disease virus]
20666	2.2	N63165	Hs.23618	ESTs
6065	2.2	X68560	Hs.44450	Sp3 transcription factor

FIG._3Ct

86 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
18238	2.2	AA205389	Hs.41145	ESTs
21627	2.2	R37410	Hs.21095	EST
3438	2.2	S72024	Hs.119140	Eukaryotic translation initiation factor 5A
34648	2.1	AA283772	Hs.79097	ACTIVATOR 1 36 KD SUBUNIT
5964	2.1	X63657	Hs.74050	Follicular lymphoma variant translocation 1
13250	2.1	AA446459	Hs.27599	ESTs
34370	2.1	AA251829	Hs.104058	ESTs Weakly similar to HYPOTHETICAL 27.4 KD PROTEIN IN MEF2-CPR7 INTERGENIC REGION [Saccharomyces cerevisiae]
27996	2.1	AA470156	Hs.80449	ESTs Weakly similar to dynein 74K chain cytosolic [R.norvegicus]
4408	2.1	U41745	Hs.8653	Human PDGF associated protein mRNA complete cds
4187	2.1	U30888	Hs.75981	Human tRNA-guanine transglycosylase mRNA complete cds
10804	2.1	AA069549	Hs.18479	ESTs
34552	2.1	AA279985	Hs.18389	Human mRNA for KIAA0372 gene complete cds
18380	2.1	AA227119	Hs.70256	ESTs
5223	2.1	U83843	EST - U83843	
37415	2.1	AA453807	Hs.99349	EST
14582	2.1	AA621340	Hs.10600	ESTs Weakly similar to HYPOTHETICAL 39.6 KD PROTEIN IN MTD1-NUP133 INTERGENIC REGION [Saccharomyces cerevisiae]
27756	2.1	AA453447	Hs.59421	ESTs
13787	2.1	AA463745	Hs.122981	ESTs Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP22 [Saccharomyces cerevisiae]
5173	2.1	U81554	Hs.5171	Homo sapiens signal recognition particle 72 (SRP72) mRNA complete cds

FIG._3Cu

87 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
40029	2.1	H68221	Hs.108332	Human E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA complete cds
19972	2.1	H83639	Hs.33576	ESTs
23301	2.1	T52847	Hs.13034	ESTs
20504	2.1	N52966	Hs.142838	ESTs
40145	2.1	H81391	Hs.81182	Human mRNA for histamine N-methyltransferase complete cds
3461	2.1	S75256		EST - S75256
41893	2.1	T23611	Hs.51251	ESTs
39298	2.1	C14805		EST - FIC_C14805
36021	2.1	AA416876	Hs.5169	ESTs Weakly similar to TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521 [H.sapiens]
8382	2.1	AA424199	Hs.106529	ESTs Weakly similar to C50B8.3 [C.elegans]
28288	2.1	AA598447	Hs.85951	Homo sapiens exportin t mRNA complete cds
5807	2.1	X55740	Hs.76856	5' nucleotidase (CD73)
19747	2.1	H53572	Hs.32407	ESTs
38155	2.1	AA486777	Hs.105698	ESTs
924	2.1	G1112-HT1112		EST - HIG1112-HT1112
9544	2.1	H72630	Hs.35982	ESTs
8384	2.1	AA424282	Hs.91728	Human 75-kD autoantigen (PM-Sc1) mRNA complete cds
25165	2.1	AA027837	Hs.30705	Retinitis pigmentosa 3 (X-linked recessive)
24348	2.1	W86469	Hs.77899	Tropomyosin alpha chain (skeletal muscle)
41401	2.1	R43334	Hs.55075	Homo sapiens KIAA0410 mRNA complete cds
35340	2.1	AA398900		EST - FIC_AA398900
10898	2.1	AA112063	Hs.15313	ESTs Weakly similar to PRE-MRNA SPLICING HELICASE BRR2 [S.cerevisiae]
381	2.1	D28473	Hs.78770	Isoleucine-tRNA synthetase

FIG.-3Cv

88 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
22051	2.1	R49047	Hs.31975	ESTs Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
3293	2.1	M94893	Hs.2051	Testis specific protein Y-linked
11528	2.1	AA236018	Hs.10724	ESTs Weakly similar to unknown [S.cerevisiae]
11890	2.1	AA278323	Hs.17481	Homo sapiens clone 24606 mRNA sequence
13643	2.1	AA458578	Hs.12017	Homo sapiens clone 24477 mRNA sequence
19927	2.1	H71829	Hs.35701	ESTs
36511	2.1	AA429632	Hs.121018	ESTs
2130	2.1	L40407	Hs.9731	Homo sapiens thyroid receptor interactor (TRIP9) gene complete cds
7193	2.1	AA046768	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat region mRNA
5448	2.1	X02751	Hs.69855	Neuroblastoma RAS viral (v-ras) oncogene homolog
35956	2.1	AA412533	Hs.109571	ESTs
7525	2.1	AA149259	Hs.69851	ESTs
39592	2.1	F09351	Hs.16492	ESTs Weakly similar to weakly similar to S. cerevisiae PTM1 precursor [C.elegans]
28029	2.1	AA478479	Hs.71992	ESTs
18425	2.1	AA232103	Hs.59112	ESTs
23494	2.1	T70045	Hs.16987	ESTs Weakly similar to HYPOTHETICAL 33.2 KD PROTEIN F26A3.7 IN CHROMOSOME I [C.elegans]
30882	2.1	N56906	Hs.47996	EST
32597	2.1	T47333	Hs.77298	Human TFIID subunit TAFII55 (TAFII55) mRNA complete cds
33368	2.1	W80814	Hs.47283	ESTs
10259	2.1	R77527	Hs.29645	ESTs
21882	2.1	R43365	Hs.22273	ESTs
20590	2.1	N58146	Hs.34227	ESTs
12907	2.1	AA427577	Hs.26502	ESTs

FIG._3Cw

89 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
22958	2.1	T10264	Hs.116122	ESTs
42044	2.1	T58753	Hs.24083	ESTs
4210	2.1	U31814	Hs.3352	Human transcriptional regulator homolog RPD3 mRNA complete cds
39	2.1	AB003698	Hs.28853	Homo sapiens mRNA for Cdc7-related kinase complete cds
14350	2.1	AA598831	Hs.17121	ESTs
29840	2.1	N21680	Hs.43047	ESTs
25593	2.1	AA113149	Hs.8130	Homo sapiens IPL (IPL) mRNA complete cds
26071	2.1	AA236880	Hs.118970	Protein phosphatase 2A regulatory subunit B' alpha-1
26529	2.1	AA278594	Hs.88461	EST
12154	2.1	AA291293	Hs.25219	ESTs
18817	2.1	F10077	Hs.12895	ESTs
6635	2.1	X99585	Hs.90182	H.sapiens mRNA for SMT3B protein
6681	2.1	Y00971	Hs.2910	Phosphoribosyl pyrophosphate synthetase 2
22077	2.1	R49482	Hs.5637	ESTs
11752	2.1	AA256042	Hs.24908	ESTs
41257	2.1	R31680	Hs.140902	ESTs
6904	2.1	Z34897	Hs.1570	Histamine receptor H1
16879	2.1	AA056538	Hs.63314	ESTs
38040	2.1	AA481403	Hs.107213	ESTs
4111	2.1	U26312	Hs.83550	Human heterochromatin protein HP1Hs-gamma mRNA complete cds
32878	2.1	W37448	Hs.41241	ESTs
21743	2.1	R40576	Hs.21590	ESTs Moderately similar to !!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!! [H.sapiens]
25968	2.1	AA234935	Hs.65032	ESTs

FIG. 3Cx

90 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
24659	2.1	Z39211	Hs.12299	Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP) mRNA complete cds
38030	2.1	AA481148	Hs.105157	ESTs
61	2.0	AC002115	Hs.83379	Cytochrome c oxidase subunit VIb
6306	2.0	X81625	Hs.77324	EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1
8203	2.0	AA382517	EST - AA382517	ESTs Highly similar to RAS-RELATED PROTEIN RAB-10 [Canis familiaris]
34357	2.0	AA251430	Hs.5850	Tyrosinase 3-monooxygenase/tryptophan 5-monooxygenase activation protein beta polypeptide
36972	2.0	AA442767	Hs.5049	H.sapiens mRNA for nuclear protein SA-2
28156	2.0	AA489057	Hs.8217	ESTs
24434	2.0	W92787	Hs.17242	Human DNA sequence from cosmid F0811 on chromosome 6. Contains Daxx BING1 Tapasin RGL2 KE2 BING4 BING5 ESTs and CpG islands
33508	2.0	W88772	Hs.50546	H.sapiens mRNA for TRE5
37681	2.0	AA460675	Hs.31748	Homo sapiens mRNA for putative RNA helicase 3' end
27125	2.0	AA405505	Hs.48295	Zinc finger protein 148 (pHZ-52)
3780	2.0	U09851	Hs.112180	Coproporphyrinogen oxidase (coproporphyrin harderoporphyria)
9112	2.0	D16611	Hs.89866	ESTs Highly similar to RSP5 PROTEIN [Saccharomyces cerevisiae]
8357	2.0	AA418921	Hs.10325	ESTs Highly similar to RSP5 PROTEIN [Saccharomyces cerevisiae]
9133	2.0	D30946	Hs.28691	ESTs Highly similar to TRANSLOCON-ASSOCIATED PROTEIN GAMMA SUBUNIT [Rattus norvegicus]
7519	2.0	AA147425	EST - AA147425_s	ESTs
14701	2.0	D59324	Hs.124852	ESTs
380	2.0	D28423	EST - D28423	ESTs

FIG.-3Cy

91 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
30571	2.0	N49595	Hs.46637	ESTs
825	2.0	D87328	Hs.79375	Holocarboxylase synthetase (biotin-[propionyl-Coenzyme A-carboxylase (ATP-hydrolysing)] ligase)
27744	2.0	AA452818	Hs.87385	ESTs Weakly similar to HYPOTHETICAL PROTEIN HI0034 [Haemophilus influenzae]
3997	2.0	U19906	Hs.2131	Arginine vasopressin receptor 1 (AVPR1)
22717	2.0	R91394		EST - FIC_R91394
377	2.0	D28364		EST - D28364
28581	2.0	C21163	Hs.68608	EST
11790	2.0	AA256678	Hs.17035	ESTs Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]
37931	2.0	AA478523	Hs.113613	ESTs Weakly similar to III ALU SUBFAMILY J WARNING ENTRY III [H.sapiens]
24678	2.0	Z39349	Hs.19575	ESTs Weakly similar to VACUOLAR ATP SYNTHASE 54 KD SUBUNIT [Saccharomyces cerevisiae]
10940	2.0	AA122217	Hs.19845	ESTs Weakly similar to HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III [C.elegans]
13964	2.0	AA479048	Hs.142620	ESTs
15665	2.0	W67631	Hs.12342	Homo sapiens clone 24538 mRNA sequence
28379	2.0	AA609710	Hs.42582	ESTs
13349	2.0	AA449269	Hs.21198	ESTs Weakly similar to MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR [Neurospora crassa]
7322	2.0	AA090692	Hs.135552	ESTs Weakly similar to The KIAA0138 gene product is novel. [H.sapiens]
29358	2.0	H70641		EST - FIC_H70641
24230	2.0	W72276	Hs.5950	ESTs

FIG._3Cz

92 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
40212	2.0	H88535	Hs.9564	Human clone 121711 defective mariner transposon Hsmar2 mRNA sequence
729	2.0	D83778	Hs.77698	Human mRNA for KIAA0194 gene partial cds
17951	2.0	AA165526	Hs.3833	Homo sapiens bifunctional ATP sulfurylase/adenosine 5'-phosphosulfate kinase mRNA complete cds
33943	2.0	AA171739	Hs.101590	ESTs
5870	2.0	X59244	Hs.74107	Zinc finger protein 43 (HTF6)
36319	2.0	AA425107	Hs.97016	ESTs
25654	2.0	AA126951	Hs.110857	ESTs Weakly similar to DNA-directed RNA polymerase [D.melkinoaster]
16344	2.0	AA018907	Hs.5427	ESTs
8118	2.0	AA328993	Hs.104558	ESTs
29962	2.0	N25228	Hs.27349	ESTs
32236	2.0	R49327	Hs.57435	Natural resistance-associated macrophage protein 2
3279	2.0	M94065	Hs.94925	DIHYDROOROTATE DEHYDROGENASE PRECURSOR
16255	2.0	AA013349	Hs.60602	ESTs
37972	2.0	AA479215	EST - FIC_AA479215	
41256	2.0	R31577	Hs.30696	ESTs
34834	2.0	AA292655	Hs.96557	ESTs
23169	2.0	T33215	Hs.112023	ESTs
29851	2.0	N22145	Hs.43094	ESTs
32862	2.0	W32519	Hs.55510	EST

FIG..3Da

93 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
33616	>10	W93726	Hs.55279	Protease inhibitor 5 (maspin)
34197	>10	AA232315	Hs.12540	Homo sapiens clone 23797 and 23917 mRNA partial cds
19387	>10	H20128	Hs.31656	ESTs
8125	>10	AA330771	Hs.82911	Human protein-tyrosine phosphatase (HU-PP-1) mRNA partial sequence
18362	>10	AA223912	Hs.12013	Ribonuclease L (2'5'-oligoadenylate synthetase-dependent) inhibitor
39995	>10	H62474	Hs.108240	EST
19328	>10	H17808	Hs.22858	ESTs
38590	>10	AA598648	Hs.78202	Human mRNA for transcriptional activator hSNF2b complete cds
38456	>10	AA504343	Hs.101074	ESTs
17559	>10	AA128407	Hs.71190	ESTs
6106	>10	X70683	Hs.83484	SRV (sex determining region Y)-box 4
8648	>10	AA465016	Hs.69423	Homo sapiens serine protease-like protease (nes1) mRNA complete cds
5619	>10	X14850	Hs.2711	HISTONE H2A.X
5603	>10	X14253	Hs.75561	Teratocarcinoma-derived growth factor 1
37677	>10	AA460530	Hs.98384	Homo sapiens orphan G protein-coupled receptor HG38 mRNA complete cds
11561	>10	AA236533	Hs.19222	Evi-1
16490	>10	AA026418	Hs.91539	ESTs
32240	>10	R50976	Hs.12013	Ribonuclease L (2'5'-oligoadenylate synthetase-dependent) inhibitor
12480	>10	AA403116	Hs.9880	Homo sapiens U-snRNP-associated cyclophilin (USA-CyP) mRNA complete cds
2144	>10	L41349	Hs.74014	Phospholipase C beta 4

FIG. 4Aa

94 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
12143	>10	AA290991	Hs.17296	ESTs
33006	>10	W46286	Hs.107039	ESTs Weakly similar to ZK1058.5 [C.elegans]
39535	>10	F02450	Hs.111980	ESTs Moderately similar to unknown protein [H.sapiens]
6449	>10	X89986	Hs.32936	H.sapiens mRNA for NBK apoptotic inducer protein
37653	>10	AA460017	Hs.99513	ESTs
4178	>10	U30246	Hs.110736	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds
1863	>10	L19161	Hs.121541	TRANSLATIONAL INITIATION FACTOR 2 GAMMA SUBUNIT
19787	>10	H56679	Hs.37362	ESTs
8092	>10	AA316272	Hs.24550	ESTs
10747	>10	AA055841	Hs.31953	ESTs
5002	>10	U72761	Hs.6990	Human karyopherin beta 3 mRNA complete cds
33791	>10	Z40883	Hs.65588	ESTs
6188	>10	X76029	Hs.2841	NEURICMEDIN U-25 PRECURSOR
13136	>10	AA436560	Hs.7327	ESTs
5963	>10	X63629	Hs.2877	Cadherin 3 (P-cadherin)
38179	>10	AA487492	Hs.76272	Homo sapiens clone 23592 mRNA sequence
30938	>10	N58561	Hs.84898	Cathepsin B
17987	>10	AA169379	Hs.72865	ESTs
36695	>10	AA433910	Hs.98786	ESTs
10233	>10	R71427	Hs.9081	ESTs Highly similar to PHENYLALANYL-TRNA SYNTHETASE ALPHA CHAIN CYTOPLASMIC [Saccharomyces cerevisiae]
38330	>10	AA490882	Hs.112227	ESTs
1349	>10	HG4747-HT5195	EST - HG4747-HT5195	
36962	>10	AA442082	Hs.131915	ESTs
5510	>10	X05360	Hs.58393	Cell division cycle 2 G1 to S and G2 to M
3021	>10	M68941	Hs.73826	Protein tyrosine phosphatase non-receptor type 4

FIG._4Ab

95 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
17734	>10	AA137246	Hs.84980	ESTs
36371	>10	AA426017	Hs.109761	ESTs
459	>10	D38293	Hs.77770	Human mRNA for clathrin-like protein complete cds
17419	>10	AA113349	Hs.69588	EST
14054	>10	AA485223	Hs.34892	ESTs
5021	>10	U73524	Hs.87465	Human putative ATP/GTP-binding protein (HEAB) mRNA complete cds
4994	>10	U72514	Hs.12045	Human C2f mRNA complete cds
26355	>10	AA256379	Hs.99291	ESTs
4455	>10	U43944	Hs.14732	MALATE OXIDOREDUCTASE
10748	>10	AA055892	Hs.14543	ESTs
8111	>10	AA323787	Hs.4770	ESTs
19389	>10	H20165	Hs.31734	EST
32195	>10	R43471	Hs.22355	ESTs Weakly similar to ORF YOR258w [S.cerevisiae]
21519	>10	R27975	Hs.12013	EST - FC_R27975
6167	>10	X74987	Hs.12013	Ribonuclease L (2'5'-oligoadenylate synthetase-dependent) inhibitor
41107	>10	R01634	Hs.119878	ESTs
5986	>10	X64810	Hs.78977	Protein convertase subtilisin/kexin type 1
11603	>10	AA243052	Hs.16389	ESTs Highly similar to GONADOTROPIN-RELEASING HORMONE RECEPTOR [Rattus norvegicus]
4702	>10	U57341	EST - U57341	EST - U57341
18676	>10	F04022	Hs.27885	ESTs
24197	>10	W67277	Hs.17546	ESTs
4713	>10	U57721	Hs.81771	Human L-kynurenine hydrolase mRNA complete cds
38460	>10	AA504462	Hs.105730	ESTs
18330	>10	AA216722	Hs.54481	Human mRNA for apolipoprotein E receptor 2 complete cds

FIG. 4Ac

96 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
18782	>10	F09739	Hs.12562	ESTs
42766	>10	Z99394	Hs.94432	ESTs Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]
34014	>10	AA191348	Hs.96178	ESTs
16835	>10	AA054438	Hs.60753	ESTs
29893	>10	N23003	Hs.42186	ESTs
11160	>10	AA164289	Hs.26006	ESTs
1158	>10	HG3344-HT3521	EST - HG3344-HT3521	
11813	>10	AA258158	Hs.22153	ESTs
10992	>10	AA132523	Hs.22900	Homo sapiens BAC clone RG119C02 from 7p15
5789	>10	X54925	Hs.83169	Matrix metalloproteinase 1 (interstitial collagenase)
16993	>10	AA065300	Hs.75337	Human mRNA for KIAA0035 gene partial cds
17654	>10	AA133250	Hs.62180	ESTs
39436	>10	D52692	Hs.74574	Human Ca2+-dependent activator protein for secretion mRNA complete cds
19727	>10	H52702	Hs.36690	ESTs
41381	>10	R42278	Hs.31748	H.sapiens mRNA for TRE5
22576	>10	R79111	Hs.29388	ESTs
35769	>10	AA406206	Hs.104746	ESTs
33980	>10	AA180223	Hs.8454	CAMP-DEPENDENT PROTEIN KINASE TYPE II-ALPHA REGULATORY CHAIN
37084	>10	AA446486	Hs.125129	Homo sapiens Ran binding protein 2 (RanBP2alpha) mRNA partial cds
26935	>10	AA347193	Hs.77831	ESTs Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 [Caenorhabditis elegans]
2188	>10	L47276		EST - L47276
4362	>10	U39817	Hs.36820	Bloom syndrome

FIG. 4Ad

97 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
9127	>10	D30037	Hs.91447	PHOSPHATIDYLINOSITOL
20614	>10	N59230	Hs.18937	ESTs
5692	>10	X17644	Hs.2707	G1 to S ₂ phase transition 1
4388	>10	U40714	Hs.109631	Human tyrosyl-tRNA synthetase mRNA complete cds
3598	>10	U01157	Hs.165	Glucagon-like peptide-1 receptor
24545	>10	Z38462	Hs.12403	ESTs
37456	>10	AA454632	Hs.123157	ESTs
10840	>10	AA084104	Hs.30177	ESTs
25179	>10	AA031268	Hs.113319	H.sapiens mRNA for kinesin-2
21	>10	AB000905	Hs.143080	H.sapiens histone H4 gene
18762	>10	F09458	Hs.12421	ESTs
39232	>10	AA621409	Hs.112986	ESTs
42602	>10	W86423	Hs.105413	ESTs
22372	>10	R62831	Hs.28366	EST
39110	>10	AA620709	Hs.20563	ESTs Weakly similar to HYPOTHETICAL 90.8 KD PROTEIN T05H10.7 IN CHROMOSOME II [C.elegans]
16810	>10	AA053636	Hs.129849	ESTs
29645	>10	H95840	Hs.42116	ESTs
36405	>10	AA426406	Hs.10801	Homo sapiens mRNA for KIAA0530 protein partial cds
4029	>10	U21090	Hs.74598	Human DNA polymerase delta small subunit mRNA complete cds
15006	>10	U30246	Hs.110736	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds
40594	>10	N35388	Hs.112227	ESTs
31484	>10	N69466	Hs.49683	ESTs
38601	>10	AA598738	Hs.109041	ESTs
40631	>10	N45124	Hs.6809	ESTs

FIG. 4Ae

98 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
236	>10	D13645	Hs.2471	Human mRNA for KIAA0020 gene complete cds
35803	>10	AA410295	Hs.97911	ESTs
19591	>10	H40688	Hs.33785	ESTs
38828	>10	AA609177	Hs.109363	ESTs
35798	>10	AA410231	Hs.98069	ESTs
3163	>10	M84424	Hs.1355	Cathepsin E
22400	>10	R64109	Hs.28487	ESTs
39062	>10	AA620333	Hs.112857	EST
25082	>10	AA017257	Hs.101139	ESTs
5857	>10	X58377	Hs.1721	Human mRNA for adipogenesis inhibitory factor
5214	>10	U83303	Hs.123029	H.sapiens mRNA for granulocyte chemotactic protein
36958	>10	AA442060	Hs.87507	ESTs
40660	>10	N49104	Hs.79108	NUCLEAR FACTOR RIP140
25951	>10	AA234556	Hs.135158	EST
22072	>10	R49406	Hs.28410	ESTs
39832	>10	H26279		EST - FIC_H26279
23198	>10	T40530	Hs.8241	ESTs Weakly similar to B0035.14 [<i>C.elegans</i>]
29331	>10	H68116	Hs.39063	ESTs
38316	>10	AA490500	Hs.18747	Homo sapiens ribonuclease P protein subunit p20 (RPP20) mRNA complete cds
37829	>10	AA470084	Hs.98358	ESTs
3870	>10	U14518	Hs.1594	Centromere protein A (17kD)
39176	>10	AA621091	Hs.72087	ESTs
41793	>10	T03887	Hs.7327	ESTs
32277	>10	R61493	Hs.26886	Human mRNA for rod photoreceptor protein complete cds
5558	>10	X07876	Hs.89791	Wingless-type MMTV integration site 2 human homolog
6382	>10	X85133	Hs.85273	H.sapiens RBQ-1 mRNA

FIG. 4A1

99 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
41040	>10	N91948	Hs.125034	ESTs
39080	>10	AA620552	EST - RC_AA620552_r	EST - RC_AA620552_r
20307	>10	N34830	Hs.37636	ESTs
18260	>10	AA206801	Hs.86277	ESTs
41065	>10	N93618	Hs.28554	ESTs
33109	>10	W59961	Hs.22564	Human mRNA for KIAA0389 gene complete cds
28015	>10	AA477421	Hs.21801	ESTs
30610	>10	N50138	Hs.47032	EST
34015	>10	AA191353	Hs.109884	ESTs
40559	>10	N33024	Hs.23450	ESTs
1445	>10	J03027	Hs.73885	MHC class I protein HLA-G
13242	>10	AA445994	Hs.21331	ESTs
37983	>10	AA479348	Hs.52871	H.sapiens mRNA for SYT
42242	>10	T89579	Hs.79353	Homo sapiens E2F-related transcription factor (DP-1) mRNA complete cds
37135	>10	AA447540	Hs.99112	EST
20564	>10	N55443	Hs.23625	ESTs
28141	>10	AA488432	Hs.56407	ESTs
21240	>10	R08613	Hs.20188	ESTs
34382	>10	AA252512	Hs.10069	ESTs
25948	>10	AA234365	Hs.102456	Homo sapiens survival of motor neuron protein interacting protein 1 (SIP1) mRNA complete cds
40913	>10	N69218	Hs.108232	ESTs
35697	>10	AA405512	Hs.104741	ESTs
34672	>10	AA284372	Hs.111471	ESTs
3659	>10	U04313	Hs.55279	Protease inhibitor 5 (maspin)
17051	>10	AA070801	Hs.51615	ESTs

FIG. 4Ag

100 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
19203	>10	H11593	Hs.28116	ESTs
20791	>10	N68057	Hs.90357	Homo sapiens telomeric repeat binding factor (TRF1) mRNA complete cds
24215	>10	W69425	Hs.15767	ESTs
37246	>10	AA449311	Hs.98658	Homo sapiens mitotic checkpoint protein kinase (BUB1) mRNA complete cds
6790	>10	Y12394	Hs.3886	Homo sapiens importin-alpha homolog (SRP1gamma) mRNA complete cds
25806	>10	AA149007	Hs.103871	EST
36307	>10	AA424803	Hs.98474	EST
25047	>10	AA011031	Hs.110182	ESTs
33343	>10	W79834	Hs.58559	ESTs Weakly similar to rhotekin [M.musculus]
5799	>10	X55330	Hs.111661	Aspartylglucosaminidase
23623	>10	T84047	Hs.15428	ESTs
29523	>10	H88353	Hs.139312	ESTs Weakly similar to line-1 protein ORF2 [H.sapiens]
26291	>10	AA253422	Hs.142179	ESTs
35801	>10	AA410291	Hs.114121	ESTs
40064	>10	H72283	Hs.38483	Human mRNA for KIAA0265 gene partial cds
29795	>10	N20641	Hs.46230	ESTs Highly similar to HYPOTHETICAL MYELOID CELL-LINE PROTEIN 3 [Homo sapiens]
5960	>10	X63575	Hs.89512	ATPase Ca++ transporting plasma membrane 2 (NOTE: redefinition of symbol)
37611	>10	AA458996	Hs.32970	Human signaling lymphocytic activation molecule (SLAM) mRNA complete cds
26274	>10	AA253011	Hs.88756	ESTs
37168	>10	AA447772	Hs.125153	ESTs
39433	>10	D52037	Hs.35650	Human thymidine kinase 2 (TK2) mRNA complete cds

FIG..4Ah

101 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
1570	>10	K01383		EST - K01383
30617	>10	N50646	Hs.47083	ESTs
35106	>10	AA371561	Hs.142355	EST Weakly similar to putative p150 [H.sapiens]
789	>10	D86971	Hs.78851	Human mRNA for KIAA0217 gene partial cds
4386	>10	U40622	Hs.21523	DNA repair protein XRCC4
31944	>10	N93193	Hs.80310	ESTs
13237	>10	AA443971	Hs.142495	ESTs Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY [H.sapiens]
4157	>10	U28811	Hs.78979	Human cysteine-rich fibroblast growth factor receptor (CFR-1) mRNA complete cds
2123	>10	L40396	Hs.26956	Homo sapiens (clone s22171) mRNA fragment
26926	>10	AA342402	Hs.48729	ESTs
6479	>10	X91653		EST - X91653
11969	>10	AA280670	Hs.24968	ESTs
37601	>10	AA458864	Hs.102946	ESTs
28644	>10	D12163	Hs.103262	ESTs
40604	>10	N38893	Hs.28578	Homo sapiens KIAA0428 mRNA complete cds
3913	>10	U16261	Hs.66576	Human MDA-7 (mda-7) mRNA complete cds
23759	>10	T90313	Hs.16732	ESTs
2857	>10	M58597	Hs.2173	Fucosyltransferase 4 (alpha (13) fucosyltransferase myeloid-specific)
34518	>10	AA278721	Hs.103104	ESTs
18008	>10	AA171895	Hs.30057	Homo sapiens clone 24749 and 24750 mRNA sequences
19001	>10	H02890	Hs.29885	ESTs
39488	>10	D60831	Hs.126021	ESTs
23360	>10	T58531	Hs.141905	ESTs
34105	>10	AA207123	Hs.130857	ESTs

FIG. 4Ai

102 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
38121	>10	AA485724	EST - RC_AA485724	
29080	>10	F13655	Hs.65638	ESTs Moderately similar to !!!! ALU SUBFAMILY SB1 WARNING ENTFY !!!! [H.sapiens]
9723	>10	L44542	Hs.126923	ESTs
25215	>10	AA035540	Hs.1255	APOLIPOPROTEIN AI REGULATORY PROTEIN-1
39218	>10	AA621330	Hs.114381	ESTs
20088	>10	N20054	Hs.20325	ESTs Weakly similar to putative p150 [H.sapiens]
33713	>10	Z39427	Hs.65748	ESTs
18392	>10	AA227751	Hs.55896	ESTs
42390	>10	W40150	Hs.24485	Homo sapiens chromosome-associated polypeptide (HCAP) mRNA complete cds
35693	>10	AA405485	Hs.96854	ESTs Weakly similar to similar to t complex testis-specific protein [C.elegans]
35500	>10	AA400715	Hs.107479	ESTs
1856	>10	L18920	Hs.36980	MELANOMA-ASSOCIATED ANTIGEN 2
36258	>10	AA423962	Hs.108465	ESTs Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTFY !!!! [H.sapiens]
37068	>10	AA446312	Hs.22143	ESTs Weakly similar to !!!! ALU CLASS C WARNING ENTFY !!!! [H.sapiens]
33020	>10	W46891	Hs.55968	ESTs Weakly similar to polypeptide N-acetyl/galactosaminyltransferase [H.sapiens]
27037	>10	AA400198	Hs.93753	ESTs
40827	>10	N64051	Hs.48920	Homo sapiens Werner syndrome gene complete cds
3375	>10	S50223	Hs.108642	HKR-11
37310	>10	AA451707	Hs.99246	ESTs
38235	>10	AA489030	Hs.105223	ESTs
22258	>10	R56432	Hs.26536	ESTs

FIG.-4Aj

103 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
36845	>10	AA436198	Hs.103902	ESTs
28323	>10	AA599639	Hs.50216	ESTs
30207	>10	N33920	Hs.44532	H.sapiens mRNA for diubiquitin
6494	>10	X92689	Hs.55823	H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylglucosaminyl transferase
36288	>10	AA424502	Hs.98402	ESTs
37546	>10	AA456641	Hs.99433	ESTs
4193	>10	U31116	Hs.77501	Human beta-sarcoglycan A3b mRNA complete cds
37777	>10	AA464860	Hs.115541	Homc sapiens Jak2 kinase mRNA complete cds
38280	>10	AA489791	Hs.79306	EST - RC_AA489791
2343	>10	M15353	Hs.102314	Eukaryotic translation initiation factor 4E
39045	>10	AA610077	Hs.111914	ESTs
35495	>10	AA400527	Hs.74101	ESTs
3522	>10	S80267	Hs.21320	Spleen tyrosine kinase
22282	>10	R59197	Hs.91077	ESTs
32740	>10	T92950	Hs.124918	ESTs
37057	>10	AA446131	Hs.96297	ESTs
34107	>10	AA209469	Hs.58174	EST - RC_AA252703
34391	>10	AA252703	Hs.495	Prostaglandin E receptor 3 (subtype EP3) (alternative products)
33301	>10	W73883	Hs.6592	EST - AA243375
765	>10	D86096	Hs.75530	ESTs
7785	>10	AA243375	Hs.97365	MITOTIC KINESIN-LIKE PROTEIN-1
34070	>10	AA196549	Hs.58940	AFFX-HUMTFRR/M11507_5
6041	>10	X67155	Hs.97365	ESTs
33890	>10	HUMTFRR/M11507	Hs.58940	ESTs
35277	>10	AA398536		
26059	>10	AA236685		

FIG..4Ak

104 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
25801	>10	AA148530		EST - RC_AA148530
32258	>10	R55623	Hs.26434	ESTs
34554	>10	AA280016	Hs.80961	DNA polymerase gamma
32034	>10	N98926	Hs.55209	ESTs Moderately similar to DMR-N9 PROTEIN [H.sapiens]
4787	>10	U61145	Hs.77256	Human enhancer of zeste homolog 2 (EZH2) mRNA complete cds
1684	>10	L07541	Hs.9969	Replication factor C (activator 1) 3 (38kD)
18718	>10	F04915	Hs.22226	ESTs
40427	>10	N21147	Hs.121688	ESTs
32635	>10	T61116	Hs.90527	ESTs
4306	>10	U36798	Hs.777	Homo sapiens platelet cG1-PDE mRNA complete cds
38211	>10	AA488687	Hs.142639	ESTs
6438	>10	X89398	Hs.78853	URACIL-DNA GLYCOSYLASE 1 PRECURSOR
38580	>10	AA598545	Hs.141444	ESTs
4945	>10	U69108	Hs.29736	Homo sapiens mRNA for TRAF5 complete cds
41654	>10	R76437	Hs.2001	THROMBOXANE-A SYNTHASE
41163	>10	R08176	Hs.20116	ESTs
34400	>10	AA253400	Hs.104326	ESTs
35822	>10	AA411144	Hs.104768	ESTs
26628	>10	AA280641	Hs.40128	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L39 [Rattus norvegicus]
40204	>10	H88296		EST - RC_H88296
19164	>10	H10395	Hs.30980	EST
26240	>10	AA252282	Hs.90438	Human mRNA for KIAA0152 gene complete cds
8963	>10	HUMTFRR/M11507		AFFX-HUMTFRR/M11507_M
35322	>10	AA398710	Hs.87195	H. sapiens RNA for CLCN3
1210	>10	HG37-HT37		EST - HG37-HT37

FIG._4A/

105 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
22793	>10	R96208	Hs.35533	ESTs
36052	>10	AA417027	Hs.104787	EST
26574	>10	AA279504	Hs.88629	ESTs
35197	>10	AA398120	Hs.97504	ESTs
37979	>10	AA479295	Hs.106290	ESTs Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]
4862	>10	U65437	Hs.95838	Human homeodomain-containing protein (HANF) mRNA
26700	>10	AA282197	Hs.89002	complete cds
35049	>10	AA350857	Hs.22507	EST
40083	>10	H73466	Hs.79086	ESTs
17541	>10	AA127459	Hs.108788	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3
19949	>10	H78263	Hs.124151	ESTs
4477	>10	U45880	Hs.37137	Human IAP-like protein ILP mRNA complete cds
26916	>10	AA331393	Hs.47378	ESTs
34188	>10	AA228030	Hs.120234	ESTs
29229	>10	H48459	Hs.36232	Human mRNA for KIAA0186 gene complete cds
42773	>10	YEL019c/MMS21	EST - YEL019c/MMS21	
32189	>10	R43183	Hs.95044	ESTs
36739	>10	AA435610	EST - RC_AA435610	
31310	>10	N66831	Hs.49268	EST
26545	>10	AA278979	Hs.88547	ESTs
21902	>10	R43822	Hs.22691	EST
25925	>10	AA164494	Hs.29417	ESTs Weakly similar to CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 [H.sapiens]
29344	>10	H68839	Hs.38782	EST
1346	>10	HG4716-HT5158	EST - HG4716-HT5158	

FIG.-4Am

106 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
218	>10	D13540	Hs.22868	PROTEIN-TYROSINE PHOSPHATASE 2C
26100	>10	AA242835	Hs.5917	Human mRNA for KIAA0391 gene complete cds
41593	>10	R64129	Hs.143745	ESTs
42290	>10	T95105	Hs.142670	ESTs
6713	>10	Y08564	EST Y08564	
33377	>10	W81219	Hs.42636	ESTs Weakly similar to F46B6.7 [C.elegans]
31619	>10	N73449	Hs.50273	ESTs
26718	10.0	AA282576	Hs.49407	ESTs
21558	10.0	R33112	Hs.100469	Human AF-6 mRNA complete cds
40113	10.0	H78003	Hs.15266	ESTs
10801	10.0	AA069285	Hs.9922	ESTs Weakly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 [C.elegans]
37491	10.0	AA455239	Hs.87630	ESTs Highly similar to CHROMOSOME CONDENSATION PROTEIN DPY-27 [Caenorhabditis elegans]
254	9.9	D14657	Hs.81892	Human mRNA for KIAA0101 gene complete cds
29693	9.9	H97819	Hs.42453	ESTs
26525	9.8	AA278392	Hs.43881	ESTs
13110	9.8	AA435840	Hs.19114	Human mRNA for high mobility group protein HMG2a
34863	9.7	AA299784	Hs.96641	EST
39432	9.7	D51691	Hs.82285	Phosphoribosylglycinamide formyltransferase
				phosphoribosylglycinamide synthetase
				phosphoribosylaminoimidazole synthetase
31572	9.6	N71294	Hs.110524	ESTs
17903	9.6	AA160259	Hs.72354	EST
20747	9.6	N66842	Hs.16395	ESTs
4676	9.6	U55206	Hs.78619	Human gamma-glutamyl hydrolase (hGH) mRNA complete cds

FIG. 4An

107 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
34363	9.6	AA251587	Hs.10801	Homo sapiens mRNA for KIAA0530 protein partial cds
39094	9.5	AA620636	Hs.112264	ESTs
3888	9.5	U15128	Hs.36573	Human beta-12-N-acetylglucosaminyltransferase II (MGAT2) gene complete cds
39386	9.5	D12184	Hs.3350	ESTs
4192	9.4	U31099	Hs.121479	Human DP prostanoid receptor (PTGDR) mRNA partial cds
4507	9.4	U47050	Hs.24852	Human putative calcium influx channel (htrp3) mRNA complete cds
35606	9.4	AA402227	Hs.97345	ESTs Moderately similar to N-tropomodulin [R.norvegicus]
19829	9.3	H58813	Hs.37629	EST
14837	9.3	T40145	Hs.21921	ESTs
17336	9.3	AA099585	Hs.41175	ESTs
29496	9.2	H85434	Hs.40672	EST
29943	9.2	N24786	Hs.42993	ESTs Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
17997	9.2	AA169633	Hs.72835	EST
13883	9.1	AA476917	Hs.34627	ESTs Weakly similar to No definition line found [C.elegans]
30539	9.1	N49072	Hs.93968	ESTs
26380	9.1	AA257012	Hs.88054	EST
40812	9.0	N63419	Hs.83389	ESTs
903	9.0	D90070	Hs.96	ATL-derived PMA-responsive (APR) peptide
22674	9.0	R87160	Hs.33665	ESTs
15244	8.9	W00904	Hs.8037	ESTs
18269	8.9	AA209467	Hs.92489	ESTs
19662	8.9	H47391	Hs.33947	ESTs
2548	8.8	M25897	Hs.81564	Platelat factor 4
7736	8.8	AA232121	Hs.109631	Human tyrosyl-tRNA synthetase mRNA complete cds

FIG._4Aa

108 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
39939	8.8	H53454		EST - RC_H53454
25111	8.7	AA020787	Hs.110291	ESTs
21655	8.7	R38239	Hs.25276	EST
27074	8.6	AA401475	Hs.39733	ESTs Weakly similar to C36B1.3 [C.elegans]
4959	8.5	U70322	Hs.82925	Human transportin (TRN) mRNA complete cds
2315	8.5	M14123		EST - M14123_xpt1
37253	8.5	AA449357	Hs.17731	ESTs
39624	8.5	F10836	Hs.101234	ESTs
23213	8.5	T40891	Hs.8330	ESTs
2798	8.5	M54995	Hs.2164	Connective tissue activation peptide III
32479	8.4	T16282	Hs.75188	WEE1-LIKE PROTEIN KINASE
19081	8.4	H06701	Hs.27948	ESTs Weakly similar to RHOMBOTIN-1 [H.sapiens]
21098	8.3	R00545	Hs.18930	ESTs
14723	8.3	D59894	Hs.34782	ESTs
37154	8.3	AA447666	Hs.77204	Human CENP-F kinetochore protein mRNA complete cds
8068	8.3	AA313387	Hs.133101	ESTs Highly similar to HYPOTHETICAL 84.7 KD PROTEIN ZK1098.1 IN CHROMOSOME III [Caenorhabditis elegans]
7485	8.3	AA129547	Hs.81688	ESTs
16501	8.3	AA026969	Hs.61423	ESTs
34527	8.2	AA279091	Hs.104420	ESTs
6700	8.2	Y07867	Hs.38842	H.sapiens mRNA for Pirin isolate 1
2852	8.2	M58460	Hs.91728	Human 75-kD autoantigen (PM-Sc1) mRNA complete cds
11188	8.2	AA172372	Hs.20608	ESTs
42293	8.2	T95333	Hs.122730	ESTs Weakly similar to coded for by C. elegans cDNA yk110j8.3 [C.elegans]
5443	8.2	X02530	Hs.2248	Interferon (gamma)-induced cell line protein 10 from
23371	8.1	T59505		EST - RC_T59505

FIG._4Ap

109 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
17306	8.1	AA086201	Hs.92702	ESTs
18497	8.1	AA233795	Hs.65828	ESTs
235	8.1	D13644	Hs.140933	Human mRNA for KIAA0019 gene complete cds
24525	8.1	Z38347	Hs.118338	ESTs
7826	8.1	AA248884	EST .. AA248884	
32142	8.1	R38715	Hs.123918	Human sapiens clone 24540 mRNA sequence
39067	8.1	AA620405	Hs.112860	ESTs
6235	8.0	X78416	Hs.3155	Casein alpha S1
29517	8.0	H88261	Hs.41116	ESTs
39344	7.9	C21034	Hs.76822	ESTs Moderately similar to initiation factor eIF-2B gamma subunit [R.norvegicus]
18951	7.9	H00580	Hs.29889	ESTs
18953	7.9	H00615	Hs.24227	ESTs
18376	7.9	AA226925	Hs.88057	ESTs
36023	7.8	AA416881	Hs.97383	ESTs
2192	7.8	L48211	Hs.20954	Human Sapiens angiotensin II receptor gene complete cds
33016	7.8	W46577	Hs.41716	H.sapiens mRNA for ESM-1 protein
40614	7.7	N39257	Hs.99291	ESTs
36295	7.7	AA424534	Hs.98415	ESTs
19564	7.7	H38833	Hs.32838	ESTs
16914	7.7	AA058665	Hs.23744	ESTs
35967	7.6	AA412694	Hs.6891	Human splicing factor SRP55-2 (SRP55) mRNA complete cds
21672	7.6	R38635	Hs.12328	ESTs
19918	7.6	H69787	Hs.14699	ESTs
17721	7.6	AA136590	Hs.71711	ESTs
26134	7.6	AA243763	Hs.87694	ESTs
18766	7.6	F09497	Hs.12755	ESTs

FIG. 4Aq

110 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
34492	7.5	AA262439	Hs.96	ATL-derived PMA-responsive (APR) peptide
270	7.5	D14822		EST · D14822
35975	7.4	AA412738	Hs.3688	ESTs
29842	7.4	N21688	Hs.43050	ESTs
5793	7.4	X54942	Hs.83758	CDC28 protein kinase 2
31571	7.4	N71250	Hs.50004	ESTs
23765	7.4	T90443	Hs.15053	ESTs Weakly similar to KIAA0376 [H.sapiens]
35123	7.3	AA380927	Hs.97113	EST
38252	7.3	AA489247	Hs.105234	ESTs
38216	7.3	AA488861	Hs.134943	ESTs
29418	7.2	H77915		EST · RC_H77915
42504	7.2	W69803	Hs.103159	ESTs
6111	7.2	X71125	Hs.79033	H.sapiens mRNA for glutamine cyclotransferase
41773	7.2	T03024	Hs.29170	ESTs Weakly similar to ribosomal protein L7 [H.sapiens]
9951	7.1	N71513	Hs.39328	ESTs
28109	7.1	AA485212	Hs.9591	ESTs
988	7.1	HG2160-HT2230		EST · HG2160-HT2230
29848	7.1	N22107	Hs.124215	ESTs
30628	7.1	N50744	Hs.124025	ESTs
22567	7.0	R77771	Hs.129445	ESTs
9347	7.0	H03686	Hs.112013	ESTs
11696	7.0	AA252894	Hs.20474	ESTs
40584	7.0	N34870	Hs.102520	EST
193	7.0	D10923	Hs.137555	PROEABLE G PROTEIN-COUPLED RECEPTOR HM74
18305	7.0	AA214048	Hs.259	Collagen type IV alpha 4
6078	7.0	X69141	Hs.48876	FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE
26741	6.9	AA283198	Hs.89113	ESTs

FIG. 4Ar

111 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
35069	6.9	AA358397	Hs.97007	EST
23504	6.9	T71042	Hs.12066	ESTs
299	6.9	D16815	Hs.37288	Homo sapiens orphan nuclear hormone receptor BD73 mRNA 3' end
40583	6.9	N34855	Hs.109099	ESTs
39524	6.9	F01905	Hs.14732	MALATE OXIDOREDUCTASE
34578	6.8	AA280837	Hs.111429	ESTs
9326	6.8	D89377	Hs.89404	Msh (Drosophila) homeo box homolog 2
19188	6.8	H11255	Hs.12887	ESTs Highly similar to ACTIN-LIKE PROTEIN [Bos taurus]
18185	6.8	AA194983	Hs.81791	Homo sapiens mRNA for osteoclastogenesis inhibitory factor (OCIF) complete cds
1566	6.7	J05614	EST - J05614	EST - J05614
25675	6.7	AA129757	Hs.54602	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L22 [Rattus norvegicus]
5814	6.7	X56088	Hs.1644	CYTICHRROME P450 VII
13861	6.6	AA470145	Hs.25130	ESTs
29794	6.6	N20598	Hs.94288	ESTs
39333	6.6	C20910	Hs.23960	Cyclin B1
3770	6.6	U09609	Hs.73090	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)
31831	6.6	N89894	Hs.91454	ESTs
33063	6.6	W53000	Hs.56155	Homo sapiens clone 24431 mRNA sequence
20326	6.6	N35583	Hs.8768	ESTs Weakly similar to PROBABLE E5 PROTEIN [Human papillomavirus type 58]
42596	6.5	W85900	Hs.109333	ESTs
39606	6.5	F10243	Hs.140873	ESTs Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]

FIG. 4As

112 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
14617	6.5	C14983	Hs.37380	ESTs
27360	6.4	AA425356	Hs.89306	ESTs
20126	6.4	N22015	Hs.18457	ESTs
6663	6.4	Y00291	Hs.82783	RETINOIC ACID RECEPTOR BETA-2
36472	6.4	AA428633	Hs.98604	EST
9578	6.4	H87652	Hs.24912	Homo sapiens bicaudal-D (BICD) mRNA complete cds
37308	6.4	AA451694	Hs.99244	EST
16101	6.4	AA002147	Hs.59952	EST
20629	6.3	N59798	Hs.18917	ESTs
36100	6.3	AA417740	Hs.96345	ESTs
32882	6.3	W37683	Hs.55080	ESTs
18072	6.3	AA180448	Hs.144300	EST
28125	6.3	AA486073	Hs.57362	ESTs
37464	6.2	AA454747	Hs.14934	ESTs
1441	6.2	J02963	Hs.785	Integrin alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex antigen-CD41B)
6061	6.1	X68314	Hs.2704	Glutathione peroxidase 2 gastrointestinal
32570	6.1	T30222	Hs.4220	ESTs Weakly similar to tetracycline transporter-like protein [M.musculus]
32504	6.1	T17063	Hs.65721	EST
10867	6.1	AA088458	Hs.19322	ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING ENTFY !!!! [H.sapiens]
14528	6.1	AA620295	Hs.99821	ESTs
29454	6.1	H81308	Hs.40253	EST
21940	6.0	R44538	Hs.140889	ESTs
29066	6.0	F10927	Hs.66163	Homo sapiens clone 23636 mRNA sequence
18062	6.0	AA179845	Hs.73625	ESTs Moderately similar to rabkinesin-6 [M.musculus]

FIG._4At

113 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
41745	6.0	R95895	Hs.142677	ESTs
8787	6.0	AA504307	Hs.96264	X-LINKED HELICASE II
693	5.9	D80007	Hs.45028	Human mRNA for KIAA0185 gene partial cds
4093	5.9	U25182	Hs.83383	Human antioxidant enzyme AOE37-2 mRNA complete cds
1192	5.9	HG3546-HT3744		EST - HG3546-HT3744
22956	5.9	T10248	Hs.4280	ESTs
36723	5.9	AA435524	Hs.97483	EST
2114	5.9	L40384		EST - L40384
26872	5.9	AA291137	Hs.109270	ESTs
6602	5.9	X98266		EST - X98266_cds2
42701	5.9	Z38612	Hs.144000	ESTs
28573	5.8	C21118	Hs.84541	ESTs
18290	5.8	AA211901	Hs.86430	ESTs
5330	5.8	U91327		EST - U91327
2553	5.8	M26167	Hs.72933	Human platelet factor 4 variation 1 (PF4var1) gene complete cds
38180	5.8	AA487495		EST - RC_AA487495
4244	5.7	U33286	Hs.90073	Human chromosome segregation gene homolog CAS mRNA complete cds
3977	5.7	U18991	Hs.2133	Retinal pigment epithelium-specific protein (65kD)
24673	5.7	Z39301	Hs.7859	ESTs
6928	5.7	Z46629	Hs.2316	SRY (sex-determining region Y)-box 9 (campomelic dysplasia autosomal sex-reversal)
38726	5.7	AA608733	Hs.138663	ESTs
39290	5.7	C14573	Hs.75383	Human mRNA for KIAA0029 gene partial cds
11405	5.7	AA232231	Hs.24596	ESTs
6329	5.6	X82279		EST - X82279

FIG. 4Au

114 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
2545	5.6	M25753	Hs.23960	Cyclin B1
33592	5.6	W93127	Hs.59422	ESTs
28843	5.6	D60252	Hs.113619	ESTs
6160	5.6	X74794	Hs.89699	CDC21 HOMOLOG
42515	5.5	W72116	Hs.106333	Homo sapiens clone 23622 mRNA sequence
4732	5.5	U58522	Hs.84713	Human huntingtin interacting protein (HIP2) mRNA complete cds
3299	5.5	M95623	Hs.82609	Hydroxymethylbilane synthase
28320	5.5	AA599574	Hs.65370	ESTs
746	5.5	D84454	Hs.21899	Human mRNA for UDP-galactose translocator complete cds
3117	5.4	M81182	Hs.76781	Peroxisomal membrane protein 1 (70kD Zellweger syndrome)
21257	5.4	R09196	Hs.20321	ESTs Moderately similar to M-phase phosphoprotein 11 [H.sapiens]
31487	5.4	N69507	Hs.129849	ESTs
28954	5.4	F03153	Hs.90383	ESTs
38928	5.4	AA609595	Hs.109960	ESTs
29903	5.4	N23366	Hs.93664	EST
28209	5.3	AA491250	Hs.54990	ESTs
9470	5.3	H46617		EST - H46617
9435	5.3	H30201		EST - H30201
27411	5.3	AA428137	Hs.86434	ESTs
30615	5.3	N50556	Hs.47076	ESTs
29934	5.3	N24194	Hs.43531	ESTs
1094	5.2	HG2846-HT2983		EST - HG2846-HT2983
11232	5.2	AA186804	Hs.25740	ESTs Weakly similar to unknown [S.cerevisiae]
26843	5.2	AA287450	Hs.93842	ESTs
8035	5.2	AA305116		EST - AA305116

FIG.-4AV

115 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
19263	5.1	H15054	Hs.22184	ESTs
24596	5.1	Z38810	Hs.27194	ESTs
28589	5.1	C21245	Hs.11171	H.sapiens mRNA for apoptosis specific protein
5684	5.1	X17098	Hs.108938	Pregnancy-specific beta-1 glycoprotein 6
30710	5.1	N51761	Hs.47338	EST
26360	5.1	AA256460	Hs.44610	ESTs
2351	5.1	M15796	Hs.78996	Proliferating cell nuclear antigen
30262	5.1	N35065	Hs.44690	Human sapiens clone 24739 mRNA sequence
41792	5.1	T03886	Hs.100265	ESTs
36710	5.1	AA434411	Hs.98806	ESTs
42185	5.1	T79951	Hs.111805	ESTs
18745	5.0	F09134	Hs.12839	ESTs
35746	5.0	AA406063	Hs.98003	ESTs
36900	5.0	AA436866	Hs.86178	H.sapiens mRNA for M-phase phosphoprotein mpp9
27595	5.0	AA443328	Hs.12544	ESTs
27117	5.0	AA405098	Hs.38178	ESTs Weakly similar to MOESIN/EZRIN/RADIXIN HOMOLOG [D.melanogaster]
33458	5.0	W86835	Hs.14158	Human sapiens mRNA for KIAA0636 protein complete cds
26693	5.0	AA282120	Hs.88975	EST
12669	5.0	AA417030	Hs.5101	Human sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds
29701	5.0	H97970	Hs.42476	EST
34828	4.9	AA292436	Hs.27621	Human sapiens semaphorin F homolog mRNA complete cds
14985	4.9	U15128	Hs.36573	Human beta-12-N-acetylglucosaminyltransferase II (MGAT2) gene complete cds
34761	4.9	AA287833	Hs.99668	ESTs
23211	4.9	T40889	Hs.8329	ESTs

FIG. 4Aw

116 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
40611	4.9	N39138	Hs.106794	Homo sapiens mRNA for KIAA0584 protein partial cds
42611	4.9	W87006	Hs.79440	Homo sapiens putative RNA binding protein KOC (koc) mRNA complete cds
17581	4.9	AA129395	Hs.71139	EST
18712	4.9	F04677	Hs.12381	ESTs
30709	4.9	N51752	Hs.47334	ESTs Weakly similar to synapse-associated protein sap47'-1 [D.melanogaster]
34179	4.9	AA227903	Hs.41127	ESTs Highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluorescens]
1285	4.8	HG4157-HT4427		EST · HG4157-HT4427
1106	4.8	HG2981-HT3127		EST · HG2981-HT3127
34367	4.8	AA251758	Hs.40323	Homo sapiens spleen mitotic checkpoint BUB3 (BUB3) mRNA complete cds
34802	4.8	AA291468	Hs.98504	ESTs
11595	4.8	AA242819	Hs.32539	ESTs
8295	4.8	AA405082	Hs.125014	ESTs
17622	4.8	AA131584	Hs.71435	ESTs Weakly similar to SOF1 PROTEIN [Saccharomyces cerevisiae]
34754	4.7	AA287642	Hs.81848	Human mRNA for KIAA0078 gene complete cds
37667	4.7	AA460318	Hs.110165	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L26 [Rattus norvegicus]
38622	4.7	AA598967	Hs.141982	ESTs
25038	4.7	AA010065	Hs.83758	CDC28 protein kinase 2
32503	4.7	T17045	Hs.90283	Collagen type I alpha-2
3278	4.7	M94055	Hs.54499	SODIUM CHANNEL PROTEIN BRAIN II ALPHA SUBUNIT
9696	4.7	L38961	Hs.89650	Integral transmembrane protein 1
36387	4.7	AA426270	Hs.98498	ESTs

FIG.-4Ax

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
31381	4.7	N67889	Hs.49397	ESTs
26723	4.7	AA282781	Hs.95321	ESTs Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP28 [Saccharomyces cerevisiae]
30594	4.6	N49967	Hs.46624	ESTs
38286	4.6	AA489847	Hs.112019	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Nycticebus coucang]
14474	4.6	AA609427	Hs.24164	ESTs Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTFY !!!! [H.sapiens]
5312	4.6	U90716	Hs.79187	Human cell surface protein HCAR mRNA complete cds
35588	4.6	AA401750	Hs.97343	EST
29739	4.6	H99626	Hs.42710	EST
7203	4.6	AA053096		EST ..AA053096
2157	4.6	L41939	Hs.89403	Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA complete cds
32086	4.6	R11510	Hs.52054	ESTs
8085	4.6	AA314779	Hs.105484	ESTs Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
224	4.6	D13633	Hs.77695	Human mRNA for KIAA0008 gene complete cds
33656	4.6	W95477	Hs.50582	ESTs
34065	4.6	AA195517	Hs.111160	ESTs Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTFY !!!! [H.sapiens]
6028	4.5	X66503	Hs.90011	Adenylosuccinate synthase
4166	4.5	U29463	Hs.108102	Cytochrome B561
41069	4.5	N93969	Hs.91107	H.sapiens mRNA for hFat protein
8264	4.5	AA401334	Hs.106941	ESTs
27588	4.5	AA443187	Hs.41181	ESTs
35882	4.5	AA412047	Hs.122578	ESTs

FIG. 4Ay

118 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
34479	4.5	AA262080	Hs.110736	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds
15921	4.5	Y12065	Hs.5092	Homc sapiens mRNA for nucleolar protein hNop56
11279	4.4	AA195399	Hs.24641	ESTs
39222	4.4	AA621348	Hs.110042	ESTs Highly similar to DOLICHYL-PHOSPHATE BETA-GLUCOSYLTRANSFERASE [Saccharomyces cerevisiae]
8771	4.4	AA491188	Hs.62273	ESTs
7898	4.4	AA263032	Hs.81634	ESTs
19902	4.4	H66736	Hs.34180	ESTs
10716	4.4	AA053319	Hs.9951	ESTs
13193	4.4	AA442763	Hs.20483	ESTs Highly similar to G2/MITOTIC-SPECIFIC CYCLIN B2 [Mesocricetus auratus]
5690	4.4	X17620	Hs.118638	NUCLEOSIDE DIPHOSPHATE KINASE A
17983	4.4	AA169226	Hs.72782	ESTs
31680	4.3	N74438	Hs.50492	ESTs
28731	4.3	D20981	Hs.92453	EST
28348	4.3	AA608752	Hs.71969	ESTs
33036	4.3	W48580	Hs.39972	ESTs Weakly similar to transposon LRE2 reverse transcriptase homolog [H.sapiens]
28106	4.3	AA485084	Hs.110462	ESTs
38690	4.3	AA600121	Hs.111467	ESTs
20203	4.3	N26855	Hs.5858	ESTs Moderately similar to !!! ALU SUBFAMILY SQ WARNING
10251	4.3	R76185	Hs.18171	ENTFY !!!! [H.sapiens]
31636	4.3	N73680	Hs.57435	ESTs Weakly similar to C01H6.7 [C.elegans]
1572	4.2	K01884		Natural resistance-associated macrophage protein 2
10923	4.2	AA116036	Hs.9329	EST - K01884
				ESTs

FIG. 4Az

119 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
34380	4.2	AA252414	Hs.104300	ESTs
10132	4.2	R35733		EST - R35733
16629	4.2	AA036811	Hs.61859	ESTs
25146	4.2	AA026356	Hs.108106	ESTs
28730	4.2	D20959	Hs.5858	ESTs Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]
10200	4.2	R64521	Hs.77361	ESTs
38695	4.2	AA600176	Hs.112345	ESTs
31365	4.2	N67550	Hs.48907	ESTs
42379	4.1	W37999	Hs.103018	ESTs
28050	4.1	AA479139	Hs.75393	Acid phosphatase 1 soluble
2620	4.1	M29474	Hs.73958	Human recombination activating protein (RAG-1) gene complete cds
8927	4.1	AF008442	Hs.5409	Human sapiens RNA polymerase I subunit hRPA39 mRNA complete cds
13379	4.1	AA449741	Hs.4029	ESTs Weakly similar to AF-9 PROTEIN [H.sapiens]
5134	4.1	U79293	Hs.90802	Human clone 23948 mRNA sequence
36575	4.1	AA431085	Hs.98706	EST
143	4.1	HUMTFRR/M11507		AFFX-HUMTFRR/M11507_5
10970	4.1	AA129390	Hs.5285	ESTs
25836	4.1	AA152305	Hs.2248	Interferon (gamma)-induced cell line protein 10 from
19735	4.1	H53038	Hs.36710	EST
40711	4.1	N53564	Hs.108159	ESTs
4149	4.1	U28386	Hs.2397	RAG (recombination activating gene) cohort 1
5767	4.1	X53793	Hs.118226	MULTIFUNCTIONAL PROTEIN ADE2
5503	4.1	X05232	Hs.83326	Stromelysin

FIG. 4Ba

120 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
20310	4.1	N34893	Hs.6153	ESTs Highly similar to HYPOTHETICAL 47.8 KD PROTEIN B0283.9 IN CHROMOSOME III [Caenorhabditis elegans]
456	4.1	D38145	Hs.61333	Prostaglandin I2 (prostacyclin) synthase
33651	4.0	W95409	Hs.59704	ESTs
19110	4.0	H08778	Hs.133521	ESTs
24408	4.0	W90146	Hs.35962	ESTs
26596	4.0	AA279943	Hs.88671	ESTs
32969	4.0	W42451	Hs.92260	ESTs
27006	4.0	AA398695	Hs.56159	ESTs Weakly similar to E04F6.2 gene product [C.elegans]
29809	4.0	N21043	Hs.42932	EST
9596	3.9	H91564	Hs.13540	ESTs
29024	3.9	F09315	Hs.76982	Homo sapiens mRNA for KIAA0583 protein partial cds
21694	3.9	R39317	Hs.89403	Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA complete cds
37865	3.9	AA476623	Hs.99819	ESTs Highly similar to PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C13A11.04C [Schistosoma haematobium]
8961	3.9	HUMTFRR/M11507		AFFX-HUMTFRR/M11507_3
24862	3.9	Z41415	Hs.6823	ESTs Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]
26685	3.9	AA281950	Hs.79656	ESTs
42300	3.9	T95850	Hs.100703	ESTs
6495	3.9	X92715	Hs.3057	Zinc finger protein 74 (Cos52)
38604	3.9	AA598803	Hs.111496	ESTs
30560	3.9	N49284	Hs.1334	MYB PROTO-ONCOGENE PROTEIN
14413	3.9	AA600150	Hs.14366	ESTs
38158	3.9	AA487021	Hs.105703	EST

FIG. 4Bb

121 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
2572	3.9	M27281	Hs.73793	Vascular endothelial growth factor
40100	3.8	H75933	Hs.75901	Laminin receptor (2H5 epitope)
20944	3.8	N74443	Hs.16247	ESTs
8513	3.8	AA446990	Hs.103135	ESTs
13877	3.8	AA476604	Hs.7114	ESTs
14509	3.8	AA609943	Hs.32793	ESTs
10281	3.8	R80333	Hs.21182	ESTs
25284	3.8	AA045074	Hs.110146	ESTs Weakly similar to 52-kD SS-A/Ro autoantigen [H.sapiens]
6730	3.8	Y09305	Hs.17154	H.sapiens mRNA for protein kinase Dyrk4 partial
16033	3.8	HUMISGF3A/M97935		AFFX-HUMISGF3A/M97935_MB
39242	3.8	AA621523	Hs.110832	ESTs
27354	3.8	AA425221	Hs.81688	ESTs
4552	3.8	U49188	Hs.76329	Human placenta (Diff33) mRNA complete cds
18385	3.8	AA227219	Hs.110826	Homo sapiens CAGF9 mRNA partial cds
16754	3.8	AA046067		EST - RC_AA046067
42463	3.8	W60180	Hs.103135	ESTs
867	3.7	D87716	Hs.90315	Human mRNA for KIAA0007 gene partial cds
31795	3.7	N80703	Hs.50473	ESTs
22828	3.7	R98192	Hs.35828	ESTs
25240	3.7	AA039713	Hs.110406	ESTs
4341	3.7	U38545	Hs.82587	Human ARF-activated phosphatidylcholine-specific phospholipase D1a (hPLD1) mRNA complete cds
17483	3.7	AA122147	Hs.64691	ESTs
16854	3.7	AA055552	Hs.71622	ESTs Weakly similar to KIAA0319 [H.sapiens]
3709	3.7	U07550	Hs.1197	Heat shock 10 kD protein 1 (chaperonin 10)
1608	3.7	L00205	Hs.111758	KERATIN TYPE II CYTOSKELETAL 6D
4951	3.7	U69546	Hs.82321	Human RNA binding protein Etr-3 mRNA complete cds

FIG. 4Bc

122 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
20418	3.6	N49209	Hs.32170	ESTs
27995	3.6	AA470155	Hs.75887	Homo sapiens coatmer protein (COPA) mRNA complete cds
7971	3.6	AA287423	Hs.126389	ESTs
27606	3.6	AA443793	Hs.94761	ESTs
24677	3.6	Z39338	Hs.21201	ESTs Highly similar to POLIOVIRUS RECEPTOR HOMOLOG PRECURSOR [Mus musculus]
9328	3.6	D89618	Hs.3886	Homo sapiens importin-alpha homolog (SRP1gamma) mRNA complete cds
17678	3.6	AA134275	Hs.134510	Human HIV1 tata element modulatory factor mRNA sequence from chromosome 3
36209	3.6	AA421266	Hs.13889	ESTs Weakly similar to LIS-1 protein [H.sapiens]
20064	3.6	H98653	Hs.16056	ESTs
9713	3.6	L44338	Hs.78494	Homo sapiens mRNA for KIAA0525 protein partial cds
28622	3.6	D11837	Hs.29846	ESTs
28628	3.6	D11888	Hs.62386	ESTs Moderately similar to PROHIBITIN [H.sapiens]
25804	3.5	AA148885	Hs.111710	ESTs
2492	3.5	M22898	Hs.1846	Tumcr protein p53 (Li-Fraumeni syndrome)
14904	3.5	T83389	Hs.107147	ESTs Highly similar to GEPHYRIN [Rattus norvegicus]
25265	3.5	AA043765	Hs.54649	H.sapiens RY-1 mRNA for putative nucleic acid binding protein
13606	3.5	AA456437	Hs.20386	ESTs Weakly similar to CLEAVAGE STIMULATION FACTOR 64 KD SUBUNIT [H.sapiens]
42307	3.5	T96595	EST - RC_T96595	
1544	3.5	J05068	Hs.2012	TRANSCOBALAMIN I PRECURSOR
42311	3.5	T97257	Hs.94560	ESTs
2023	3.5	L34600	Hs.3823	INITIATION FACTOR IF-2 MITOCHONDRIAL PRECURSOR
4540	3.5	U48807	Hs.2359	Human MAP kinase phosphatase (MKP-2) mRNA complete cds

FIG..4Bd

123 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
33707	3.5	Z39297	Hs.3281	Neuronal pentraxin II
17220	3.5	AA083070		EST - RC_AA083070_s
24332	3.5	W85782	Hs.18529	ESTs
35887	3.5	AA412067	Hs.98117	ESTs
8338	3.4	AA417152	Hs.5101	Human sapiens protein regulating cytokinesis 1 (PRC1)
				mRNA complete cds
387	3.4	D28589		EST - D28589
12319	3.4	AA398109	Hs.20890	ESTs
15643	3.4	W58247	Hs.27437	ESTs Highly similar to KINESIN-LIKE PROTEIN KIF4 [Mus musculus]
11218	3.4	AA180488	Hs.33746	ESTs
16539	3.4	AA029328	Hs.1191	Human mRNA for KIAA0073 gene partial cds
29203	3.4	H28581	Hs.92711	ESTs
13838	3.4	AA465342	Hs.34045	ESTs
25585	3.4	AA112389	Hs.107932	H4(D10S170)
34018	3.4	AA191488	Hs.73614	Human high-affinity copper uptake protein (hCTR1)
				mRNA complete cds
251	3.4	D14520	Hs.84728	Basic transcription element binding protein 2
3778	3.4	U09848	Hs.363	Zinc finger protein 139 (clone pHZ-37)
24535	3.4	Z38409	Hs.8053	ESTs
16127	3.4	AA004669	Hs.39441	ESTs
26149	3.4	AA250824	Hs.60478	ESTs Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]
4011	3.4	U20536	Hs.3280	Human cysteine protease Mch2 isoform alpha (Mch2)
				mRNA complete cds
5660	3.4	X16396	Hs.37791	NAD-DEPENDENT METHYLENETETRAHYDROFOLATE
				DEHYDROGENASE
26928	3.4	AA342580	Hs.47232	ESTs

FIG..4Be

124 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
36267	3.4	AA424046	Hs.98385	ESTs
32257	3.4	R54726	Hs.98493	DNA-REPAIR PROTEIN XRCC1
17365	3.4	AA101551	Hs.68900	ESTs
15296	3.3	W16684	Hs.74284	ESTs Moderately similar to S.cerevisiae hypothetical protein L3111 [H.sapiens]
17675	3.3	AA134064	Hs.44045	ESTs
10006	3.3	N81193	Hs.43133	Homo sapiens mRNA for KIAA0628 protein complete cds
33985	3.3	AA181580	Hs.81690	Homo sapiens importin beta subunit mRNA complete cds
9570	3.3	H85169	Hs.24837	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene complete cds
37551	3.3	AA456679	Hs.7256	ESTs
18367	3.3	AA224180	Hs.93332	ESTs Moderately similar to ovarian-specific protein [R.noivegicus]
14310	3.3	AA598412	Hs.8739	ESTs Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN PMT6-PCT1 INTERGENIC REGION [Saccharomyces cerevisiae]
19233	3.3	H12634	Hs.8104	ESTs
12809	3.3	AA424406	Hs.31839	ESTs
21555	3.3	R33073	Hs.24595	EST
13767	3.3	AA463234	Hs.119387	ESTs
4738	3.3	U58766	Hs.75801	Human FX protein mRNA complete cds
7258	3.3	AA075427	Hs.17296	ESTs
17041	3.3	AA070364	EST - RC_AA070364	
15504	3.3	W28362	Hs.44131	ESTs
18214	3.3	AA196635	Hs.86081	ESTs
7401	3.3	AA094800	Hs.55682	Human translation initiation factor eIF3 p66 subunit mRNA complete cds

FIG..4Bf

125 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
18912	3.3	F10913	Hs.12475	Homo sapiens clone 23617 unknown mRNA partial cds
36317	3.3	AA425089	Hs.50722	Human mRNA for KIAA0334 gene complete cds
9410	3.3	H20443	Hs.31748	H.sapiens mRNA for TRE5
2146	3.2	L41390		EST - L41390
18683	3.2	F04258	Hs.36454	ESTs Highly similar to INORGANIC PYROPHOSPHATASE [Bos taurus]
33891	3.2	HUMTFRR/M11507		AFFX-HUMTFRR/M11507_M
15840	3.2	X70944	Hs.91379	PTB-ASSOCIATED SPLICING FACTOR
3256	3.2	M92439	Hs.87157	130 kD LEUCINE-RICH PROTEIN
4400	3.2	U41387	Hs.5122	Human Gu protein mRNA partial cds
21350	3.2	R15846	Hs.21738	ESTs
11981	3.2	AA280928	Hs.24287	ESTs
23930	3.2	T96690	Hs.125123	ESTs Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTFY !!!! [H.sapiens]
30399	3.2	N45226	Hs.46495	EST
13494	3.2	AA453431	Hs.21043	ESTs
12908	3.2	AA427579	Hs.9347	ESTs
31309	3.1	N66818	Hs.42179	ESTs
31192	3.1	N64406	Hs.54174	ESTs
11288	3.1	AA196512	Hs.25916	ESTs
170	3.1	D00596	Hs.82962	Thymidylate synthase
26105	3.1	AA243133	Hs.48915	Homo sapiens serine/threonine kinase (BTAK) mRNA complete cds
11659	3.1	AA251909	Hs.36708	Homo sapiens MAD3-like protein kinase mRNA complete cds
19177	3.1	H10984	Hs.12338	ESTs
17380	3.1	AA102566	Hs.69149	ESTs
42397	3.1	W42928	Hs.103046	ESTs

FIG..4Bg

126 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
14935	3.1	T94828	Hs.63220	ESTs Weakly similar to GA BINDING PROTEIN BETA-2 CHAIN [H.sapiens]
3190	3.1	M86808	Hs.131361	PYRUVATE DEHYDROGENASE E1 COMPONENT ALPHA SUBUNIT TESTIS-SPECIFIC FORM PRECURSOR
17406	3.1	AA112979	Hs.48269	Homo sapiens mRNA for VRK1 complete cds
14130	3.1	AA489041	Hs.15140	ESTs
14134	3.1	AA489080	Hs.3566	ESTs Highly similar to phosphorylation regulatory protein HP-1) [H.sapiens]
42421	3.1	W45491	Hs.106835	ESTs Weakly similar to T23G11.7 [C.elegans]
15723	3.1	W79060	Hs.5337	ESTs Highly similar to ribosome-binding protein p34 [R.novgicus]
11140	3.1	AA158132	Hs.11817	ESTs Highly similar to YSA1 PROTEIN [Saccharomyces cerevisiae]
14522	3.1	AA610108	Hs.27693	ESTs Highly similar to PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C21E11.05C [Schizosaccharomyces pombe]
15962	3.1	Z21420	Hs.30819	ESTs
13229	3.0	AA443811	Hs.23363	ESTs
27315	3.0	AA424038	Hs.58197	ESTs
35929	3.0	AA412429	Hs.48642	ESTs
17925	3.0	AA164209	Hs.31730	Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA complete cds
5053	3.0	U76992	Hs.71134	Human Tat-SF1 mRNA complete cds
15060	3.0	U54999	Hs.93121	Human LGN protein mRNA complete cds
17757	3.0	AA147224	Hs.71814	EST
26530	3.0	AA278650	Hs.73291	ESTs
22960	3.0	T10272	Hs.4287	ESTs

FIG. 4Bh

127 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
4298	3.0	U36448	Hs.74574	Human Ca2+-dependent activator protein for secretion mRNA complete cds
7445	3.0	AA104023	Hs.110048	ESTs
18055	3.0	AA179387	Hs.73596	ESTs
7282	3.0	AA083339	Hs.126781	ESTs
806	3.0	D87009	Hs.43834	Human (lambda) DNA for immunoglobulin light chain
38447	3.0	AA504255	Hs.54404	Human protein kinase ATR mRNA complete cds
41464	3.0	R46837	Hs.107450	ESTs
9662	3.0	L19161	Hs.121541	TRANSLATIONAL INITIATION FACTOR 2 GAMMA SUBUNIT
15174	3.0	U82987	Hs.87246	Human Bcl-2 binding component 3 (bbc3) mRNA partial cds
33620	3.0	W93943	Hs.59509	ESTs
41077	3.0	N95028	Hs.125031	ESTs
1932	3.0	L24804	Hs.75839	Human (p23) mRNA complete cds
39556	3.0	F03738	Hs.3657	ESTs
32156	3.0	R40381	Hs.142852	ESTs
13617	3.0	AA456646	Hs.28661	ESTs
11989	3.0	AA281251	Hs.35696	ESTs Weakly similar to trithorax protein trxl [D.melanogaster]
6056	2.9	X68194	Hs.80919	Pantrcophysin [human keratinocyte line HaCaT mRNA 2106 nt]
1605	2.9	L00058	Hs.79070	V-myc: avian myelocytomatosis viral oncogene homolog
4536	2.9	U48705	Hs.75562	Receptor protein-tyrosine kinase EDDR1
10173	2.9	R56678	Hs.102963	ESTs Weakly similar to cell division control protein CDC21 [H.sapiens]
21009	2.9	N90401	Hs.28928	ESTs
36200	2.9	AA421164	Hs.107213	ESTs
35299	2.9	AA398622	Hs.75133	Transcription factor 6-like 1 (mitochondrial transcription factor 1-like)
9804	2.9	M74558	Hs.142965	Human SIL mRNA complete cds

FIG..4Bi

128 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
12313	2.9	AA397916	Hs.22595	ESTs
5928	2.9	X62048	Hs.75188	WEE1-LIKE PROTEIN KINASE
18199	2.9	AA195318	Hs.63311	ESTs
19867	2.9	H61476	Hs.15641	ESTs
6081	2.9	X69398	Hs.82685	CD47 antigen (Rh-related antigen integrin-associated signal transducer)
5254	2.9	U86782	Hs.76887	Human 26S proteasome-associated pad1 homolog (POH1) mRNA complete cds
13579	2.9	AA455967	Hs.106705	Human neuronal PAS2 (NPAS2) mRNA complete cds
38495	2.9	AA505118	Hs.112255	Human nucleoporin 98 (NUP98) mRNA complete cds
2028	2.9	L35035	Hs.79886	RIBOSE 5-PHOSPHATE ISOMERASE
27374	2.9	AA425816	Hs.64641	ESTs Weakly similar to Y53C12A.3 [C.elegans]
26108	2.9	AA243189	Hs.53652	ESTs
4189	2.8	U30930	Hs.57700	UDP glycosyltransferase 8 (UDP-galactose ceramide galactosyltransferase)
16708	2.8	AA043944	Hs.62663	ESTs
357	2.8	D26156	Hs.78202	Human mRNA for transcriptional activator hSNF2b complete cds
26045	2.8	AA236276	Hs.87287	ESTs
8059	2.8	AA310967	Hs.5080	ESTs Weakly similar to T04A8.11 [C.elegans]
21358	2.8	R16079	Hs.14775	ESTs
3572	2.8	S87759	Hs.57764	Protein phosphatase 2C alpha [human teratocarcinoma mRNA 2346 nt]
11877	2.8	AA262727	Hs.9591	ESTs
35830	2.8	AA411448	Hs.139386	ESTs
20151	2.8	N22895	Hs.6831	Homc sapiens clone 1400 unknown protein mRNA partial cds
38648	2.8	AA599267		EST - RC_AA599267

FIG.-4Bj

129 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
7777	2.8	AA236820	Hs.118236	ESTs
32845	2.8	W31566	Hs.55459	EST
28258	2.8	AA505133	Hs.62273	ESTs
35944	2.8	AA412488	Hs.98150	ESTs
30648	2.8	N50971	Hs.42116	ESTs
8616	2.8	AA460077	Hs.28555	ESTs
34929	2.8	AA342084	EST .. RC_AA342084	
326	2.8	D21262	Hs.75337	Human mRNA for KIAA0035 gene partial cds
6480	2.8	X91788	Hs.84974	H.sapiens mRNA for lcln protein
25202	2.8	AA034527	Hs.95182	EST
1681	2.8	L07493	Hs.1608	Replication protein A (E coli RecA homolog RAD51 homolog)
14566	2.8	AA621122	Hs.5198	ESTs
14182	2.8	AA490885	Hs.21766	ESTs
18253	2.7	AA206370	Hs.86248	ESTs
22911	2.7	T03865	Hs.27047	ESTs
35549	2.7	AA401274	Hs.31730	Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA complete cds
35955	2.7	AA412528	Hs.20183	ESTs Weakly similar to ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH [R.noirvegicus]
17642	2.7	AA132983	Hs.44155	ESTs Moderately similar to C-1-TETRAHYDROFOLATE SYNTHASE CYTOPLASMIC [H.sapiens]
6131	2.7	X72841	Hs.2758	Human retinoblastoma-binding protein (RbAp46) mRNA complete cds
41429	2.7	R44994	Hs.108182	ESTs
22937	2.7	T10065	Hs.4214	Homo sapiens TLS-associated protein TASR-2 mRNA complete cds

FIG..4Bk

130 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
16243	2.7	AA012902	Hs.60556	ESTs
6444	2.7	X89750	Hs.90077	H.sapiens mRNA for TGIF protein
6240	2.7	X78627	Hs.75066	H.sapiens mRNA for translin
42116	2.7	T69924		EST - RC_T69924
7701	2.7	AA215333	Hs.97101	ESTs
17568	2.7	AA128905	Hs.22587	ESTs
42534	2.7	W73189	Hs.89403	Homc sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA complete cds
29813	2.7	N21111	Hs.42946	ESTs
35273	2.7	AA398507	Hs.97361	ESTs
32563	2.7	T27697	Hs.21603	Human mRNA for KIAA0036 gene complete cds
13223	2.7	AA443720	Hs.7551	ESTs
8494	2.7	AA443460	Hs.3430	ESTs
1130	2.7	HG3132-HT3308		EST - HG3132-HT3308
2379	2.7	M16937	Hs.819	Human homeo box c1 protein mRNA complete cds
18906	2.7	F10868	Hs.46571	Human SH3 domain-containing protein SH3P18 mRNA complete cds
34796	2.7	AA291259	Hs.97101	ESTs
33688	2.7	Z38501	Hs.8768	ESTs Weakly similar to PROBABLE E5 PROTEIN [Human papillomavirus type 58]
30733	2.7	N52078	Hs.13604	Homo sapiens mRNA for KIAA0637 protein complete cds
21256	2.7	R09195	Hs.86013	Homo sapiens mRNA for KIAA0564 protein partial cds
9296	2.7	D82775	Hs.10724	ESTs Weakly similar to unknown [S.cerevisiae]
3154	2.7	M83712	Hs.1614	Cholinergic receptor nicotinic alpha polypeptide 5
7383	2.7	AA093834	Hs.109822	ESTs Weakly similar to HYPOTHETICAL 16.8 KD PROTEIN IN SMY2-RPS101 INTERGENIC REGION [S.cerevisiae]
1923	2.7	L23808	Hs.1695	Matrix metalloproteinase 12 (macrophage elastase)

FIG..4BI

131 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
30407	2.6	N45983	Hs.46572	ESTs
26286	2.6	AA253351	Hs.44439	ESTs
9558	2.6	H81497	Hs.12063	ESTs
18104	2.6	AA188801	Hs.85634	ESTs
8865	2.6	AB002359	Hs.105478	Human mRNA for KIAA0361 gene KIAA0361 protein
20422	2.6	N49300	Hs.24908	ESTs
41602	2.6	R67258	Hs.58215	ESTs Moderately similar to rhotekin [M.musculus]
4821	2.6	U62801	Hs.79361	Human protease M mRNA complete cds
16807	2.6	AA053296	Hs.63136	ESTs
15288	2.6	W07562	Hs.26198	ESTs Moderately similar to rA8 [R.norvegicus]
23822	2.6	T91715	Hs.14574	ESTs Highly similar to HYPOTHETICAL 103.6 KD PROTEIN IN COX5B-PFK26 INTERGENIC REGION [Saccharomyces cerevisiae]
10951	2.6	AA126719	Hs.25282	ESTs
26891	2.6	AA292659	Hs.93667	ESTs
7699	2.6	AA215299	Hs.70830	Homo sapiens chromosome 19 cosmid R30783
11308	2.6	AA207114	Hs.27842	ESTs
4086	2.6	U24704	Hs.111709	Human antiselectory factor-1 mRNA complete cds
38615	2.6	AA598938		EST - RC_AA598938
11819	2.6	AA258189	Hs.32471	ESTs
37433	2.6	AA454103	Hs.110031	ESTs
5587	2.6	X13482	Hs.80506	U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A'
19841	2.6	H59617	Hs.5199	ESTs Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD [Drosophila melanogaster]
10655	2.6	AA040882	Hs.10290	ESTs
31574	2.6	N71303	Hs.50015	EST
7614	2.6	AA187579	Hs.102696	ESTs Weakly similar to Yel007c-ap [S.cerevisiae]

FIG. 4Bm

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
7090	2.6	AA009913	Hs.103300	Homo sapiens diphthamide biosynthesis protein-2 (DPH2) mRNA complete cds
24219	2.6	W69960	Hs.19416	ESTs
19070	2.6	H05970	Hs.133828	Human clone 23960 mRNA sequence
17719	2.6	AA136569	Hs.144295	EST
11362	2.6	AA227261	Hs.20922	ESTs
8613	2.6	AA459555	Hs.31921	Homo sapiens mRNA for KIAA0648 protein partial cds
13866	2.6	AA476319	Hs.5327	ESTs
39552	2.6	F03605	Hs.75574	PUTATIVE 60S RIBOSOMAL PROTEIN
1795	2.6	L13434	Hs.84162	Human chromosome 3p21.1 gene sequence complete cds
14746	2.6	D60354	Hs.90315	Human mRNA for KIAA0007 gene partial cds
2993	2.6	M64929	Hs.75200	Protein phosphatase 2 (formerly 2A) regulatory subunit B (PR 52) alpha isoform
12986	2.6	AA430032	Hs.7487	ESTs Moderately similar to PTTG gene product [R.norvegicus]
18003	2.5	AA171692	Hs.70980	ESTs
42653	2.5	W92703	Hs.103239	ESTs
30438	2.5	N47204	Hs.46680	ESTs Weakly similar to C50F4.12 [C.elegans]
26135	2.5	AA243765	Hs.76977	ESTs
15457	2.5	W27560	Hs.90789	ESTs
27748	2.5	AA453159	Hs.41723	Human kinesin-like spindle protein HKSP (HKSP) mRNA complete cds
32315	2.5	R69840	Hs.70189	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE
25310	2.5	AA046745	Hs.110457	HOMOLOG [Nycticebus coucang]
9658	2.5	L16991	Hs.79006	Deoxythymidylate kinase
12210	2.5	AA293774	Hs.21261	ESTs Weakly similar to PROBABLE TRYPTOPHANYL-TRNA SYNTHETASE MITOCHONDRIAL [C.elegans]

132 / 454

FIG. 4Bn

133 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
32826	2.5	W20391	Hs.20830	Human mRNA for kinesin-related protein partial cds
9692	2.5	L37747	Hs.89497	LAMIN B1
27862	2.5	AA458908	Hs.50883	ESTs
17288	2.5	AA085178	Hs.24382	ESTs
9888	2.5	N35449	Hs.111449	ESTs Highly similar to HYPOTHETICAL 30.3 KD PROTEIN IN APE1/LAP4-CWP1 INTERGENIC REGION [Saccharomyces cerevisiae]
5932	2.5	X62153	Hs.82479	Minichromosome maintenance deficient (S. cerevisiae) 3
26834	2.5	AA287138	Hs.59346	ESTs Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus]
5157	2.5	U80034	Hs.68583	Human mitochondrial intermediate peptidase precursor (MIPEP) mRNA mitochondrial gene encoding mitochondrial protein complete cds
38434	2.5	AA497013	Hs.142592	ESTs
7590	2.5	AA173505	Hs.35353	ESTs Weakly similar to HYPOTHETICAL 46.1 KD PROTEIN IN PHC2-POL3 INTERGENIC REGION [S.cerevisiae]
14960	2.5	U05237	Hs.99872	Human fetal Alz-50-reactive clone 1-(FAC1) mRNA complete cds
13585	2.5	AA455999	Hs.22151	ESTs Highly similar to NEUROLYSIN PRECURSOR [Sus scrofa]
38185	2.5	AA487508	Hs.9877	Homo sapiens mRNA for KIAA0688 protein complete cds
34678	2.5	AA284744	Hs.75510	Annexin XI (56kD autoantigen)
1424	2.5	J02645	Hs.81613	Eukaryotic translation initiation factor 2A
21876	2.5	R43286		EST - FC_R43286
34290	2.5	AA236866	Hs.111314	ESTs
18109	2.5	AA188981	Hs.58169	Homo sapiens retinoblastoma-associated protein HEC mRNA complete cds

FIG. 4Bo

134 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
6485	2.5	X92098	Hs.75914	H.sapiens mRNA for transmembrane protein rnp24
27444	2.5	AA430160	Hs.42785	ESTs Weakly similar to F25H9.7 [C.elegans]
30037	2.5	N27439	Hs.51652	ESTs
27602	2.5	AA443702	Hs.29835	ESTs Weakly similar to W02B12.7 [C.elegans]
3390	2.5	S59184	Hs.79350	RYK receptor-like tyrosine kinase
25040	2.5	AA010188	Hs.103305	ESTs
40477	2.4	N24006	Hs.99348	Homo sapiens BAC clone RG300E22 from 7q21-q31.1
18620	2.4	F02506	Hs.9417	ESTs
15120	2.4	U73524	Hs.87465	Human putative ATP/GTP-binding protein (HEAB) mRNA complete cds
28813	2.4	D59257	Hs.91161	Human C-1 mRNA complete cds
34723	2.4	AA287115	Hs.99697	ESTs
7960	2.4	AA285277	Hs.8932	Homo sapiens brain expressed ring finger protein mRNA complete cds
18927	2.4	F11087	Hs.12544	ESTs
28443	2.4	AA621611	Hs.70877	ESTs
452	2.4	D38076	Hs.24763	RAN binding protein 1
11701	2.4	AA253031	Hs.31730	Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA complete cds
12672	2.4	AA417067	Hs.13055	ESTs
4836	2.4	U63717	Hs.95821	Human osteoclast stimulating factor mRNA complete cds
42200	2.4	T83729		EST - FC_I83729
28395	2.4	AA610064	Hs.73602	ESTs
36390	2.4	AA426291	Hs.108527	ESTs Weakly similar to No definition line found [C.elegans]
12916	2.4	AA427745	Hs.37747	ESTs
36786	2.4	AA435815	Hs.77965	Human Clk-associated RS cyclophilin CARS-Cyp mRNA complete cds

FIG. 4Bd

135 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
39462	2.4	D60063	Hs.9012	ESTs
14420	2.4	AA600322	Hs.19574	ESTs Highly similar to AAC-RICH MRNA CLONE AAC3 PROTEIN [Dictyostelium discoideum]
27431	2.4	AA429038	Hs.40541	ESTs
6387	2.4	X85372	Hs.105465	H.sapiens mRNA for Sm protein F
11342	2.4	AA223874	Hs.14843	Homo sapiens mRNA for KIAA0704 protein partial cds
1497	2.4	J04088	Hs.3378	Topoisomerase (DNA) II alpha (170kD)
11454	2.4	AA233854	Hs.23348	ESTs
32978	2.4	W42788	Hs.1098	Human terminal transferase mRNA complete cds
27872	2.4	AA459254	Hs.48855	ESTs
11623	2.4	AA243617	Hs.31082	ESTs
22142	2.4	R51382	Hs.124275	Homo sapiens mRNA for KIAA0659 protein partial cds
13533	2.4	AA454607	Hs.38114	ESTs Highly similar to HYPOTHETICAL 40.2 KD PROTEIN K12H4.3 IN CHROMOSOME III [Caenorhabditis elegans]
6231	2.4	X78121	Hs.2010	Choroideremia
24371	2.4	W87415	Hs.16918	ESTs Weakly similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII [H.sapiens]
25286	2.4	AA045261	Hs.108259	ESTs
8163	2.4	AA357394	Hs.98073	ESTs
12233	2.4	AA343513	Hs.28813	ESTs Weakly similar to LINE/Ig H-chain fusion protein [M.musculus]
14371	2.4	AA599219	Hs.30272	ESTs Moderately similar to ALR [H.sapiens]
26169	2.4	AA251089	Hs.94576	ESTs Weakly similar to ORF YOR281c [S.cerevisiae]
23065	2.4	T23539	Hs.7165	ESTs Highly similar to zinc finger protein [M.musculus]
20524	2.4	N53965	Hs.15741	ESTs
20837	2.4	N69263	Hs.20524	ESTs Highly similar to HEXOKINASE TYPE I [Homo sapiens]
21195	2.4	R07210	Hs.19913	ESTs

FIG. 4Ba

136 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
13377	2.4	AA449720	Hs.20201	Homo sapiens clone 24706 mRNA sequence
17352	2.3	AA100925	Hs.20990	ESTs
11914	2.3	AA278907	Hs.24549	ESTs
28796	2.3	D51272		EST - RC_D51272_s
22491	2.3	R70012	Hs.29055	EST
40847	2.3	N66354	Hs.109437	ESTs
42022	2.3	T53138	Hs.19582	Homo sapiens mRNA for hTCF-4
8053	2.3	AA309880	Hs.109957	ESTs
363	2.3	D26528	Hs.123058	Human mRNA for RNA helicase complete cds
26679	2.3	AA281733	Hs.4310	ESTs
31858	2.3	N90680	Hs.54642	EST
24092	2.3	W42845	Hs.14611	Homo sapiens protein tyrosine phosphatase PIR1 mRNA complete cds
19428	2.3	H22949	Hs.31942	EST
27264	2.3	AA418389	Hs.42219	ESTs
13600	2.3	AA456286	Hs.30794	ESTs
13552	2.3	AA454943	Hs.29911	ESTs
26583	2.3	AA279774	Hs.142497	ESTs
3674	2.3	U05237	Hs.99872	Human fetal Alz-50-reactive clone 1 (FAC1) mRNA complete cds
33694	2.3	Z38770	Hs.71623	ESTs
16977	2.3	AA064616	Hs.66983	ESTs
5948	2.3	X63337		EST - X63337
24247	2.3	W73010	Hs.108761	Ribosomal protein L37
40879	2.3	N67816	Hs.53263	ESTs Moderately similar to !!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]

FIG._4Br

137 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
5875	2.3	X59405	Hs.83532	Membrane cofactor protein (CD46 trophoblast-lymphocyte cross-reactive antigen)
9239	2.3	D79100	Hs.83196	ESTs
41997	2.3	T47788	Hs.109628	ESTs
39565	2.3	F04320	Hs.35120	Replication factor C 37-kD subunit
7404	2.3	AA094989	Hs.7381	Homo sapiens voltage dependent anion channel protein mRNA complete cds
6388	2.3	X85373	Hs.77496	H.sapiens mRNA for Sm protein G
14529	2.3	AA620307	Hs.27379	ESTs
21197	2.3	R07320	Hs.19936	ESTs
28203	2.3	AA490969	Hs.59838	ESTs
38320	2.3	AA490611	Hs.99838	ESTs
4674	2.3	U54999	Hs.93121	Human LGN protein mRNA complete cds
26756	2.3	AA283832	Hs.86619	ESTs
11567	2.3	AA236747	Hs.30327	Homo sapiens mitogen activated protein kinase activated protein kinase gene complete cds
25050	2.3	AA011134	Hs.25863	ESTs Weakly similar to renin [H.sapiens]
41935	2.3	T29681	Hs.75761	Human serine kinase mRNA complete cds
26895	2.3	AA292765	Hs.42650	H.sapiens mRNA for M-phase phosphoprotein mpp5
3343	2.3	M97936	Hs.21486	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA
42435	2.3	W46994	Hs.109903	ESTs
5937	2.2	X62534	Hs.80684	High-mobility group (nonhistone chromosomal) protein 2
25756	2.2	AA135868	Hs.95783	ESTs
34184	2.2	AA227959	Hs.3280	Human cysteine protease Mch2 isoform alpha (Mch2) mRNA complete cds
8672	2.2	AA477046	Hs.59838	ESTs

FIG. 4Bs

138 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
7387	2.2	AA093977	Hs.71475	ESTs
18016	2.2	AA173223	Hs.44426	ESTs
20843	2.2	N69352	Hs.5683	Homo sapiens mRNA for ATP-dependent RNA helicase #46 complete cds
10054	2.2	R10266	Hs.120997	ESTs Highly similar to HYPOTHETICAL GTP-BINDING PROTEIN IN PMI40-PAC2 INTERGENIC REGION [Saccharomyces cerevisiae]
34094	2.2	AA206088	Hs.104139	ESTs
41246	2.2	R27296	Hs.23240	ESTs
22634	2.2	R82837	Hs.103329	ESTs
19686	2.2	H48502	Hs.28212	ESTs
28448	2.2	AA621752	Hs.76887	Human 26S proteasome-associated pad1 homolog (POH1) mRNA complete cds
651	2.2	D78129		EST - [78129
20221	2.2	N29345	Hs.28917	ESTs
5792	2.2	X54941	Hs.77550	CDC28 protein kinase 1
28656	2.2	D19708	Hs.5122	Human Gu protein mRNA partial cds
19240	2.2	H13265	Hs.31196	ESTs
11688	2.2	AA252672	Hs.103300	Homo sapiens diphthamide biosynthesis protein-2 (DPH2) mRNA complete cds
14152	2.2	AA489790	Hs.4976	Homo sapiens Ran-GTP binding protein mRNA partial cds
38341	2.2	AA490967	Hs.105276	ESTs
11803	2.2	AA257971	Hs.21214	ESTs
39085	2.2	AA620599	Hs.24766	ESTs
4046	2.2	U22376	Hs.1334	MYB PROTO-ONCOGENE PROTEIN
11600	2.2	AA242868	Hs.7395	ESTs Weakly similar to house-keeping protein [M.musculus]

FIG. 4Bt

139 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
5051	2.2	U76638	Hs.54089	Human BRCA1-associated RING domain protein (BARD1)
20674	2.2	N63392	Hs.128003	mRNA complete cds
41031	2.2	N91246	Hs.102897	ESTs
24711	2.2	Z39645	Hs.21470	ESTs
4733	2.2	U58658	Hs.57689	ESTs
				Human unknown protein mRNA within the p53 intron 1 complete cds
29733	2.2	H99398	Hs.42680	EST
23155	2.2	T30550	Hs.22615	ESTs
34638	2.2	AA282987	Hs.104473	EST
1889	2.2	L20591	Hs.1378	Annexin III (lipocortin III)
4136	2.2	U28014	Hs.74122	IGH-2 PROTEASE PRECURSOR
20276	2.2	N32919	Hs.27931	ESTs
18238	2.2	AA205389	Hs.41145	ESTs
13250	2.1	AA446459	Hs.27599	ESTs
34370	2.1	AA251829	Hs.104058	ESTs Weakly similar to HYPOTHETICAL 27.4 KD PROTEIN IN MEF2-CPR7 INTERGENIC REGION
				[Saccharomyces cerevisiae]
27996	2.1	AA470156	Hs.80449	ESTs Weakly similar to dynein 74K chain cytosolic [R.norvegicus]
10804	2.1	AA069549	Hs.18479	ESTs
34552	2.1	AA279985	Hs.18389	Human mRNA for KIAA0372 gene complete cds
18380	2.1	AA227119	Hs.70256	ESTs
37415	2.1	AA453807	Hs.99349	EST
14582	2.1	AA621340	Hs.10600	ESTs Weakly similar to HYPOTHETICAL 39.6 KD PROTEIN IN MTD1-NUP133 INTERGENIC REGION
				[Saccharomyces cerevisiae]

FIG. 4Bu

140 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
5173	2.1	U81554	Hs.5171	Homo sapiens signal recognition particle 72 (SRP72) mRNA complete cds
19972	2.1	H83639	Hs.33576	ESTs
23301	2.1	T52847	Hs.13034	ESTs
20504	2.1	N52966	Hs.142838	ESTs
40145	2.1	H81391	Hs.81182	Human mRNA for histamine N-methyltransferase complete cds
3461	2.1	S75256	EST - S75256	EST - S75256
41893	2.1	T23611	Hs.51251	ESTs
36021	2.1	AA416876	Hs.5169	ESTs Weakly similar to TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521 [H.sapiens]
5807	2.1	X55740	Hs.76856	5' nucleotidase (CD73)
38155	2.1	AA486777	Hs.105698	ESTs
924	2.1	HG1112-HT1112	EST - HG1112-HT1112	EST - HG1112-HT1112
8384	2.1	AA424282	Hs.91728	Human 75-kD autoantigen (PM-Sc1) mRNA complete cds
25165	2.1	AA027837	Hs.30705	Retinitis pigmentosa 3 (X-linked recessive)
24348	2.1	W86469	Hs.77899	Tropomyosin alpha chain (skeletal muscle)
35340	2.1	AA398900	EST - FIC_AA398900	EST - FIC_AA398900
10898	2.1	AA112063	Hs.15313	ESTs Weakly similar to PRE-MRNA SPLICING HELICASE BRR2 [S.cerevisiae]
381	2.1	D28473	Hs.78770	Isoleucine-tRNA synthetase
22051	2.1	R49047	Hs.31975	ESTs Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
11528	2.1	AA236018	Hs.10724	ESTs Weakly similar to unknown [S.cerevisiae]
11890	2.1	AA278323	Hs.17481	Homo sapiens clone 24606 mRNA sequence
5448	2.1	X02751	Hs.69855	Neuroblastoma RAS viral (v-ras) oncogene homolog
35956	2.1	AA412533	Hs.109571	ESTs
7525	2.1	AA149259	Hs.69851	ESTs

FIG. 4Bv

141 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
39592	2.1	F09351	Hs.16492	ESTs Weakly similar to weakly similar to <i>S. cerevisiae</i> PTM1 precursor [<i>C.elegans</i>]
28029	2.1	AA478479	Hs.71992	ESTs
18425	2.1	AA232103	Hs.59112	ESTs
33368	2.1	W80814	Hs.47283	ESTs
20590	2.1	N58146	Hs.34227	ESTs
12907	2.1	AA427577	Hs.26502	ESTs
22958	2.1	T10264	Hs.116122	ESTs
39	2.1	AB003698	Hs.28853	Homo sapiens mRNA for Cdc7-related kinase complete cds
14350	2.1	AA598831	Hs.17121	ESTs
25593	2.1	AA113149	Hs.8130	Homo sapiens IPL (IPL) mRNA complete cds
26529	2.1	AA278594	Hs.88461	EST
6681	2.1	Y00971	Hs.2910	Phosphoribosyl pyrophosphate synthetase 2
16879	2.1	AA056538	Hs.63314	ESTs
38040	2.1	AA481403	Hs.107213	ESTs
4111	2.1	U26312	Hs.83550	Human heterochromatin protein HP1Hs-gamma mRNA complete cds
32878	2.1	W37448	Hs.41241	ESTs
25968	2.1	AA234935	Hs.65032	ESTs
24659	2.1	Z39211	Hs.12299	Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP) mRNA complete cds
38030	2.1	AA481148	Hs.105157	ESTs
61	2.0	AC002115	Hs.83379	Cytochrome c oxidase subunit VIb
37681	2.0	AA460675	Hs.31748	H.sapiens mRNA for TRE5
27125	2.0	AA405505	Hs.48295	Homo sapiens mRNA for putative RNA helicase 3' end
3780	2.0	U09851	Hs.112180	Zinc finger protein 148 (pHZ-52)
9112	2.0	D16611	Hs.89866	Coproporphyrinogen oxidase (coproporphyrin harderoporphyria)

FIG. 4Bw

142 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
7519	2.0	AA147425		EST - AA147425_s
14701	2.0	D59324	Hs.124852	ESTs
380	2.0	D28423		EST - D28423
825	2.0	D87328	Hs.79375	Holocarboxylase synthetase (biotin-[propionyl-Coenzyme A-carboxylase (ATP-hydrolysing)] ligase)
3997	2.0	U19906	Hs.2131	Arginine vasopressin receptor 1 (AVPR1)
377	2.0	D28364		EST - D28364
28379	2.0	AA609710	Hs.42582	ESTs
7322	2.0	AA090692	Hs.135552	ESTs Weakly similar to The KIAA0138 gene product is novel. [H.sapiens]
29358	2.0	H70641		EST - FC_H70641
24230	2.0	W72276	Hs.5950	ESTs
40212	2.0	H88535	Hs.9564	Human clone 121711 defective mariner transposon Hsmar2 mRNA sequence
36319	2.0	AA425107	Hs.97016	ESTs
25654	2.0	AA126951	Hs.110857	ESTs Weakly similar to DNA-directed RNA polymerase [D.melanogaster]
16344	2.0	AA018907	Hs.5427	ESTs
8118	2.0	AA328993	Hs.104558	ESTs
29962	2.0	N25228	Hs.27349	ESTs
32236	2.0	R49327	Hs.57435	Natural resistance-associated macrophage protein 2
37972	2.0	AA479215		EST - RC_AA479215
34834	2.0	AA292655	Hs.96557	ESTs

FIG. 4Bx

143 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
2348	>10	M15656	Hs.75592	Aldolase B fructose-bisphosphate
6463	>10	X90908	Hs.74126	H.sapiens mRNA for l-15P (l-BABP) protein
42139	>10	T73335	Hs.93194	APOLIPOPROTEIN A-I PRECURSOR
4544	>10	U48959	Hs.75950	H.sapiens mRNA for myosin light chain kinase
1583	>10	K02765	Hs.58512	COMPLEMENT C3 PRECURSOR
2426	>10	M19828	Hs.585	Apolipoprotein B (including Ag(x) antigen)
8859	>10	AB002351	Hs.10587	Human mRNA for KIAA0353 gene partial cds
24572	>10	Z38688	Hs.24192	ESTs
17810	>10	AA151402	Hs.46531	ESTs
7006	>10	Z70295	Hs.32966	H.sapiens mRNA for GCAP-II/uroguanylin precursor
1304	>10	HG4310	EST - HG4310-HT4580	EST - HG4310-HT4580
5980	>10	X64559	Hs.65424	Tetranectin (plasminogen-binding protein)
41987	>10	T47089	Hs.121713	Cytochrome P450 subfamily XXI (steroid 21-hydroxylase congenital adrenal hyperplasia)
24461	>10	W94427	Hs.3807	ESTs Weakly similar to SODIUM/POTASSIUM-TRANSPORTING ATPASE GAMMA-CHAIN [Mus
2372	>10	M16594	Hs.89552	Glutathione S-transferase A2
6001	>10	X65727	Hs.89552	Glutathione S-transferase A2
1750	>10	L10955	Hs.89485	Carbonic anhydrase IV
15130	>10	U77643	Hs.95655	Homo sapiens K12 protein precursor mRNA complete cds
12467	>10	AA402656	Hs.28264	ESTs
41148	>10	R06984	EST - RC_R06984_s	EST - RC_R06984_s
31652	>10	N73958	Hs.50404	Human chemokine (TECK) mRNA complete cds
4605	>10	U51010	EST - U51010	EST - U51010
28359	>10	AA609133	Hs.58115	ESTs

FIG. 5Aa

144 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
24066	>10	W32506	Hs.111676	ESTs Weakly similar to HEAT SHOCK 27 KD PROTEIN [H.sapiens]
33282	>10	W73194	Hs.80552	ESTs
12084	>10	AA284767	Hs.21910	ESTs
41473	>10	R48732	Hs.11006	ESTs
27108	>10	AA404397	Hs.58414	ESTs Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]
2848	>10	M58286	Hs.159	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR
19537	>10	H30270	Hs.32583	ESTs
18784	>10	F09748	Hs.7974	ESTs
5773	>10	X54162	Hs.79386	64 KD AUTOANTIGEN D1
27387	>10	AA426330	Hs.78264	ESTs
2866	>10	M59815	Hs.76682	Complement component 4A
42530	>10	W72859	Hs.74669	ESTs Weakly similar to SYNAPTOBREVIN 2 [H.sapiens]
827	>10	D87433	Hs.84753	Human mRNA for KIAA0246 gene partial cds
650	>10	D78014	Hs.74566	Human mRNA for dihydropyrimidinase related protein-3 complete cds
7026	>10	Z80345	Hs.127610	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
16736	>10	AA045306	Hs.42996	ESTs
4630	>10	U52101	Hs.9999	Human 5'UTR mRNA complete cds
4655	>10	U52969	Hs.80296	BRAIN SPECIFIC POLYPEPTIDE PEP-19
42758	>10	Z41411	Hs.107040	ESTs
35637	>10	AA402933	Hs.29283	ESTs
40392	>10	H99587	Hs.108880	ESTs
7354	>10	AA092348	Hs.7858	ESTs

FIG. 5Ab

145 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
9034	>10	C01833	Hs.29759	ESTs Weakly similar to !!!! ALU SUBFAMILY SX WARNING ENTRY III! [H.sapiens]
10935	>10	AA121534	Hs.6923	ESTs Highly similar to TUBULIN BETA-5 CHAIN [Gallus gallus]
5520	>10	X06256	Hs.119218	Integrin alpha 5 (fibronectin receptor alpha polypeptide)
2547	>10	M25809	Hs.1009	ATPase H+ transporting lysosomal (vacuolar proton pump) beta polypeptide 56/58kD isoform 1
9003	>10	C00808	Hs.107882	ESTs
41628	>10	R70212	Hs.79630	Immunoglobulin-associated alpha
21934	>10	R44449	Hs.48778	ESTs
11129	8	AA156873	Hs.15970	ESTs
40387	7	H99460	Hs.108873	ESTs

FIG..5Ac

146 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
2348	>10	M15656	Hs.75592	Aldolase 3 fructose-bisphosphate
6463	>10	X90908	Hs.74126	H.sapiens: mRNA for I-15P (-BABP) protein
42139	>10	T73335	Hs.93194	APOLIPROTEIN A-I PRECURSOR
4544	>10	U48959	Hs.75950	H.sapiens: mRNA for myosin light chain kinase
1583	>10	K02765	Hs.58512	COMPLEMENT C3 PRECURSOR
2426	>10	M19828	Hs.585	Apolipoprotein B (including Ag(x) antigen)
8859	>10	AB002351	Hs.10587	Human mRNA for KIAA0353 gene partial cds
24572	>10	Z38688	Hs.24192	ESTs
17810	>10	AA151402	Hs.46531	ESTs
7006	>10	Z70295	Hs.32966	H.sapiens: mRNA for GCAP-II/uroguanylin precursor
1304	>10	HG4310-		EST - HG4310-HT4580
5980	>10	X64559		Tetranectin (plasminogen-binding protein)
41987	>10	T47089	Hs.65424	Cytochrome P450 subfamily XXI (steroid 21-hydroxylase congenital adrenal hyperplasia)
			Hs.121713	ESTs Weakly similar to SODIUM/POTASSIUM-TRANSPORTING ATPASE GAMMA CHAIN [Mus musculus]
24461	>10	W94427	Hs.3807	Glutathione S-transferase A2
2372	>10	M16594	Hs.89552	Glutathione S-transferase A2
6001	>10	X65727	Hs.89552	Glutathione S-transferase A2
1750	>10	L10955	Hs.89485	Carbonic anhydrase IV
15130	>10	U77643	Hs.95655	Homo sapiens K12 protein precursor mRNA complete cds
12467	>10	AA402656	Hs.28264	ESTs
41148	>10	R06984		EST - RC_R06984_s
31652	>10	N73958	Hs.50404	Human chemokine (TECK) mRNA complete cds
23483	>10	T68873	Hs.143289	H.sapiens mRNA for metallothionein isoform 1R
4605	>10	U51010		EST - U51010
28359	>10	AA609133	Hs.58115	ESTs

FIG. 6Aa

147 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
24066	>10	W32506	Hs.111676	ESTs Weakly similar to HEAT SHOCK 27 KD PROTEIN [H.sapiens]
33282	>10	W73194	Hs.80552	ESTs
12084	>10	AA284767	Hs.21910	ESTs
41473	>10	R48732	Hs.11006	ESTs
32568	>10	T29248	Hs.143113	Human pancreatic lipase related protein 2 (PLRP2) mRNA complete cds
6413	>10	X87159	Hs.37129	Sodium channel nonvoltage-gated 1 beta (Liddle syndrome)
20707	>10	N64436	Hs.20813	ESTs
27108	>10	AA404397	Hs.58414	ESTs Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]
12477	>10	AA403032	Hs.21701	ESTs
42059	>10	T61654	Hs.93194	APOLIPOPROTEIN A-I PRECURSOR
25468	>10	AA079072	Hs.1477	Insulin-like growth factor binding protein 6
26910	>10	AA303081	Hs.78293	ESTs
16938	>10	AA059473	Hs.66783	ESTs
41788	>10	T03735	Hs.26885	ESTs
7754	>10	AA234634	Hs.76722	Human N ^F -IL6-beta protein mRNA complete cds
6122	>10	X72012	Hs.75962	Endoglin (Osler-Rendu-Weber syndrome 1)
2848	>10	M58286	Hs.159	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR
23013	>10	T16661	Hs.6725	ESTs
19537	>10	H30270	Hs.32583	ESTs
4584	>10	U50360	EST - U50360	EST - U50360
37410	>10	AA453652	Hs.99344	ESTs
27969	>10	AA464594	Hs.63382	ESTs
35497	>10	AA400606	Hs.144344	EST

FIG. 6Ab

148 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
37013	>10	AA443690	Hs.136268	ESTs Highly similar to ZINC FINGER PROTEIN HF.12 [Homo sapiens]
39247	>10	AA621553	Hs.112998	ESTs
13471	>10	AA452598	Hs.109590	ESTs
42110	>10	T68878	Hs.76688	Carboxylesterase 2 (liver)
10965	>10	AA128997	Hs.18953	Homo sapiens cGMP-specific phosphodiesterase (PDE9A2) mRNA complete cds
4918	>10	U67733	Hs.3831	Human cGMP-stimulated 3'5'-cyclic nucleotide phosphodiesterase PDE2A3 (PDE2A) mRNA complete cds
40737	>10	N54950	Hs.81454	H.sapiens: KHK mRNA for ketohexokinase clone pHKHK3a
30403	>10	N45300	Hs.110647	Meis1 (mouse) homolog
11432	>10	AA233369	Hs.361	ESTs
18784	>10	F09748	Hs.7974	ESTs
40662	>10	N49281		EST - RC_N49281
5773	>10	X54162	Hs.79386	64 KD ALTOANTIGEN D1
35041	>10	AA350586	Hs.30862	ESTs
20868	>10	N70068	Hs.7243	ESTs
39729	>10	H11489	Hs.105805	ESTs
27387	>10	AA426330	Hs.78264	ESTs
39758	>10	H15814	Hs.80485	Human apM1 mRNA for GS3109 (novel adipose specific collagen-like factor) complete cds
4319	>10	U37283	Hs.58882	Human microfibril-associated glycoprotein-2 MAGP-2 mRNA complete cds
2866	>10	M59815	Hs.76682	Complement component 4A
30332	>10	N39075	Hs.44934	EST
41344	>10	R40189	Hs.6985	ESTs

FIG.-6Ac

149 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
28271	>10	AA521200	Hs.48778	ESTs
5834	>10	X57129	Hs.7644	HISTONE H1D
19048	>10	H05464	Hs.100251	ESTs
1429	>10	J02854	Hs.9615	Human 20-kDa myosin light chain (MLC-2) mRNA complete cds
19491	>10	H27910	Hs.107384	ESTs
29992	>10	N26386	Hs.33084	Solute carrier family 2 (facilitated glucose transporter) member 5
2041	>10	L36033	Hs.77423	Stromal cell-derived factor 1
22865	>10	R99909	Hs.36186	ESTs
11624	>10	AA243654	Hs.17998	ESTs
12512	>10	AA405199	Hs.20733	ESTs
41443	>10	R45577	Hs.10683	ESTs
5055	>10	U77180	Hs.50002	Human α RNA for EBI1-ligand chemokine complete cds
6038	>10	X66945	Hs.748	Basic fibroblast growth factor (bFGF) receptor (shorter form)
42530	>10	W72859	Hs.74669	ESTs Weakly similar to SYNAPTOBREVIN 2 [H.sapiens]
827	>10	D87433	Hs.84753	Human α RNA for KIAA0246 gene partial cds
650	>10	D78014	Hs.74566	Human α RNA for dihydropyrimidinase related protein-3 complete cds
37350	>10	AA452606	Hs.99289	EST
37488	>10	AA455178	Hs.99397	ESTs
36646	>10	AA431797	Hs.98763	EST
38999	>10	AA609907		EST - RC_AA609907
38191	>10	AA487895	Hs.17311	ESTs
9944	>10	N57464	Hs.74670	Human mRNA for KIAA0146 gene partial cds
8139	>10	AA341723	Hs.107374	ESTs
41522	>10	R53966	Hs.75092	N-CHIMAERIN

FIG. 6Ad

150 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
38090	>10	AA482603	Hs.111301	Matrix metalloproteinase 2 (gelatinase A 72kD gelatinase 72kD type IV collagenase)
41175	>10	R09241		EST - R09241
36947	>10	AA437388	Hs.115726	ESTs
4175	>10	U29953	Hs.76110	Pigment epithelium-derived factor
35421	>10	AA399686	Hs.97669	EST
4358	>10	U39487	Hs.250	Xanthine dehydrogenase
35463	>10	AA400272	Hs.97758	EST
7026	>10	Z80345	Hs.127610	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
34625	>10	AA282238	Hs.118463	Homo sapiens clone 24519 unknown mRNA partial cds
20179	>10	N24879	Hs.9693	ESTs
36805	>10	AA435901	Hs.56874	ESTs Weakly similar to p20 protein [R.norvegicus]
24447	>10	W93121	Hs.23841	Human mRNA for KIAA0355 gene complete cds
10247	>10	R74386	Hs.108924	ESTs
3618	>10	U02388	Hs.101	Leukotriene B4 omega hydroxylase (cytochrome P450 subfamily IVF)
1464	>10	J03474	Hs.3157	SERUM AMYLOID A PROTEIN PRECURSOR
16842	>10	AA055163	Hs.57975	Homo sapiens mRNA for cardiac calsequestrin complete cds
16736	>10	AA045306	Hs.42996	ESTs
22666	>10	R85880	Hs.33455	ESTs
5248	>10	U86358	Hs.50404	Human chemokine (TECK) mRNA complete cds
7510	>10	AA136353	Hs.38022	ESTs
34683	>10	AA284920	Hs.13716	ESTs
19986	>10	H89980	Hs.12112	ESTs Moderately similar to protein phosphatase 1 binding protein PTG [M.musculus]
9959	>10	N75215	Hs.43148	ESTs

FIG. 6Ae

151 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
38136	>10	AA486185	Hs.125176	ESTs
36702	>10	AA434108	Hs.101393	ESTs Moderately similar to DNAJ PROTEIN HOMOLOG 1 [Homo sapiens]
3357	>10	M99487	Hs.1915	PROSTATE-SPECIFIC MEMBRANE ANTIGEN
36783	>10	AA435805	Hs.112065	EST
4876	>10	U66061	Hs.2048	Protease serine 2 (trypsin 2)
41149	>10	R06986	Hs.76487	ESTs
15925	>10	Y13492	Hs.78483	Homo sapiens mRNA for smoothelin
12944	>10	AA428258	Hs.8769	ESTs
9317	>10	D87468	Hs.40888	Human mRNA for KIAA0278 gene partial cds
19331	>10	H17865	Hs.23213	ESTs
5032	>10	U74382	Hs.90357	Homo sapiens telomeric repeat binding factor (TRF1) mRNA complete cds
34239	>10	AA235009	Hs.32246	ESTs
32852	>10	W31906	Hs.116428	ESTs
6432	>10	X89066	Hs.94413	Transient receptor potential channel 1
37001	>10	AA443311	Hs.98998	ESTs
4630	>10	U52101	Hs.9999	Human Y11P mRNA complete cds
19489	>10	H27852	Hs.28137	ESTs
23028	>10	T17215	Hs.6952	ESTs
35359	>10	AA399061	Hs.112961	ESTs Moderately similar to PANCREATITIS-ASSOCIATED PROTEIN 1 PRECURSOR [H.sapiens]
4655	>10	U52969	Hs.80296	BRAIN SPECIFIC POLYPEPTIDE PEP-19
26030	>10	AA235984	Hs.87469	ESTs
41348	>10	R40395	Hs.112125	Lecithin-cholesterol acyltransferase
14494	>10	AA609645	Hs.25632	ESTs Weakly similar to PNG gene [H.sapiens]

FIG. 6A1

152 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
4453	>10	U43916	Hs.79368	Human epithelial membrane protein-(CL-20) mRNA complete cds
42758	>10	Z41411	Hs.107040	ESTs
35637	>10	AA402933	Hs.29283	ESTs
40392	>10	H99587	Hs.108880	ESTs
19366	>10	H19204	Hs.133466	ESTs
5184	>10	U82169	Hs.87234	Human frizzled homolog (FZD3) mRNA complete cds
859	>10	D87468	Hs.40888	Human mRNA for KIAA0278 gene partial cds
1595	>10	K03207	Hs.103972	Salivary proline-rich protein
15574	>10	W38778	Hs.26216	ESTs
8985	>10	C00125	Hs.24332	ESTs Weakly similar to similar to deoxyribose-phosphate aldolase [<i>C.elegans</i>]
33995	>10	AA182845	Hs.139088	Homo sapiens FIP2 alternatively translated mRNA complete cds
7949	>10	AA283620	Hs.34956	ESTs
11670	>10	AA252191	Hs.25199	Homo sapiens PAC clone DJ130H16 from 22q12.1-qter
7354	>10	AA092348	Hs.7858	ESTs
36151	>10	AA419011	Hs.96744	ESTs
42136	>10	T72491	Hs.73849	Apolipoprotein C-III
289	>10	D16480	Hs.75860	Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein) alpha subunit
41379	>10	R42233	Hs.106487	Homo sapiens mRNA for KIAA0673 protein partial cds
34764	>10	AA287870	Hs.890	Lymphotoxin-beta
24515	>10	Z38289	Hs.12701	ESTs
18652	>10	F03111	Hs.22505	ESTs

FIG.-6Aa

153 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
37815	>10	AA469952	Hs.97899	ESTs
9034	>10	C01833	Hs.29759	ESTs Weakly similar to !!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!! [H.sapiens]
34805	>10	AA291522	Hs.97250	EST
12246	>10	AA348198	Hs.14829	Homo sapiens mRNA for GABA-BR1a (hGB1a) receptor
42153	>10	T77729	Hs.89890	Pyruvate carboxylase
27110	>10	AA404494	Hs.84112	CTP synthetase
28831	>10	D59722	Hs.92924	ESTs
6333	>10	X82494	Hs.2653	Fibulin 2
10935	>10	AA121534	Hs.6923	ESTs Highly similar to TUBULIN BETA-5 CHAIN [Gallus gallus]
27257	>10	AA418001	Hs.46146	ESTs Weakly similar to mitogen-activated kinase kinase 5 [H.sapiens]
3631	>10	U03090	Hs.290	Homo sapiens Ca2+-dependent phospholipase A2 mRNA complete cds
4752	>10	U59632	Hs.3847	Glycoprotein Ib (platelet) beta polypeptide
3766	>10	U09579	Hs.74984	CYCLIN-DEPENDENT KINASE INHIBITOR 1
4310	>10	U37055	Hs.76034	Macrophage stimulating 1 (hepatocyte growth factor-like)
26923	>10	AA342302	Hs.55036	ESTs
5520	>10	X06256	Hs.119218	Integrin alpha 5 (fibronectin receptor alpha polypeptide)
16720	>10	AA044732	Hs.77208	ESTs
25336	>10	AA053405	Hs.101404	ESTs
2547	>10	M25809	Hs.1009	ATPase H+ transporting lysosomal (vacuolar proton pump) beta polypeptide 56/58kD isoform 1
9796	>10	M63509	Hs.73974	Glutathione S-transferase M2 (muscle)
5206	>10	U82979	Hs.67846	Human clone HM18 monocyte inhibitory receptor precursor mRNA complete cds

FIG.--6Ah

154 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
9377	>10	H12674	Hs.9396	ESTs
41960	>10	T33511	Hs.4844	ESTs
21911	>10	R43980	Hs.26320	ESTs
16225	>10	AA011305	Hs.10029	Cathepsin C
16071	>10	AA001426	Hs.40863	ESTs
29335	>10	H68239	Hs.39122	ESTs
34966	>10	AA344866	Hs.1285	Complement component 8 gamma polypeptide
21076	>10	N99976	Hs.8016	ESTs
4402	>10	U41518	Hs.74602	AQUAPCRIN-CHIP
20423	>10	N49308	Hs.104938	ESTs
16575	>10	AA031948	Hs.57548	ESTs
28264	>10	AA521080	Hs.46765	ESTs
9003	>10	C00808	Hs.107882	ESTs
5632	>10	X15357	EST - X15357	
20852	>10	N69540	Hs.17713	ESTs
34585	>10	AA281002	Hs.40735	ESTs
33690	>10	Z38607	Hs.62248	ESTs
8904	>10	AF002256	Hs.86180	Homo sapiens killer cell receptor (KIR103) mRNA allele ASD1 complete cds
3307	>10	M95809	Hs.89578	BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT
39200	>10	AA621246	Hs.112956	EST
24712	>10	Z39652	Hs.27457	ESTs
2199	>10	L49169	Hs.75678	Human GOS3 mRNA complete cds
38942	>10	AA609646	Hs.94970	Human mRNA for KIAA0306 gene partial cds
41628	>10	R70212	Hs.79630	Immunoglobulin-associated alpha
6834	>10	Z18954	Hs.2960	S100 calcium-binding protein A5 (formerly S100D)

FIG. 6A

155 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
40562	>10	N33212	Hs.107197	ESTs
37333	>10	AA452158	Hs.75122	TRANSFORMING PROTEIN RHOB
3992	>10	U19713	Hs.76364	Allograft inflammatory factor 1
38734	>10	AA608792	Hs.112591	EST
37836	>10	AA470135	Hs.112238	ESTs
10000	>10	N79674	Hs.7915	ESTs
30658	>10	N51105	Hs.111223	ESTs
17629	>10	AA131919	Hs.69009	ESTs
36260	>10	AA423970	Hs.98378	ESTs
24122	>10	W46947	Hs.4188	ESTs
1066	>10	HG2705-		EST - HG2705-HT2801
12389	>10	AA399633	Hs.24872	ESTs
26025	>10	AA235874	Hs.88888	PUTATIVE DNA BINDING PROTEIN A20
41104	>10	R01398		EST - RC_R01398
33586	>10	W93015	Hs.73166	Treacher Collins syndrome susceptibility protein
25379	>10	AA058893	Hs.111841	Human a-tenyl cyclase-associated protein homolog CAP2 (CAP2) mRNA complete cds
17907	>10	AA160530	Hs.72447	ESTs
36838	>10	AA436163	Hs.95851	Homo sapiens Pig12 (PIG12) mRNA complete cds
19524	>10	H29566	Hs.83466	Homo sapiens clone 23579 mRNA sequence
21934	>10	R44449	Hs.48778	ESTs
32456	>10	T15829	Hs.65264	ESTs
15440	>10	W27301	Hs.111652	ESTs Moderately similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA [Thermomonospora curvata]
2807	>10	M55210	Hs.87428	Laminin gamma 1 (formerly LAMB2)
34193	>10	AA232251	Hs.128630	ESTs

FIG. 6A

156 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
14584	>10	AA621414	Hs.110903	Homo sapiens transmembrane protein mRNA complete cds
38752	>10	AA608852	Hs.112603	EST
5294	>10	U90065	Hs.79351	Human two P-domain K+ channel TWIK-1 mRNA complete cds
84	>10	AF001359		EST - AF001359_f
4856	>10	U65093	Hs.82071	Human msg1-related gene 1 (mrg1) mRNA complete cds
13974	>10	AA479299	Hs.21107	ESTs
26151	>10	AA250836	Hs.108509	ESTs
5938	>10	X62535	Hs.74044	Diacylglycerol kinase alpha (80kD)
17717	>10	AA136541	Hs.71647	EST
12404	>10	AA400292	Hs.23786	ESTs
2407	>10	M18737	Hs.90708	GRANZYME A PRECURSOR
26620	10	AA280413	Hs.89843	Spleen focus forming virus (SFFV) proviral integration oncogene spi1
37675	10	AA460377	Hs.99816	ESTs
41827	10	T15445	Hs.99491	H.sapiens: mRNA for F25B3.3 kinase like protein from C.elegans
82	10	AF000959	Hs.110903	Homo sapiens transmembrane protein mRNA complete cds
203	10	D12620	Hs.106242	CYTOCHROME P450 IVF3
24159	10	W57862	Hs.21289	ESTs
5302	10	U90543	Hs.79041	Human b.tyrophilin (BTF1) mRNA complete cds
2219	10	L76670	Hs.109610	Homo sapiens nkat7 mRNA complete cds
24392	10	W88568	Hs.58589	Homo sapiens glycogenin-2 gamma (glycogenin-2) mRNA complete cds
36159	10	AA419279	Hs.82813	Colony-stimulating factor 1 (M-CSF)
28251	10	AA504512	Hs.76852	ESTs Weakly similar to ZK792.1 [C.elegans]
37592	10	AA458668	Hs.95898	ESTs
39619	9	F10640	Hs.12354	ESTs

FIG. 6A

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
8240	9	AA397841	Hs.106879	ESTs
10887	9	AA101632	Hs.22971	ESTs
37500	9	AA455474	Hs.100530	ESTs
42650	9	W92272	Hs.25601	Homo sapiens zinc-finger helicase (hZFh) mRNA complete cds
9011	9	C01394	Hs.106823	Homo sapiens clone 24818 mRNA sequence
3490	9	S77763	Hs.75643	Homo sapiens NF-E2 protein (NF-E2) mRNA complete cds
36691	9	AA432381	Hs.97357	ESTs Moderately similar to NITRIC OXIDE SYNTHASE INDUCIBLE [H.sapiens]
3478	9	S76992	Hs.104005	Vav 2 oncogene
42034	9	T56281	Hs.110440	Human metallothionein (MT)I-F gene
11845	9	AA259064	Hs.10839	ESTs Weakly similar to unknown [S.cerevisiae]
19317	9	H17476	Hs.11615	ESTs Weakly similar to dual specificity phosphatase [H.sapiens]
42395	8	W42733	Hs.109870	ESTs
11425	8	AA233257	Hs.25511	Homo sapiens mRNA for Hic-5 partial cds
15310	8	W19098	Hs.7921	ESTs
36601	8	AA431337	Hs.98017	ESTs
13499	8	AA453458	Hs.7301	ESTs
37514	8	AA455914	Hs.1019	Parathyroid hormone receptor 1
5998	8	X65644	Hs.75063	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 ENHANCER-BINDING PROTEIN 2
33589	8	W93074	Hs.59342	ESTs
5801	8	X55448	Hs.3118	H.sapiens mRNA for 2.19 gene
11129	8	AA156873	Hs.15970	ESTs
31987	8	N94551	Hs.55060	ESTs
40438	8	N21684	Hs.80500	Human mRNA for KIAA0061 gene partial cds
34471	8	AA258843	Hs.111376	ESTs

FIG. 6A1

158 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
25530	8	AA098834	Hs.83428	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)
39471	7	D60265	Hs.107894	ESTs
25100	7	AA019426	Hs.103343	EST
15915	7	Y09858	Hs.82577	Human DNA sequence from clone 323P24 on chromosome Xp11.21-11.23 Contains SPIN (spindlin homolog (PROTEIN DXF34) hypothetical protein E
19097	7	H08171	Hs.30842	ESTs
35353	7	AA398962	Hs.97699	ESTs
36822	7	AA435978	Hs.98852	EST
35530	7	AA400893	Hs.41717	Human 3'5' cyclic nucleotide phosphodiesterase (HSPDE1A3A) mRNA complete cds
3869	7	U14417	Hs.106185	Human Fial guanine nucleotide dissociation stimulator mRNA partial cds
1979	7	L29339	Hs.1964	Solute carrier family 5 (sodium/glucose cotransporter) member 1
26178	7	AA251153	Hs.27910	Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA complete cds
36428	7	AA427605	Hs.98551	Human cardiac myosin binding protein-C (MyBP-C) gene complete cds
26333	7	AA256075	Hs.82280	Homo sapiens regulator of G protein signaling 10 mRNA complete cds
40387	7	H99460	Hs.108873	ESTs
27236	7	AA417037	Hs.67805	ESTs
20083	7	H99879	Hs.28029	ESTs Highly similar to EPIDERMAL GROWTH FACTOR PRECURSOR [Mus musculus]

FIG. 6Am

159 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
21561	7	R33245	Hs.23076	ESTs
21223	7	R08175	Hs.110130	Homo sapiens chromosome 19 cosmid F22329
13405	7	AA450118	Hs.25722	ESTs Weakly similar to KRUPPEL-RELATED ZINC FINGER PROTEIN 1 [Homo sapiens]
34845	7	AA293420	Hs.95464	ESTs Moderately similar to transcription enhancer factor TEF1 [H.sapiens]
15059	7	U53831	Hs.85280	Human interferon regulatory factor 7 (humirf7) mRNA complete cds
1945	7	L25878	Hs.89649	Epoxide hydrolase 1 microsomal (xenobiotic)
42648	7	W92150	Hs.79310	Human GAP SH3 binding protein mRNA complete cds
20041	7	H97012	Hs.11050	ESTs Weakly similar to L8004.7 gene product [S.cerevisiae]
7053	6	Z84721	Hs.75792	Hemoglobin alpha 1
23843	6	T92561	Hs.110422	ESTs
25815	6	AA149889	Hs.96200	ESTs Weakly similar to A-kinase anchor protein 95 AKAP95 [R.norvegicus]
8473	6	AA437346	Hs.2967	SHB adaptor protein (a Src homology2 protein)
34618	6	AA282143	Hs.58094	H.sapiens mRNA for melanoma growth regulatory protein MIA
11074	6	AA148983	Hs.29068	ESTs
17533	6	AA127098	Hs.71057	EST
28973	6	F04014	Hs.65996	ESTs
17042	6	AA070397		EST - RC_AA070397
15246	6	W01094	Hs.84628	ESTs
2247	6	M10321	Hs.110802	VON WILLEBRAND FACTOR PRECURSOR
30810	6	N53419	Hs.47646	ESTs
13348	6	AA449267	Hs.17914	ESTs Weakly similar to HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT [M.musculus]

FIG._6An

160 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
1789	6	L13258	Hs.936	Solute carrier family 17 (sodium phosphate) member 2
16627	5	AA036779	Hs.61826	Homo sapiens clone 23928 mRNA sequence
27103	5	AA404282	Hs.63481	ESTs Weakly similar to kynurenine/alpha-aminoadipate aminotransferase [R.norvegicus]
12631	5	AA412293	Hs.21258	ESTs
11599	5	AA242829	Hs.7508	ESTs
9010	5	C01360	Hs.67364	Homo sapiens clone 23904 mRNA sequence
4660	5	U53225	Hs.75283	Sorting nexin 1
5244	5	U85992	Hs.87197	Human clone IMAGE:35527 unknown protein mRNA partial cds
7953	5	AA284403	Hs.74750	Homo sapiens mRNA for KIAA0554 protein partial cds
27617	5	AA446114	Hs.55409	ESTs
39480	5	D60419	Hs.81915	STATHMIN
37529	5	AA456112	Hs.99410	ESTs
11858	5	AA262308	Hs.106385	ESTs
37294	5	AA450127	Hs.110571	ESTs Highly similar to MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD118 [Mus musculus]
23201	5	T40652	Hs.8279	ESTs
28767	5	D45608	Hs.83792	Surfactant pulmonary-associated protein D
3151	4	M83652	Hs.53155	Properdin P factor complement
29196	4	H24456	Hs.85053	Homo sapiens clone 24440 mRNA sequence
12863	4	AA425782	Hs.27973	ESTs
42486	4	W68410	Hs.106857	Calbindin 2 (29kD calretinin)
23571	4	T80628	Hs.108169	ESTs
12376	4	AA399271	Hs.19610	ESTs
27894	4	AA460319	Hs.48469	ESTs
24935	4	AFFX-	AFFX-HLUMGAPDH/M33197_M	

FIG.-6A0

161 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
4238	4	U33053	Hs.2499	Human lipid-activated protein kinase PRK1 mRNA complete cds
41844	4	T15833	Hs.100227	EST
20111	4	N21380	Hs.25497	H.sapiens mRNA for ROX protein
8316	4	AA410529	Hs.30732	ESTs
39794	4	H21819	Hs.14896	Homo sapiens clone 24590 mRNA sequence
1517	4	J04501	Hs.772	Glycogen synthase 1 (muscle)
9164	4	D38081	Hs.89887	Thromboxane A2 receptor
35027	4	AA349996	Hs.96937	ESTs
14158	4	AA490182	Hs.118598	ESTs
41950	4	T33137	Hs.7967	ESTs
34360	4	AA251547	Hs.104358	EST
6547	4	X95808	Hs.9568	Human mRNA for KIAA0385 gene complete cds
20863	4	N69989	Hs.19167	ESTs
12734	4	AA419200	Hs.5737	ESTs
39497	4	D80154	Hs.56340	ESTs
1600	4	K03474	EST - K03474	
27148	4	AA406231	Hs.100113	Human mRNA for KIAA0381 gene partial cds
10763	4	AA057620	Hs.30807	ESTs
17007	4	AA069696	Hs.67317	ESTs
13522	4	AA454115	Hs.6000	ESTs
18444	4	AA232646	Hs.68061	ESTs
27665	3	AA447759	Hs.134724	ESTs
21382	3	R16896	Hs.89615	PROTEIN KINASE C THETA TYPE
2052	3	L36818	Hs.75339	Inositol polyphosphate phosphatase-like protein 1 (51C protein)
9039	3	C02049	Hs.106291	ESTs
34888	3	AA303078	Hs.94479	Human GT334 protein (GT334) gene mRNA complete cds

FIG. 6A

162 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
11047	3	AA142849	Hs.22660	ESTs
19451	3	H23747	Hs.31697	ESTs
2822	3	M55621	Hs.117946	N-acetylglucosaminyltransferase I
13928	3	AA478441	Hs.11590	ESTs
12064	3	AA283848	Hs.11367	ESTs Weakly similar to KIAA0009 [H.sapiens]
3836	3	U12707	Hs.2157	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)
4528	3	U48251	Hs.75871	Homo sapiens protein kinase C-binding protein RACK7 mRNA partial cds
42064	3	T63364	Hs.9225	ESTs Highly similar to FIBRINOGEN-LIKE PROTEIN A PRECURSOR [Parastichopus parvimensis]
4596	3	U50743	Hs.19520	Sodium/potassium ATPase gamma subunit
4914	3	U67611	Hs.2799	EST - U67611
20168	3	N24106	Hs.16511	Cartilage linking protein 1
24281	3	W79773	Hs.31597	ESTs
19634	3	H44866	Hs.8023	ESTs
10989	3	AA132366	Hs.8135	Homo sapiens mRNA for SPOP
6587	3	X97748	Hs.8944	EST - X97748
14096	3	AA487558	Hs.95870	ESTs
13350	3	AA449297	Hs.104252	ESTs Weakly similar to type 1 procollagen C-proteinase enhancer protein precursor [H.sapiens]
33930	3	AA169539	Hs.95870	ESTs
34215	3	AA233855	Hs.104252	UTROPHIN
22509	3	R71393	Hs.29190	ESTs
20065	3	H98657	Hs.27291	ESTs
31091	3	N63076	Hs.138746	EST
2493	3	M22919	Hs.77385	MYOSIN LIGHT CHAIN ALKALI SMOOTH-MUSCLE ISOFORM

FIG._6Aa

163 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
28913	3	F01560	Hs.22583	ESTs Highly similar to co-repressor protein [M.musculus]
14323	3	AA598575	Hs.12851	ESTs
34914	3	AA338729	Hs.133096	ESTs
14236	3	AA496891	Hs.5011	ESTs Weakly similar to The ha1237 gene product is related to S.pombe rad21 gene product. [H.sapiens]
24594	3	Z38804	Hs.22555	ESTs Highly similar to OPIOID BINDING PROTEIN/CELL ADHESION MOLECULE PRECURSOR [Bos taurus]
22589	3	R79580	Hs.29874	ESTs
22156	3	R52145	Hs.25894	ESTs
16404	3	AA021284	Hs.60554	ESTs Moderately similar to sodium-calcium exchanger form 3 [R.norvegicus]
29310	3	H66642	Hs.88729	ESTs
9758	3	M26393	Hs.127610	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
9806	2	M79462	Hs.89633	Probable transcription factor PML {alternative products}
19289	2	H16568	Hs.23748	ESTs
34031	2	AA192614	Hs.83577	Human LIM protein MLP mRNA complete cds
33299	2	W73790	Hs.73803	IMMUNOGLOBULIN-RELATED 14.1 PROTEIN PRECURSOR
3276	2	M93718	Hs.76983	Nitric oxide synthase 3 (endothelial cell)
31704	2	N75055	Hs.14632	ESTs
10310	2	R87373	Hs.75429	ESTs
22388	2	R63695	Hs.1432	Protein kinase C substrate 80K-H
20938	2	N73988	Hs.37477	ESTs Weakly similar to No definition line found [C.elegans]
5935	2	X62466	Hs.108338	CDW52 antigen (CAMPATH-1 antigen)
41485	2	R49689	Hs.5260	ESTs Weakly similar to C06G8.3 [C.elegans]-
25403	2	AA063316		EST - RC_AA063316
27965	2	AA464267	Hs.24912	Homo sapiens bicaudal-D (BICD) mRNA complete cds

FIG. 6A

164 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
40632	2	N45221	EST - RC_N45221	
15527	2	W28798	Hs.63260	Phosphodiesterase 6A cGMP-specific rod alpha
31672	2	N74336	Hs.91681	ESTs
964	2	HG1804-	EST - HG1804-HT1829	
12439	2	AA401452	Hs.32060	ESTs
24223	2	W70158	Hs.29696	ESTs
21052	2	N93764	Hs.10175	ESTs Weakly similar to hypothetical protein [H.sapiens]
34140	2	AA215637	Hs.104186	ESTs
5130	2	U79288	Hs.85053	Homo sapiens clone 24440 mRNA sequence
30041	2	N27628	Hs.132744	Homo sapiens clone 24525 mRNA sequence
19202	2	H11509	Hs.22482	ESTs
41350	2	R40442	Hs.75652	Glutathione S-transferase M5
914	2	HG1019-	EST - HG1019-HT1019	
31958	2	N93495	Hs.54960	ESTs
12014	2	AA281769	Hs.7214	Human Hpast (HPAST) mRNA complete cds
39777	2	H18412	Hs.75253	Human clone ID 193225 NAD (H)-specific isocitrate dehydrogenase gamma subunit mRNA alternatively spliced partial cds
19147	2	H09751	Hs.117619	ESTs
11199	2	AA176446	Hs.10024	ESTs
6477	2	X91504	Hs.64904	Transcription factor COUP 2 (a.k.a. ARP1)
16336	2	AA018601	Hs.75649	EXTRACELLULAR SIGNAL-REGULATED KINASE 3
24058	2	W23709	Hs.109047	ESTs
26180	2	AA251230	Hs.112272	ESTs
37177	2	AA447988	Hs.7765	ESTs
41994	2	T47601	Hs.138805	ESTs

FIG. 6As

165 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
36532	2	AA429889	Hs.68882	Acrosin
1450	2	J03071	Hs.115352	Growth hormone 1
24819	2	Z40923	Hs.24812	ESTs
6532	2	X95325	Hs.89491	DNA-BINDING PROTEIN A
27085	2	AA402495	Hs.77978	ESTs
20487	2	N52322	Hs.19978	ESTs
724	2	D83703	Hs.30729	Peroxisomal biogenesis factor 6
4132	2	U27655	Hs.82294	Human HGP3 mRNA complete cds
13375	2	AA449716	Hs.5723	ESTs
13988	2	AA480045	Hs.7934	ESTs
22306	2	R59906	Hs.100530	ESTs
23167	2	T33164	Hs.12840	Homo sapiens germline mRNA sequence
11320	2	AA213667	Hs.22222	ESTs
24608	2	Z38888	Hs.25046	ESTs
13163	2	AA437225	Hs.22410	ESTs
1139	2	HG3227-	EST - HG3227-HT3404	
35572	2	AA401489	EST - RC_AA401489	
6964	2	Z49105	H.sapiens HD21 mRNA	
30963	2	N59373	Hs.137591	ESTs
16164	2	AA007509	Hs.26812	ESTs
2174	2	L42611	Hs.75395	Human mRNA for TPRD complete cds
38958	2	AA609707	Hs.111758	KERATIN TYPE II CYTOSKELETAL 6D
37919	2	AA478162	Hs.112751	ESTs
28905	2	D81123	Hs.104965	ESTs
3745	2	U09117	Hs.57475	ESTs
19545	2	H37834	Hs.80776	Human phospholipase c delta 1 mRNA complete cds
			Hs.32699	ESTs

FIG. 6A1

166 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
8416	2	AA428531		EST - AA428531
17569	2	AA128926		EST - RC_AA128926
19354	2	H18829	Hs.121515	ESTs
7598	2	AA174185	Hs.3354	Homo sapiens ezrin-radixin-moesin binding phosphoprotein-50 mRNA complete cds
25385	2	AA059099	Hs.109727	ESTs
14176	2	AA490620	Hs.11809	ESTs
29487	2	H85120	Hs.80881	N-ACETYLACTOSAMINE SYNTHASE
10197	2	R64199	Hs.50785	Homo sapiens vesicle trafficking protein sec22b mRNA complete cds
19488	2	H27675	Hs.25604	ESTs
10568	2	AA029703	Hs.36574	ESTs
30799	2	N53143	Hs.64001	ESTs
9638	2	L07592	Hs.106415	Human peroxisome proliferator activated receptor mRNA complete cds
27195	2	AA411473	Hs.65311	ESTs
17438	2	AA115508	Hs.2780	Jun D proto-oncogene
24932	2	AFFX-		AFFX-HSAC07X00351_M
10944	2	AA125969	Hs.34769	ESTs Weakly similar to F35G12.9 [C.elegans]
42324	2	T98199	Hs.142702	ESTs
34756	2	AA287665	Hs.8245	ESTs
12743	2	AA421050	Hs.24545	ESTs
13676	2	AA459389	Hs.26350	Homo sapiens mRNA for tyrosyl sulfotransferase-2
13009	2	AA430474	Hs.16466	ESTs
7403	2	AA094921	Hs.79788	ESTs
35669	2	AA404707	Hs.54865	ESTs

FIG.-6Au

167 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
17701	2	AA135941	Hs.71626	ESTs
18713	2	F04686	Hs.21782	ESTs
8314	2	AA410355	Hs.103081	ESTs Highly similar to RIBOSOMAL PROTEIN S6 KINASE [Homo sapiens]
7990	2	AA291786	Hs.32822	ESTs Weakly similar to HYPOTHETICAL PROTEIN KIAA0168 [H.sapiens]
42791	2	AFFX-		AFFX-HIJMGAPDH/M33197_M
6893	1	Z30643	Hs.123123	H.sapiens mRNA for chloride channel (putative) 2139bp
35607	1	AA402267	Hs.133475	ESTs Weakly similar to zinc finger protein [H.sapiens]
9468	1	H46074	Hs.31562	ESTs
29469	1	H82929		EST - RC_H82929
18692	1	F04444	Hs.6217	ESTs
35205	1	AA398161	Hs.97602	ESTs
22184	1	R53520	Hs.102755	ESTs
28815	1	D59267	Hs.56782	ESTs
17813	1	AA151480	Hs.91202	ESTs
24655	1	Z39191	Hs.27262	ESTs Weakly similar to Lph17p [S.cerevisiae]
15611	1	W51743	Hs.35096	ESTs
15700	1	W73859	Hs.78061	Homo sapiens mesoderm-specific basic-helix-loop-helix protein (POD1) mRNA complete cds
36770	1	AA435753		EST - RC_AA435753
32400	1	R97176	Hs.110783	ESTs
10802	1	AA069425	Hs.20573	ESTs
17593	1	AA129856		EST - RC_AA129856
20266	1	N32118	Hs.107365	ESTs Highly similar to THREONYL-TRNA SYNTHETASE CYTOPLASMIC [Homo sapiens]

FIG.-6Av

168 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
14447	1	AA609045	Hs.11759	ESTs
12892	1	AA426521	Hs.18528	Homo sapiens mRNA for NA14 protein
19738	1	H53059	Hs.15548	ESTs
14471	1	AA609346	Hs.20102	ESTs
5796	1	X55019	Hs.99975	Cholinergic receptor nicotinic delta polypeptide
18441	1	AA232508	Hs.77480	ESTs
10164	1	R54743	Hs.19400	ESTs Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisiae]
8830	1	AB002319	Hs.8663	Human rRNA for KIAA0321 gene partial cds
8682	1	AA477891	Hs.104476	ESTs
35620	1	AA402493	Hs.10552	ESTs Highly similar to c-Jun leucine zipper interactive [M.musculus]
35401	1	AA399593	Hs.97682	EST
10901	1	AA112307	Hs.25224	ESTs
19546	1	H37901	Hs.32706	ESTs
30292	1	N35978	Hs.82364	ESTs
39087	1	AA620607	Hs.111591	ESTs
37896	1	AA477463	Hs.77039	Ribosomal protein S28
41552	1	R59352	Hs.101253	Human mRNA for KIAA0296 gene complete cds
11467	1	AA234089	Hs.14593	ESTs
8215	1	AA389673	Hs.84344	ESTs Weakly similar to No definition line found [C.elegans]
15505	1	W28366	Hs.7252	Homo sapiens clone 24800 mRNA sequence
9834	1	M92299	Hs.22554	Homeo box B5 (2.1 protein)
9159	1	D31483	Hs.90062	Homo sapiens clone 23565 unknown mRNA partial cds
42218	1	T86444	Hs.110095	ESTs
15526	1	W28790	Hs.8124	ESTs

FIG.-6AW

169 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
17790	1	AA150182	Hs.42262	ESTs Weakly similar to HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOME III [C.elegans]
9777	1	M57888	Hs.95946	GRANZYME H PRECURSOR
15373	1	W26376	Hs.74563	THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR
12076	1	AA284362	Hs.6448	ESTs Weakly similar to No definition line found [C.elegans]
15391	1	W26651	Hs.15961	ESTs
12905	1	AA427537	Hs.32419	ESTs
39820	1	H24085	Hs.25443	ESTs
13109	1	AA435838	Hs.7985	ESTs
24249	1	W73069	Hs.12600	ESTs
16514	1	AA027946	Hs.44608	ESTs
16767	1	AA046650	Hs.40342	ESTs
15381	1	W26496	Hs.107725	ESTs Weakly similar to LIS-1 protein [H.sapiens]
11690	1	AA252762	Hs.31235	ESTs
22999	1	T16510	Hs.6624	ESTs
24490	1	Z38153	Hs.26921	ESTs
24368	1	W87280	Hs.124800	ESTs
22565	1	R77631	Hs.29126	ESTs
15358	1	W26105	Hs.8961	ESTs
24186	1	W61319	Hs.37482	ESTs Highly similar to COATOMER ZETA SUBUNIT [Bos taurus]
22272	1	R58922	Hs.26590	ESTs
16434	1	AA024494	Hs.61199	ESTs
22692	1	R88711	Hs.34183	ESTs
38830	1	AA609189	Hs.116415	ESTs
42547	1	W73946		EST - RC_W73946
34885	1	AA302831	Hs.57732	Homo sapiens p38beta2 MAP kinase mRNA complete cds

FIG.-6Ax

170 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
18445	1	AA232648	Hs.87068	ESTs
18070	1	AA180352	Hs.72733	ESTs
23923	1	T96407	Hs.17812	ESTs

FIG. 6Ay

171 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
2348	>10	M15656	Hs.75592	Aldolase B fructose-bisphosphate
6463	>10	X90908	Hs.74126	H.sapiens mRNA for I-15P (I-BABP) protein
42139	>10	T73335	Hs.93194	APOLIPOPROTEIN A-I PRECURSOR
4544	>10	U48959	Hs.75950	H.sapiens mRNA for myosin light chain kinase
1583	>10	K02765	Hs.58512	COMPLEMENT C3 PRECURSOR
2426	>10	M19828	Hs.585	Apolipoprotein B (including Ag(x) antigen)
8859	>10	AB002351	Hs.10587	Human mRNA for KIAA0353 gene partial cds
24572	>10	Z38688	Hs.24192	ESTs
17810	>10	AA151402	Hs.46531	ESTs
7006	>10	Z70295	Hs.32966	H.sapiens mRNA for GCAP-II/uroguanylin precursor
1304	>10	HG4310		EST - H134310-HT4580
5980	>10	X64559	Hs.65424	Tetranectin (plasminogen-binding protein)
41987	>10	T47089	Hs.121713	Cytochrome P450 subfamily XXI (steroid 21-hydroxylase congenital adrenal hyperplasia)
24461	>10	W94427	Hs.3807	ESTs Weakly similar to SODIUM/POTASSIUM-TRANSPORTING ATPASE GAMMA CHAIN [Mus musculus]
2372	>10	M16594	Hs.89552	Glutathione S-transferase A2
6001	>10	X65727	Hs.89552	Glutathione S-transferase A2
1750	>10	L10955	Hs.89485	Carbonic anhydrase IV
15130	>10	U77643	Hs.95655	Homo sapiens K12 protein precursor mRNA complete cds
12467	>10	AA402656	Hs.28264	ESTs
41148	>10	R06984		EST - RC_R06984_s
31652	>10	N73958	Hs.50404	Human chemokine (TECK) mRNA complete cds
23483	>10	T68873	Hs.143289	H.sapiens mRNA for metallothionein isoform.1R
4605	>10	U51010		EST - U51010
28359	>10	AA609133	Hs.58115	ESTs

FIG..7Aa

172 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
24066	>10	W32506	Hs.111676	ESTs Weakly similar to HEAT SHOCK 27 KD PROTEIN [H.sapiens]
33282	>10	W73194	Hs.80552	ESTs
12084	>10	AA284767	Hs.21910	ESTs
41473	>10	R48732	Hs.11006	ESTs
32568	>10	T29248	Hs.143113	Human pancreatic lipase related protein 2 (PLRP2) mRNA complete cds
6413	>10	X87159	Hs.37129	Sodium channel nonvoltage-gated 1 beta (Liddle syndrome)
20707	>10	N64436	Hs.20813	ESTs
27108	>10	AA404397	Hs.58414	ESTs Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]
12477	>10	AA403032	Hs.21701	ESTs
42059	>10	T61654	Hs.93194	APOLIPOPROTEIN A-I PRECURSOR
25468	>10	AA079072	Hs.1477	Insulin-like growth factor binding protein 6
26910	>10	AA303081	Hs.78293	ESTs
16938	>10	AA059473	Hs.66783	ESTs
41788	>10	T03735	Hs.26885	ESTs
7754	>10	AA234634	Hs.76722	Human NF-IL6-beta protein mRNA complete cds
6122	>10	X72012	Hs.75962	Endoglin (Osler-Rendu-Weber syndrome 1)
2848	>10	M58286	Hs.159	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR
23013	>10	T16661	Hs.6725	ESTs
19537	>10	H30270	Hs.32583	ESTs
4584	>10	U50360		EST - U50360
37410	>10	AA453652	Hs.99344	ESTs
27969	>10	AA464594	Hs.63382	ESTs
35497	>10	AA400606	Hs.144344	EST

FIG.-7Ab

173 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
37013	>10	AA443690	Hs.136268	ESTs Highly similar to ZINC FINGER PROTEIN HF.12 [Homo sapiens]
39247	>10	AA621553	Hs.112998	ESTs
13471	>10	AA452598	Hs.109590	ESTs
42110	>10	T68878	Hs.76688	Carboxylesterase 2 (liver)
10965	>10	AA128997	Hs.18953	Homo sapiens cGMP-specific phosphodiesterase (PDE9A2) mRNA complete cds
4918	>10	U67733	Hs.3831	Human cGMP-stimulated 3'5'-cyclic nucleotide phosphodiesterase PDE2A3 (PDE2A) mRNA complete cds
40737	>10	N54950	Hs.81454	H.sapiens KHK mRNA for ketohexokinase clone pHKHK3a
30403	>10	N45300	Hs.110647	Meis1 (mouse) homolog
11432	>10	AA233369	Hs.361	ESTs
18784	>10	F09748	Hs.7974	ESTs
40662	>10	N49281		EST - RC_N49281
5773	>10	X54162	Hs.79386	64 KD AUTOANTIGEN D1
35041	>10	AA350586	Hs.30862	ESTs
20868	>10	N70068	Hs.7243	ESTs
39729	>10	H11489	Hs.105805	ESTs
27387	>10	AA426330	Hs.78264	ESTs
39758	>10	H15814	Hs.80485	Human apM1 mRNA for GS3109 (novel adipose specific collagen-like factor) complete cds
4319	>10	U37283	Hs.58882	Human ricrofibril-associated glycoprotein-2 MAGP-2 mRNA complete cds
2866	>10	M59815	Hs.76682	Complement component 4A
30332	>10	N39075	Hs.44934	EST
41344	>10	R40189	Hs.6985	ESTs

FIG. 7Ac

174 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
28271	>10	AA521200	Hs.48778	ESTs
5834	>10	X57129	Hs.7644	HISTONE H1D
19048	>10	H05464	Hs.100251	ESTs
1429	>10	J02854	Hs.9615	Human 20-kDa myosin light chain (MLC-2) mRNA complete cds
19491	>10	H27910	Hs.107384	ESTs
29992	>10	N26386	Hs.33084	Solute carrier family 2 (facilitated glucose transporter) member 5
2041	>10	L36033	Hs.77423	Stromal cell-derived factor 1
22865	>10	R99909	Hs.36186	ESTs
11624	>10	AA243654	Hs.17998	ESTs
12512	>10	AA405199	Hs.20733	ESTs
41443	>10	R45577	Hs.10683	ESTs
5055	>10	U77180	Hs.50002	Human mRNA for EBI1-ligand chemokine complete cds
6038	>10	X66945	Hs.748	Basic fibroblast growth factor (bFGF) receptor (shorter form)
42530	>10	W72859	Hs.74669	ESTs Weakly similar to SYNAPTOBREVIN 2 [H.sapiens]
827	>10	D87433	Hs.84753	Human mRNA for KIAA0246 gene partial cds
650	>10	D78014	Hs.74566	Human mRNA for dihydropyrimidinase related protein-3 complete cds
37350	>10	AA452606	Hs.99289	EST
37488	>10	AA455178	Hs.99397	ESTs
36646	>10	AA431797	Hs.98763	EST
38999	>10	AA609907		EST - RC_AA609907
38191	>10	AA487895	Hs.17311	ESTs
9944	>10	N57464	Hs.74670	Human mRNA for KIAA0146 gene partial cds
8139	>10	AA341723	Hs.107374	ESTs
41522	>10	R53966	Hs.75092	N-CHIMAERIN

FIG. 7Ad

175 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
38090	>10	AA482603	Hs.111301	Matrix metalloproteinase 2 (gelatinase A 72kD gelatinase 72kD type IV collagenase)
41175	>10	R09241		EST - RC_R09241
36947	>10	AA437388	Hs.115726	ESTs
4175	>10	U29953	Hs.76110	Pigment epithelium-derived factor
35421	>10	AA399686	Hs.97669	EST
4358	>10	U39487	Hs.250	Xanthine dehydrogenase
35463	>10	AA400272	Hs.97758	EST
7026	>10	Z80345	Hs.127610	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
34625	>10	AA282238	Hs.118463	Homo sapiens clone 24519 unknown mRNA partial cds
20179	>10	N24879	Hs.9693	ESTs
36805	>10	AA435901	Hs.56874	ESTs Weakly similar to p20 protein [R.norvegicus]
24447	>10	W93121	Hs.23841	Human mRNA for KIAA0355 gene complete cds
10247	>10	R74386	Hs.108924	ESTs
3618	>10	U02388	Hs.101	Leukotriene B4 omega hydroxylase (cytochrome P450 subfamily IVF)
18730	>10	F08876	Hs.8008	ESTs
22529	>10	R73075	Hs.29327	EST
37520	>10	AA455960	Hs.99405	ESTs
41122	>10	R05483	Hs.138500	ESTs
4417	>10	U42031	Hs.7557	Human 54 kDa progesterone receptor-associated immunophilin FKBP54 mRNA partial cds
9742	>10	M14777	Hs.89552	Glutathione S-transferase A2
36194	>10	AA421142	Hs.104672	ESTs
4445	>10	U43653	Hs.3261	Leptin (r urine obesity homolog)
19749	>10	H53728	Hs.36808	ESTs

FIG. 7Ae

176 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
19793	>10	H56965	Hs.34564	ESTs
12713	>10	AA418398	Hs.17778	ESTs
1464	>10	J03474	Hs.3157	SERUM AMYLOID A PROTEIN PRECURSOR
16842	>10	AA055163	Hs.57975	Homo sapiens mRNA for cardiac calsequestrin complete cds
34229	>10	AA234383	Hs.3576	ESTs
35563	>10	AA401404	Hs.112087	ESTs
16736	>10	AA045306	Hs.42996	ESTs
33607	>10	W93497	Hs.59486	ESTs
16146	>10	AA005236	Hs.60162	ESTs
22666	>10	R85880	Hs.33455	ESTs
22562	>10	R77493	Hs.29653	EST
22985	>10	T16211	Hs.6326	Homo sapiens clone 23798 and 23825 mRNA sequence
5248	>10	U86358	Hs.50404	Human chemokine (TECK) mRNA complete cds
27608	>10	AA443800	Hs.43125	ESTs
7510	>10	AA136353	Hs.38022	ESTs
34683	>10	AA284920	Hs.13716	ESTs
27633	>10	AA446659	Hs.2563	Tachykinin 2 (substance K neurokinin A neurokinin 2 neuromedin L neurokinin alpha neuropeptide K neuropeptide gamma)
32485	>10	T16335	Hs.65325	EST
38791	>10	AA609018	Hs.112629	ESTs
32020	>10	N95796	Hs.55181	ESTs
19986	>10	H89980	Hs.12112	ESTs Moderately similar to protein phosphatase 1 binding protein PTG [M.musculus]
30748	>10	N52254	Hs.47438	ESTs
8903	>10	AF002246	Hs.21226	Homo sapiens neural cell adhesion molecule (CALL) mRNA complete cds

FIG.-7A1

177 / 454.

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
9959	>10	N75215	Hs.43148	ESTs
38136	>10	AA486185	Hs.125176	ESTs
19845	>10	H59887	Hs.35167	ESTs
1127	>10	HG3117-		EST - HG3117-HT3293
23637	>10	T85315	Hs.15903	ESTs
16699	>10	AA043349	Hs.62630	ESTs
36702	>10	AA434108	Hs.101393	ESTs Moderately similar to DNAJ PROTEIN HOMOLOG 1 [Homo sapiens]
28930	>10	F02702	Hs.141503	Small inducible cytokine A5 (RANTES)
9226	>10	D62584	Hs.109439	ESTs Highly similar to OSTEOINDUCTIVE FACTOR PRECURSOR [Bos taurus]
3357	>10	M99487	Hs.1915	PROSTATE-SPECIFIC MEMBRANE ANTIGEN
36783	>10	AA435805	Hs.112065	EST
4876	>10	U66061	Hs.2048	Protease serine 2 (trypsin 2)
41149	>10	R06986	Hs.76487	ESTs
22200	>10	R54179	Hs.26100	ESTs
15925	>10	Y13492	Hs.78483	Homo sapiens mRNA for smoothelin
10911	>10	AA113387	Hs.24305	ESTs
3336	>10	M97675	Hs.1944	Human protein tyrosine kinase t-Ror1 (Ror1) mRNA complete cds
31889	>10	N91897	Hs.50652	ESTs
10406	>10	AA007629	Hs.25478	ESTs
17737	>10	AA142875	Hs.71719	ESTs
38939	>10	AA609632	Hs.112737	EST
16206	>10	AA010611	Hs.60418	EST
32810	>10	W15376	Hs.122656	ESTs

FIG.-7Aa

178 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
18210	>10	AA196306	Hs.86045	ESTs
24054	>10	W15580	Hs.15342	ESTs
23047	>10	T23457	Hs.7120	ESTs
12944	>10	AA428258	Hs.8769	ESTs
34172	>10	AA227469	Hs.139171	EST
9317	>10	D87468	Hs.40888	Human rRNA for KIAA0278 gene partial cds
19331	>10	H17865	Hs.23213	ESTs
21035	>10	N92824	Hs.14898	ESTs
34208	>10	AA233380	Hs.104249	EST
5974	>10	X64072	Hs.83968	Integrin beta 2 (antigen CD18 (p95) lymphocyte function-associated antigen 1 macrophage antigen 1 (mac-1) beta subunit)
5032	>10	U74382	Hs.90357	Homo sapiens telomeric repeat binding factor (TRF1) mRNA complete cds
41941	>10	T32561	Hs.5476	ESTs
34239	>10	AA235009	Hs.32246	ESTs
32852	>10	W31906	Hs.116428	ESTs
7662	>10	AA203527	Hs.18747	Homo sapiens ribonuclease P protein subunit p20 (RPP20) mRNA complete cds
6432	>10	X89066	Hs.94413	Transient receptor potential channel 1
37001	>10	AA443311	Hs.98998	ESTs
4630	>10	U52101	Hs.9999	Human YMP mRNA complete cds
19489	>10	H27852	Hs.28137	ESTs
28483	>10	C14270	Hs.66357	ESTs
19801	>10	H57357	Hs.18767	ESTs Weakly similar to unknown protein [H.sapiens]
24672	>10	Z39300	Hs.124952	ESTs
31153	>10	N63688	EST - RC_N63688	

FIG. 7Ah

179 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
40250	>10	H92451	Hs.110	Solute carrier family 3 (cystine dibasic and neutral amino acid transporters activator of cystine dibasic and neutral amino acid transport) mem
23028	>10	T17215	Hs.6952	ESTs
28072	>10	AA480886	Hs.86693	ESTs
11868	>10	AA262556	Hs.28802	ESTs Weakly similar to centaurin alpha [R.norvegicus]
35359	>10	AA399061	Hs.112961	ESTs Moderately similar to PANCREATITIS-ASSOCIATED PROTEIN 1 PRECURSOR [H.sapiens]
4285	>10	U35139	Hs.50130	Human NEECDIN related protein mRNA complete cds
4655	>10	U52969	Hs.80296	BRAIN SPECIFIC POLYPEPTIDE PEP-19
26030	>10	AA235984	Hs.87469	ESTs
2042	>10	L36051	Hs.1166	Thrombopoietin (myeloproliferative leukemia virus oncogene ligand megakaryocyte growth and development factor)
25262	>10	AA043501	Hs.30250	Homo sapiens short form transcription factor C-MAF (c-maf) mRNA complete cds
34821	>10	AA291983	Hs.144599	ESTs
42405	>10	W44682	Hs.109896	ESTs
41348	>10	R40395	Hs.112125	Lecithin:cholesterol acyltransferase
14494	>10	AA609645	Hs.25632	ESTs Weakly similar to PNG gene [H.sapiens]
4453	>10	U43916	Hs.79368	Human epithelial membrane protein (CL-20) mRNA complete cds
42758	>10	Z41411	Hs.107040	ESTs
2098	>10	L39009		EST - L39009
35637	>10	AA402933	Hs.29283	ESTs
16549	>10	AA029697	Hs.94854	ESTs
1220	>10	HG3733-		EST - HG3733-HT4003

FIG._7A1

180 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
39934	>10	H52185	Hs.124994	ESTs
7735	>10	AA232121	Hs.109631	Human tyrosyl-tRNA synthetase mRNA complete cds
40392	>10	H99587	Hs.108880	ESTs
37170	>10	AA447779	Hs.99145	EST
18361	>10	AA223902	Hs.86899	ESTs
19366	>10	H19204	Hs.133466	ESTs
38429	>10	AA496965	Hs.108694	Glycophorin A
38021	>10	AA481059	Hs.105152	ESTs
5184	>10	U82169	Hs.87234	Human frizzled homolog (FZD3) mRNA complete cds
27863	>10	AA458923	Hs.70202	ESTs Weakly similar to F23B2.4 [C.elegans]
37476	>10	AA455051	Hs.99386	EST
859	>10	D87468	Hs.40888	Human mRNA for KIAA0278 gene partial cds
27185	>10	AA410895	Hs.62348	ESTs
41010	>10	N80686	Hs.21639	Human APEG-1 mRNA complete cds
38241	>10	AA489076	Hs.105101	ESTs
22701	>10	R89477	Hs.34299	ESTs
12152	>10	AA291271	Hs.10886	ESTs Weakly similar to uroporphyrinogen III synthase UROIIIIS [H.sapiens]
38913	>10	AA609531	Hs.112050	ESTs
34034	>10	AA192871	Hs.83760	Troponin I (skeletal fast)
37644	>10	AA459857	Hs.99503	EST
4173	>10	U29725	Hs.3080	Human EMK1 alpha kinase mRNA complete cds
16178	>10	AA009839	Hs.1632	CD27L RECEPTOR PRECURSOR
20527	>10	N54161	Hs.124044	ESTs
41918	>10	T25873	Hs.102243	ESTs

FIG.-7Ai

181 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
1525	>10	J04621	Hs.1501	Syndecan 2 (heparan sulfate proteoglycan 1 cell surface-associated fibroglycan)
19160	>10	H10208	Hs.30972	EST
16860	>10	AA055833	Hs.58152	ESTs Weakly similar to Natsu [M.musculus]
36927	>10	AA437259	Hs.104944	EST
1595	>10	K03207	Hs.103972	Salivary proline-rich protein
15574	>10	W38778	Hs.26216	ESTs
8985	>10	C00125	Hs.24332	ESTs Weakly similar to similar to deoxyribose-phosphate aldolase [C.elegans]
33995	>10	AA182845	Hs.139088	Homo sapiens FIP2 alternatively translated mRNA complete cds
7949	>10	AA283620	Hs.34956	ESTs
16607	>10	AA034918	Hs.85079	ESTs
11670	>10	AA252191	Hs.25199	Homo sapiens PAC clone DJ130H16 from 22q12.1-qter
7354	>10	AA092348	Hs.7858	ESTs
4277	>10	U34879	Hs.85279	ESTRADIOL 17 BETA-DEHYDROGENASE 1
23214	>10	T40895	Hs.11937	Human protein tyrosine phosphatase PTPCAAX1 (hPTPCAAX1) mRNA complete cds
22209	>10	R54594	Hs.25209	ESTs
36151	>10	AA419011	Hs.96744	ESTs
23372	>10	T59537		EST - RC_T59537
42136	>10	T72491	Hs.73849	Apolipoprotein C-III
289	>10	D16480	Hs.75860	Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein) alpha subun
15974	>10	Z36531	Hs.2659	H.sapiens mRNA for fibrinogen-like protein (pT49 protein)
41379	>10	R42233	Hs.106487	Homo sapiens mRNA for KIAA0673 protein partial cds

FIG. 7A

182 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
34764	>10	AA287870	Hs.890	Lymphotxin-beta
24027	>10	W01875	Hs.5734	Homo sapiens mRNA for KIAA0679 protein partial cds
36197	>10	AA421158	Hs.97514	ESTs
37211	>10	AA448334		EST - RC: AA448334
27684	>10	AA448625	Hs.57929	ESTs
31790	>10	N80279	Hs.50891	ESTs
24515	>10	Z38289	Hs.12701	ESTs
18652	>10	F03111	Hs.22505	ESTs
16635	>10	AA037433	Hs.46987	ESTs
37815	>10	AA469952	Hs.97899	ESTs
6364	>10	X83857	Hs.495	Prostaglandin E receptor 3 (subtype EP3) {alternative products}
9034	>10	C01833	Hs.29759	ESTs Weakly similar to !!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!! [H.sapiens]
16469	>10	AA025728	Hs.61307	ESTs
27034	>10	AA400102	Hs.49051	ESTs
42746	>10	Z40646	Hs.124953	ESTs
35368	>10	AA399269	Hs.15250	Homo sapiens DBI-related protein mRNA complete cds
34805	>10	AA291522	Hs.97250	EST
19983	>10	H89355	Hs.6598	ESTs
31126	>10	N63444	Hs.47566	ESTs
22616	>10	R81949	Hs.124964	ESTs
12246	>10	AA348198	Hs.14829	Homo sapiens mRNA for GABA-BR1a (hGB1a) receptor
8777	>10	AA495865	Hs.7974	ESTs
13486	>10	AA453034	Hs.21041	ESTs Highly similar to FIBROPELLIN C PRECURSOR [Strongylocentrotus purpuratus]
25512	>10	AA085721	Hs.95511	ESTs

FIG.-7AI

183 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
29073	>10	F12567		EST - RC_F12567
5541	>10	X07203	Hs.89751	CD20 RECEPTOR
41689	>10	R82942	Hs.107755	ESTs Weakly similar to GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE [E.coli]
32343	>10	R80965	Hs.125052	ESTs
38335	>10	AA490916	Hs.112157	ESTs
41729	>10	R92458	Hs.89554	Hemoglobin gamma-G
36707	>10	AA434246	Hs.98802	EST
28491	>10	C14784	Hs.12382	ESTs
41702	>10	R86970	Hs.123363	ESTs
32246	>10	R52163	Hs.144526	ESTs
17314	>10	AA086487	Hs.107365	ESTs Highly similar to THREONYL-TRNA SYNTHETASE CYTOPLASMIC [Homo sapiens]
30325	>10	N38967	Hs.44904	EST
19823	>10	H58692	Hs.9520	ESTs Highly similar to FORMYL-TETRAHYDROFOLATE DEHYDROGENASE [Rattus norvegicus]
42153	>10	T77729	Hs.89890	Pyruvate carboxylase
19321	>10	H17511	Hs.24963	ESTs
27110	>10	AA404494	Hs.84112	CTP synthetase
28831	>10	D59722	Hs.92924	ESTs
6333	>10	X82494	Hs.2653	Fibulin 2
37679	>10	AA460661	Hs.99562	ESTs
40829	>10	N64344	Hs.78362	Human clone 23839 mRNA sequence
19132	>10	H09343	Hs.27261	ESTs
19353	>10	H18706	Hs.31604	ESTs
10935	>10	AA121534	Hs.6923	ESTs Highly similar to TUBULIN BETA-5 CHAIN [Gallus gallus]

FIG..7Am

184 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
11621	>10	AA243574	Hs.14691	ESTs
38538	>10	AA521370	Hs.104423	ESTs
10095	>10	R22139	Hs.30343	ESTs
30014	>10	N26740	Hs.42771	ESTs
4464	>10	U44429	Hs.16611	Human L53 (hD53) mRNA partial cds
3650	>10	U03877	Hs.76224	Human extracellular protein (S1-5) mRNA complete cds
36377	>10	AA426056	Hs.98450	ESTs
20437	>10	N50550	Hs.24587	Homo sapiens mRNA for Efs1 complete cds
1576	>10	K02100	Hs.117050	ORNITHINE CARBAMOYLTRANSFERASE PRECURSOR
42078	>10	T64891	Hs.144323	ESTs
27257	>10	AA418001	Hs.46146	ESTs Weakly similar to mitogen-activated kinase kinase
30582	>10	N49848	Hs.46974	kinase 5 [H.sapiens]
3631	>10	U03090	Hs.290	EST
19026	>10	H04768	Hs.30484	Homo sapiens Ca2+-dependent phospholipase A2 mRNA complete cds
4752	>10	U59632	Hs.3847	ESTs
3766	>10	U09579	Hs.74984	Glycoprotein Ib (platelet) beta polypeptide
1437	>10	J02923	Hs.76506	CYCLIN-DEPENDENT KINASE INHIBITOR 1
33905	>10	AFFX-		Lymphocyte cytosolic protein 1 (L-plastin)
4310	>10	U37055	Hs.76034	AFFX-TrpX-5
26923	>10	AA342302	Hs.55036	Macrophage stimulating 1 (hepatocyte growth factor-like)
5520	>10	X06256	Hs.119218	ESTs
37571	>10	AA457409	Hs.99458	Integrin alpha 5 (fibronectin receptor alpha polypeptide)
38800	>10	AA609052	Hs.112636	EST
27952	>10	AA463700	Hs.47042	EST
				Homo sapiens CD39L3 (CD39L3) mRNA complete cds

FIG. 7An

185 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
27621	>10	AA446242	Hs.56589	ESTs
38784	>10	AA608988	Hs.2051	Testis specific protein Y-linked
291	>10	D16532	Hs.73729	Very low density lipoprotein receptor
18014	>10	AA173168	Hs.57672	ESTs Weakly similar to myosin heavy chain [C.elegans]
16720	>10	AA044732	Hs.77208	ESTs
25336	>10	AA053405	Hs.101404	ESTs
2547	>10	M25809	Hs.1009	ATPase H+ transporting lysosomal (vacuolar proton pump) beta polypeptide 56/58kD isoform 1
39953	>10	H56010	Hs.108144	ESTs Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
13777	>10	AA463504	Hs.6052	ESTs
13419	>10	AA450336	Hs.22269	ESTs
1403	>10	J00123	Hs.93557	PROENKEPHALIN A PRECURSOR
42373	>10	W35362	Hs.103012	ESTs
21520	>10	R28267	Hs.24258	ESTs
9796	>10	M63509	Hs.73974	Glutathione S-transferase M2 (muscle)
35650	>10	AA404271	Hs.22631	Human glutamate receptor (GLUR5) mRNA complete cds
42501	>10	W69586	Hs.103156	ESTs
33812	>10	Z41239	Hs.106960	ESTs
42473	>10	W63731	Hs.122531	ESTs
25195	>10	AA033790	Hs.75736	Apolipoprotein D
28607	>10	C21481	Hs.84630	ESTs Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]
3712	>10	U07620	Hs.89661	Human MAP kinase mRNA complete cds
6214	>10	X77307	Hs.2507	5-HYDROXYTRYPTAMINE 2B RECEPTOR

FIG.-7Aa

186 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
23575	>10	T80833	Hs.14794	ESTs
31775	>10	N79765	Hs.50847	ESTs
5206	>10	U82979	Hs.67846	Human clone HM18 monocyte inhibitory receptor precursor mRNA complete cds
22769	>10	R94521	Hs.124693	ESTs
9377	>10	H12674	Hs.9396	ESTs
29268	>10	H61046	Hs.70405	EST Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
11061	>10	AA147537	Hs.4811	ESTs
41960	>10	T33511	Hs.4844	ESTs
29416	>10	H77734	Hs.36702	Homo sapiens roundabout 1 (robo1) mRNA complete cds
38248	>10	AA489218	Hs.105229	ESTs
37256	>10	AA449424	Hs.98428	ESTs
21911	>10	R43980	Hs.26320	ESTs
23184	>10	T34622	Hs.8108	ESTs Weakly similar to HYPOTHETICAL 35.8 KD PROTEIN IN PRP15-SRP40 INTERGENIC REGION [S.cerevisiae]
16225	>10	AA011305	Hs.10029	Cathepsin C
27766	>10	AA453656	Hs.88417	ESTs
16071	>10	AA001426	Hs.40863	ESTs
17343	>10	AA100152	Hs.5921	ESTs
10643	>10	AA040154	Hs.32478	ESTs
29335	>10	H68239	Hs.39122	ESTs
34966	>10	AA344866	Hs.1285	Complement component 8 gamma polypeptide
26303	>10	AA255483	Hs.88042	EST
1030	>10	HG2416-	EST - HG2416-HT2512	
28370	>10	AA609559	Hs.38550	ESTs Moderately similar to alfa subunit [H.sapiens]

FIG. 7Aa

187 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
29303	>10	H65881	Hs.38427	ESTs
21076	>10	N99976	Hs.8016	ESTs
27100	>10	AA404231		EST - RC_AA404231
11329	>10	AA216589	Hs.28462	ESTs
4402	>10	U41518	Hs.74602	AQUAPORIN-CHIP
11050	>10	AA142919	Hs.5558	ESTs
22844	>10	R98947		EST - RC_R98947
31581	>10	N71371	Hs.39938	ESTs
7253	>10	AA074407	Hs.139119	ESTs
20423	>10	N49308	Hs.104938	ESTs
39264	>10	AA621750		EST - RC_AA621750
36415	>10	AA426598	Hs.24897	Homo sapiens chromosome 21q22.1 anonymous mRNA sequence
16575	>10	AA031948	Hs.57548	ESTs
37505	>10	AA455659	Hs.103233	ESTs
28264	>10	AA521080	Hs.46765	ESTs
23886	>10	T95325	Hs.16545	ESTs
11781	>10	AA256485	Hs.33413	ESTs
25603	>10	AA114250	Hs.48924	Homo sapiens mRNA for KIAA0512 protein complete cds
9003	>10	C00808	Hs.107882	ESTs
5632	>10	X15357		EST - X15357
7680	>10	AA206946	Hs.8059	ESTs
22783	>10	R95689	Hs.35437	ESTs
20852	>10	N69540	Hs.17713	ESTs
16795	>10	AA047896	Hs.49169	ESTs
37558	>10	AA456975	Hs.75736	Apolipoprotein D

FIG. 7Aa

188 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
35957	>10	AA412537	Hs.98149	EST
42129	>10	T71561	Hs.84824	ESTs
34585	>10	AA281002	Hs.40735	ESTs
33690	>10	Z38607	Hs.62248	ESTs
8904	>10	AF002256	Hs.86180	Homo sapiens killer cell receptor (KIR103) mRNA allele ASD1 complete cds
2689	>10	M32373	Hs.1256	Arylsulfatase B
40909	>10	N69084	Hs.49608	ESTs
22377	>10	R63090	Hs.28391	ESTs
21208	>10	R07651	Hs.20023	EST
27304	>10	AA421783	Hs.56808	Homo sapiens mRNA for zinc finger protein FPM315 complete cds
3307	>10	M95809	Hs.89578	BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT
25370	>10	AA057556	Hs.28478	ESTs
41423	>10	R44717	Hs.22917	ESTs
2570	>10	M27160	Hs.2053	Tyrosinase (oculocutaneous albinism IA)
14557	>10	AA620965	Hs.108300	ESTs Highly similar to ADENYLOSUCCINATE SYNTHETASE
7023	>10	Z78291		MUSCLE ISOZYME [Mus musculus]
31051	>10	N62696	Hs.48607	EST - Z73291
39200	>10	AA621246	Hs.112956	EST
24712	>10	Z39652	Hs.27457	ESTs
23296	>10	T52497	Hs.9444	ESTs Moderately similar to !!!!! ALU CLASS A WARNING ENTRY !!!!! [H.sapiens]
12826	>10	AA424806	Hs.134646	ESTs
2199	>10	L49169	Hs.75678	Human COS3 mRNA complete cds

FIG. 7A

189 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
27226	>10	AA416767	Hs.43498	ESTs
7135	>10	AA028976	Hs.8175	ESTs
17102	>10	AA074955		EST - RC_AA074955
38942	>10	AA609646	Hs.94970	Human mRNA for KIAA0306 gene partial cds
29288	>10	H64973	Hs.38336	ESTs
34336	>10	AA250843	Hs.54434	Interferon regulatory factor 5
30816	>10	N53566	Hs.47681	ESTs
16739	>10	AA045461	Hs.65093	ESTs
42317	>10	T97599	Hs.113025	ESTs
2228	>10	L77563		EST - L77563
30862	>10	N55171	Hs.47927	ESTs
35954	>10	AA412526	Hs.97951	ESTs
36403	>10	AA426383	Hs.98467	ESTs
36949	>10	AA441812	Hs.98959	ESTs
41628	>10	R70212	Hs.79630	Immunoglobulin-associated alpha
39175	>10	AA621076	Hs.111996	ESTs
37657	>10	AA460147		EST - RC_AA460147
36279	>10	AA424242	Hs.98397	ESTs Weakly similar to precursor of major fibrous sheath protein [M.musculus]
6834	>10	Z18954	Hs.2960	S100 calcium-binding protein A5 (formerly S100D)
40562	>10	N33212	Hs.107197	ESTs
13770	>10	AA463272	Hs.22636	ESTs
5101	>10	U79249	Hs.78362	Human clone 23839 mRNA sequence
3355	>10	M99438	Hs.31305	Human transducin-like enhancer protein (TLE3) mRNA complete cds
8476	>10	AA442119	Hs.29790	ESTs

FIG.-7As

190 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
34231	>10	AA234527	Hs.75772	Glucocorticoid receptor
42046	>10	T59148	Hs.50966	Carbamoyl-phosphate synthetase 1 mitochondrial
23913	>10	T96123	Hs.17749	ESTs
37333	>10	AA452158	Hs.75122	TRANSFORMING PROTEIN RHOB
27946	>10	AA463434	Hs.42658	ESTs
34407	>10	AA255523		EST - RC_AA255523
16542	>10	AA029428	Hs.61555	ESTs
6248	>10	X78712	Hs.98008	Glycerol kinase 2 (testis specific)
8227	>10	AA393666	Hs.75709	Mannose-6-phosphate receptor (cation dependent)
3507	>10	S78774		EST - S78774
40907	>10	N68830	Hs.25717	ESTs
33340	>10	W79698	Hs.58550	ESTs
19079	>10	H06371	Hs.20945	ESTs
3992	>10	U19713	Hs.76364	Allograft inflammatory factor 1
36059	>10	AA417063	Hs.98189	ESTs
37634	>10	AA459662	Hs.99489	EST
41581	>10	R62313	Hs.126270	ESTs Weakly similar to RTP60 [R.norvegicus]
38734	>10	AA608792	Hs.112591	EST
37836	>10	AA470135	Hs.112238	ESTs
21303	>10	R11157	Hs.12610	ESTs
20125	>10	N22006	Hs.6202	ESTs
35516	>10	AA400795	Hs.97450	ESTs
26771	>10	AA284067	Hs.89267	EST
33558	>10	W90735	Hs.59332	EST
2830	>10	M57399	Hs.44	Pleiotrophin (heparin binding growth factor 8 neurite growth-promoting factor 1)

FIG. 7A

191 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
42625	>10	W88426	Hs.110128	ESTs
26152	>10	AA250845	Hs.87762	ESTs
31988	>10	N94581	Hs.55062	ESTs
17763	>10	AA148213	Hs.71873	ESTs Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Gallus gallus]
21959	>10	R44949	Hs.22906	ESTs
10000	>10	N79674	Hs.7915	ESTs
30658	>10	N51105	Hs.111223	ESTs
17629	>10	AA131919	Hs.69009	ESTs
36260	>10	AA423970	Hs.98378	ESTs
285	>10	D16227	Hs.3618	Hippocalcin-like 1
26123	>10	AA243598	Hs.20887	ESTs
34535	>10	AA279391	Hs.104425	EST
29100	>10	H01428	Hs.92350	ESTs
24122	>10	W46947	Hs.4188	ESTs
19894	>10	H65942	Hs.36030	ESTs
22987	>10	T16258	Hs.25420	ESTs
5985	>10	X64728	Hs.34514	H.sapiens CHML mRNA
42461	>10	W60008	Hs.89717	Human preprocarboxypeptidase A2 (proCPA2) mRNA complete cds
5422	>10	X00588	Hs.77432	Epidermal growth factor receptor
16603	>10	AA034366	Hs.144627	ESTs
33389	>10	W81607	Hs.58663	EST
6931	>10	Z46788	Hs.3232	H.sapiens mRNA for cylicin II
19324	>10	H17618	Hs.28180	ESTs
32166	>10	R41836	Hs.9657	ESTs

FIG. 7Au

192 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
39967	>10	H58415	Hs.102160	EST
17958	>10	AA166917	Hs.72639	ESTs
38569	>10	AA598437	Hs.29385	ESTs Highly similar to MITOCHONDRIAL RESPIRATORY CHAIN COMPLEXES ASSEMBLY PROTEIN RCA1
1006	>10	HG2260-		[Saccharomyces cerevisia
23552	>10	T79638	Hs.105618	EST - HG2260-HT2349
38228	>10	AA488997	Hs.137530	ESTs
1066	>10	HG2705-		ESTs
23815	>10	T91283		EST - HG2705-HT2801
4699	>10	U57099	Hs.21639	EST - RC_T91283
31306	>10	N66796	Hs.144212	Human APEG-1 mRNA complete cds
12389	>10	AA399633	Hs.24872	ESTs
34539	>10	AA279662	Hs.142462	ESTs Moderately similar to snRNP protein B [H.sapiens]
20358	>10	N39584	Hs.17404	ESTs
26070	>10	AA236868	Hs.87564	ESTs
38210	>10	AA488659	Hs.105686	ESTs
26025	>10	AA235874	Hs.88888	PUTATIVE DNA BINDING PROTEIN A20
4978	>10	U71207	Hs.29279	Homo sapiens clone 24534 eyes absent homolog (Eab1)
4935	>10	U68162		mRNA partial cds
3501	>10	S78467	Hs.84171	THROMBOPOEITIN RECEPTOR PRECURSOR
14281	>10	AA505136	Hs.12420	EST - S78467
31859	>10	N90688	Hs.54643	ESTs
41104	>10	R01398		EST
				EST - RC_R01398

FIG. 7Av

193 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
5293	>10	U89995	Hs.95206	Human DNA binding protein FKHL15 (FKHL15) mRNA complete cds
3543	>10	S81957		EST - S81957
27615	>10	AA443958	Hs.90960	ESTs
7152	>10	AA036753	Hs.78494	Homo sapiens mRNA for KIAA0525 protein partial cds
16197	>10	AA010328	Hs.39379	ESTs
20176	>10	N24772	Hs.30213	Homo sapiens putative transmembrane protein (CLN5) mRNA complete cds
33586	>10	W93015	Hs.73166	Treacher Collins syndrome susceptibility protein
27265	>10	AA418392	Hs.46784	ESTs
12453	>10	AA402000	Hs.20415	ESTs Weakly similar to GS3786 [H.sapiens]
36302	>10	AA424652	Hs.124985	ESTs
23192	>10	T40448	Hs.8204	ESTs
17423	>10	AA114071	Hs.26270	ESTs
23464	>10	T67026	Hs.13019	ESTs
42762	>10	Z41697	Hs.106296	ESTs
32628	>10	T56470	Hs.119190	Chromogranin A (parathyroid secretory protein 1)
12805	>10	AA424331	Hs.29640	ESTs
25379	>10	AA058893	Hs.111841	Human adenyl cyclase-associated protein homolog CAP2 (CAP2) mRNA complete cds
39318	>10	C20617	Hs.108945	Homo sapiens mRNA for KIAA0515 protein partial cds
29699	>10	H97938	Hs.75772	Glucocorticoid receptor
17907	>10	AA160530	Hs.72447	ESTs
35819	>10	AA411011	Hs.8038	ESTs
36838	>10	AA436163	Hs.95851	Homo sapiens Pig12 (PIG12) mRNA complete cds
29611	>10	H94043	Hs.41949	ESTs

FIG.-7AW

194 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
19650	>10	H46167	Hs.31542	ESTs
33221	>10	W70305	Hs.64859	ESTs
18840	>10	F10265	Hs.13287	ESTs
2580	>10	M27533	EST - M27533	EST - M27533
7274	>10	AA082171	Hs.8261	ESTs
19524	>10	H29566	Hs.83466	Homo sapiens clone 23579 mRNA sequence
40571	>10	N33558	Hs.103102	ESTs Weakly similar to WWP2 [H.sapiens]
31178	>10	N64191	Hs.46584	ESTs
29894	>10	N23009	Hs.43296	ESTs
22201	>10	R54416	Hs.140932	ESTs
26719	>10	AA282583	Hs.88617	ESTs
32493	>10	T16497	Hs.65339	EST
37179	>10	AA448004	Hs.99150	ESTs
17980	>10	AA169173	Hs.72754	ESTs
21934	>10	R44449	Hs.48778	ESTs
36792	>10	AA435848	EST - RC_AA435848	EST - RC_AA435848
34056	>10	AA194851	Hs.110575	ESTs
39102	>10	AA620674	Hs.112882	EST
26283	>10	AA253217	Hs.41271	ESTs
23989	>10	T98529	Hs.18398	ESTs
32456	>10	T15829	Hs.65264	ESTs
15440	>10	W27301	Hs.111652	ESTs Moderately similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA [Thermomonospora curvata]
19004	>10	H03299	Hs.30390	EST
27839	>10	AA456309	Hs.58831	ESTs
18848	>10	F10338	Hs.106309	ESTs Moderately similar to FOG [M.musculus]

FIG.-7Ax

195 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
13112	>10	AA435896	Hs.18397	ESTs
1850	>10	L17325	Hs.278	Human pre-T/NK cell associated protein (1D12A2) mRNA complete cds
9101	>10	C17938	Hs.25536	ESTs
2807	>10	M55210	Hs.87428	Laminin gamma 1 (formerly LAMB2)
3383	>10	S57153	Hs.91797	Retinoblastoma-binding protein 1{alternative products}
23142	>10	T26444	Hs.101248	ESTs
5367	>10	U95019	Hs.30941	Myastheric syndrome antigen B [human fetal brain mRNA 3477 nt]
32205	>10	R44234	Hs.75169	ESTs
26515	>10	AA262972	Hs.87298	ESTs
15332	>10	W24127	Hs.16003	ESTs Weakly similar to keratin 8 type II cytoskeletal embryonic [M.musculus]
34193	>10	AA232251	Hs.128630	ESTs
6392	>10	X85753	Hs.25283	CELL DIVISION PROTEIN KINASE 8
33784	>10	Z40689	Hs.65973	ESTs
33474	>10	W87484	Hs.50429	ESTs
34964	>10	AA344854	Hs.96837	ESTs
14584	>10	AA621414	Hs.110903	Homo sapiens transmembrane protein mRNA complete cds
22640	>10	R83664	Hs.33416	EST
4339	>10	U38372	EST - U33372	EST - U33372
37557	>10	AA456966	Hs.41548	Human MHC Class I region proline rich protein mRNA complete cds
4937	>10	U68385	Hs.117313	Human Meis1-related protein 2 (MRG2) mRNA partial cds
30795	>10	N53043	Hs.47606	ESTs
30966	>10	N59432	Hs.48382	EST

FIG. 7AV

196 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
33991	>10	AA181935	Hs.104059	EST
2265	>10	M11591		EST - M11591
24315	>10	W84413	Hs.23017	ESTs
38752	>10	AA608852	Hs.112603	EST
5119	>10	U79271	Hs.7571	Human clones 23920 and 23921 mRNA sequence
15037	>10	U44798	Hs.93502	Human U1-snRNP binding protein homolog mRNA complete cds
37045	>10	AA446000	Hs.99043	ESTs
37627	>10	AA459392	Hs.105042	ESTs
21935	>10	R44477	Hs.22646	ESTs
18669	>10	F03889	Hs.27278	ESTs Highly similar to PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A [Bos taurus Sus scrofa]
22737	>10	R92512		EST - RC_R92512_s
30727	>10	N51987	Hs.47390	EST
16086	>10	AA001879	Hs.59890	EST
23293	>10	T52201	Hs.9410	ESTs
5294	>10	U90065	Hs.79351	Human tivo P-domain K+ channel TWIK-1 mRNA complete cds
17769	>10	AA148923	Hs.93675	ESTs
25549	>10	AA101056		EST - RC_AA101056
84	>10	AF001359		EST - AF001359_f
4856	>10	U65093	Hs.82071	Human msg1-related gene 1 (mrg1) mRNA complete cds
7697	>10	AA214730	Hs.107256	ESTs
36296	>10	AA424535	Hs.98416	ESTs
17490	>10	AA125781	Hs.57489	ESTs
36976	>10	AA442779	Hs.98983	ESTs
10425	>10	AA010619	Hs.16446	ESTs

FIG..7Az

197 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
41196	>10	R11654	Hs.20526	ESTs
42285	>10	T94409		EST - RC_T94409
33185	>10	W69435	Hs.58009	EST
13974	>10	AA479299	Hs.21107	ESTs
19868	>10	H61560		EST - RC_H61560
1378	>10	HG831-		EST - HG831-HT831
621	>10	D63813	Hs.26886	Human mRNA for rod photoreceptor protein complete cds
5346	>10	U92459	Hs.86204	Human metabotropic glutamate receptor 8 mRNA complete cds
6029	>10	X66533	Hs.77890	GUANYLATE CYCLASE SOLUBLE BETA-1 CHAIN
22196	>10	R53972	Hs.26026	ESTs
24609	>10	Z38900	Hs.26615	ESTs
37196	>10	AA448226		EST - RC_AA448226
26151	>10	AA250836	Hs.108509	ESTs
5938	>10	X62535	Hs.74044	Diacylglycerol kinase alpha (80kD)
16373	>10	AA019603	Hs.60992	ESTs
28356	>10	AA609080	Hs.41585	ESTs
20070	>10	H98854	Hs.20423	ESTs
17717	>10	AA136541	Hs.71647	EST
20069	>10	H98768	Hs.13121	ESTs
40985	>10	N74604	Hs.124694	ESTs
10194	>10	R63545	Hs.11553	ESTs Weakly similar to putative type III alcohol dehydrogenase [D.melanogaster]
40200	>10	H87229	Hs.82963	Gonadotropin-releasing hormone (leutinizing-releasing hormone)
34983	>10	AA347417	Hs.96869	EST
23543	>10	T79203	Hs.14480	ESTs
12770	>10	AA421778	Hs.8861	ESTs

FIG.-7Ba

198 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
25085	>10	AA017518	Hs.115241	Homo sapiens G protein beta 5 subunit mRNA complete cds
37746	>10	AA463627	Hs.99598	ESTs
2370	>10	M16505	Hs.79876	STERYL-SULFATASE PRECURSOR
31244	>10	N66062	Hs.49112	EST
31716	>10	N75507	Hs.50628	ESTs Weakly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP17 [Rattus norvegicus]
28306	>10	AA598959	Hs.59163	ESTs
2220	>10	L76687	Hs.83070	Homo sapiens Grb14 mRNA complete cds
12404	>10	AA400292	Hs.23786	ESTs
41050	>10	N92882	Hs.109494	ESTs Weakly similar to putative progesterone binding protein [H.sapiens]
2407	>10	M18737	Hs.90708	GRANZYME A PRECURSOR
23462	>10	T66948	Hs.12992	ESTs
18614	>10	F02418	Hs.107614	ESTs
40553	>10	N32060	Hs.104010	Homo sapiens CAG-isl 7 mRNA complete cds
27826	>10	AA455949	Hs.61232	ESTs
207	>10	D12763	Hs.66	Suppression of tumorigenicity 2
41064	>10	N93608	Hs.102923	EST
10845	>10	AA084405	Hs.106313	ESTs Weakly similar to P24 protein [M.musculus]
21813	10	R42039	Hs.23084	ESTs
18463	10	AA233151	Hs.81796	ESTs
17507	10	AA126419	Hs.74876	ESTs
23957	10	T97487	Hs.18070	ESTs
13317	10	AA448212	Hs.38095	ESTs
29550	10	H90133	Hs.41352	ESTs
39068	10	AA620411	Hs.141503	Small inducible cytokine A5 (RANTES)

FIG. 7Bb

199 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
26620	10	AA280413	Hs.89843	Spleen focus forming virus (SFFV) proviral integration
37675	10	AA460377	Hs.99816	oncogene spi1
31437	10	N68821	Hs.49573	ESTs
32657	10	T66867	Hs.76889	ESTs
34952	10	AA342828	Hs.73734	ESTs
26475	10	AA262264	Hs.87640	PLATELET GLYCOPROTEIN V PRECURSOR
41827	10	T15445	Hs.99491	ESTs
20073	10	H98985	Hs.111911	H.sapiens mRNA for F25B3.3 kinase like protein from C.elegans
42336	10	T99713	Hs.139933	ESTs
26412	10	AA258224	Hs.86646	ESTs
21352	10	R15880	Hs.21745	ESTs
22583	10	R79239	Hs.29855	EST
34020	10	AA191543	Hs.144302	EST
25913	10	AA161106		EST - RC_AA161106
82	10	AF000959	Hs.110903	Homo sapiens transmembrane protein mRNA complete cds
37531	10	AA456140	Hs.99235	ESTs
13314	10	AA448169	Hs.6728	ESTs
31430	10	N68610		EST - RC_N68610
30570	10	N49587	Hs.46633	EST
7302	10	AA089688	Hs.103668	EST
27732	10	AA452167	Hs.55778	ESTs
22533	10	R73468	Hs.140996	ESTs
31079	10	N62969	Hs.48682	EST
35470	10	AA400393	Hs.97803	EST Weakly similar to precursor polypeptide [H.sapiens]
37102	10	AA446869	Hs.119316	ESTs

FIG.-7Bc

200 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
203	10	D12620	Hs.106242	CYTOCHROME P450 IVF3
11427	10	AA233277	Hs.74947	ESTs
24159	10	W57862	Hs.21289	ESTs
17870	10	AA157772	Hs.72185	ESTs
5302	10	U90543	Hs.79041	Human butyrophilin (BTF1) mRNA complete cds
27256	10	AA417998	Hs.62781	ESTs
2219	10	L76670	Hs.109610	Homo sapiens nkat7 mRNA complete cds
30858	10	N55081	Hs.47915	EST
8870	10	AB002367	Hs.21355	Human mRNA for KIAA0369 gene complete cds
40870	10	N67262	Hs.358	Zinc finger protein 135 (clone pHZ-17)
11811	10	AA258130	Hs.11530	ESTs
33254	10	W72633	Hs.58187	ESTs
17162	10	AA079094	Hs.58589	EST - RC_AA079094
24392	10	W88568	Hs.58589	Homo sapiens glycogenin-2 gamma (glycogenin-2) mRNA complete cds
27456	10	AA430539	Hs.57760	ESTs
25419	10	AA069386	Hs.57760	EST - RC_AA069386
7100	10	AA012885	Hs.60548	ESTs
31586	10	N71571	Hs.50050	ESTs
29995	10	N26401	Hs.43802	EST
31973	10	N93875	Hs.55015	EST
36159	10	AA419279	Hs.82813	Colony-stimulating factor 1 (M-CSF)
12419	10	AA400888	Hs.7159	ESTs
27076	10	AA401630	Hs.62592	ESTs
28251	10	AA504512	Hs.76852	ESTs Weakly similar to ZK792.1 [C.elegans]
4219	10	U32324	Hs.64310	Human interleukin-11 receptor alpha chain mRNA complete cds

FIG.-7Bd

201 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
27991	10	AA465650	Hs.87306	ESTs
37702	10	AA461119	Hs.99539	ESTs
25251	10	AA040792	Hs.54421	Bradykinin receptor B2
27064	10	AA401253	Hs.87677	ESTs
37592	10	AA458668	Hs.95898	ESTs
39619	9	F10640	Hs.12354	ESTs
31053	9	N62724	Hs.48614	EST
33338	9	W79524	Hs.58585	ESTs
23368	9	T59005	Hs.10476	EST
8240	9	AA397841	Hs.106879	ESTs
21778	9	R41389	Hs.26159	EST
31168	9	N63965	Hs.48903	ESTs
3440	9	S72370	Hs.89890	Pyruvate carboxylase
25930	9	AA164928		EST - RC_AA164928
29971	9	N25657	Hs.93692	EST
39771	9	H17463	Hs.101735	ESTs
21481	9	R26141	Hs.24032	ESTs Highly similar to transmembrane receptor [M.musculus]
10887	9	AA101632	Hs.22971	ESTs
31431	9	N68666	Hs.76798	ESTs
30756	9	N52398	Hs.39252	ESTs
35829	9	AA411438	Hs.74635	Dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex 2-oxo-glutarate complex branched chain keto acid dehydrog
24540	9	Z38435	Hs.19235	ESTs
37500	9	AA455474	Hs.100530	ESTs
19007	9	H03358		EST- RC_H03358

FIG.-7Be

202 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
42650	9	W92272	Hs.25601	Homo sapiens zinc-finger helicase (hZFH) mRNA complete cds
16705	9	AA043675	Hs.62633	EST
40275	9	H94647	Hs.102329	ESTs
24372	9	W87423	Hs.35598	ESTs
9011	9	C01394	Hs.106823	Homo sapiens clone 24818 mRNA sequence
40780	9	N59568	Hs.108107	ESTs
17177	9	AA079331	EST - RC_AA079331	
20878	9	N70305	Hs.34492	ESTs
38140	9	AA486273	Hs.100472	ESTs
3490	9	S77763	Hs.75643	Homo sapiens NF-E2 protein (NF-E2) mRNA complete cds
39112	9	AA620724	Hs.112890	ESTs
27347	9	AA424940	Hs.43590	ESTs
14747	9	D60364	Hs.34882	ESTs
23599	9	T82307	EST - RC_T82307	
23979	9	T98262	EST - RC_T98262	
27759	9	AA453472	ESTs	
36691	9	AA432381	Hs.95111	ESTs
			Hs.97357	ESTs Moderately similar to NITRIC OXIDE SYNTHASE INDUCIBLE [H.sapiens]
26782	9	AA284181	Hs.89310	ESTs
26818	9	AA285145	Hs.50446	ESTs
22334	9	R61290	Hs.25870	ESTs
29892	9	N22995	Hs.42829	ESTs
22945	9	T10134	Hs.9877	Homo sapiens mRNA for KIAA0688 protein complete cds
30618	9	N50656	Hs.93996	ESTs Highly similar to mosaic protein LR11 [H.sapiens]
29715	9	H98700	Hs.60887	ESTs
37560	9	AA457023	EST - RC_AA457023	

FIG. 7Bf

203 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
23264	9	T50062	Hs.9092	EST
31001	9	N62200	Hs.47566	ESTs
17841	9	AA156109	Hs.66180	ESTs
3478	9	S76992	Hs.104005	Vav 2 oncogene
11605	9	AA243139	Hs.4863	ESTs
19032	9	H04822	Hs.30494	EST
29933	9	N24182	Hs.93677	ESTs
26622	9	AA280431	Hs.88756	ESTs
4289	9	U35376	Hs.37138	Human repressor transcriptional factor (ZNF85) mRNA complete cds
42034	9	T56281	Hs.110440	Human metallothionein (MT)-I-F gene
30447	9	N47439	Hs.44603	ESTs
25238	9	AA039568		EST - RC_AA039568
20238	9	N30077	Hs.14855	ESTs
30232	9	N34500	Hs.44600	EST
17017	9	AA069920		EST - RC_AA069920
11845	9	AA259064	Hs.10839	ESTs Weakly similar to unknown [S.cerevisiae]
30229	9	N34457		EST - RC_N34457
30737	9	N52137	Hs.47442	EST
30555	9	N49259		EST - RC_N49259
981	9	HG2139-		EST - HG2139-HT2208_f
30498	9	N48325	Hs.93956	EST
40434	9	N21461		EST - RC_N21461
36788	9	AA435824	Hs.95594	Homo sapiens BAC clone RG113D17 from 7p14-p15
28991	9	F04652	Hs.66195	ESTs
25942	9	AA234187	Hs.87267	ESTs

FIG. 7Ba

204 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
30466	9	N47951	Hs.57485	ESTs
19317	9	H17476	Hs.11615	ESTs Weakly similar to dual specificity phosphatase [H.sapiens]
13859	8	AA470066	Hs.24309	ESTs Highly similar to S-ACYL FATTY ACID SYNTHASE THIOESTERASE MEDIUM CHAIN [Rattus norvegicus]
23445	8	T65992	Hs.11722	EST
24448	8	W93273	Hs.9270	ESTs Weakly similar to isopentenyl-diphosphate Delta-isomerase [H.sapiens]
7583	8	AA167824	Hs.63559	ESTs Highly similar to PROTEIN CDC27HS [Homo sapiens]
22778	8	R94840	Hs.35372	ESTs Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]
16439	8	AA024835	Hs.47584	Homo sapiens Shab-related delayed-rectifier K+ channel alpha subunit (KCNS3) mRNA complete cds
42395	8	W42733	Hs.109870	ESTs
19991	8	H90887	Hs.18357	ESTs
23690	8	T87648		EST - RC_T87648
7111	8	AA018804	Hs.125175	ESTs Highly similar to RAS-RELATED PROTEIN RAB-14 [Rattus norvegicus]
6400	8	X86163	Hs.54421	Bradykinin receptor B2
42474	8	W63747	Hs.109918	H.sapiens: TTF mRNA for small G protein
11425	8	AA233257	Hs.25511	Homo sapiens mRNA for Hic-5 partial cds
27039	8	AA400277	Hs.48849	ESTs
32206	8	R44386	Hs.91703	ESTs
15310	8	W19098	Hs.7921	ESTs
36601	8	AA431337	Hs.98017	ESTs
463	8	D38462		EST - D33462
31674	8	N74357	Hs.50482	ESTs

FIG..7Bh

205 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
31182	8	N64339	Hs.48956	EST
13499	8	AA453458	Hs.7301	ESTs
37514	8	AA455914	Hs.1019	Parathyroid hormone receptor 1
5998	8	X65644	Hs.75063	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 ENHANCER-BINDING PROTEIN 2
962	8	HG180-		EST - HG180-HT180
40790	8	N62328	Hs.3786	Glutamate receptor metabotropic 3
25700	8	AA131512	Hs.103820	EST
36880	8	AA436706	Hs.98895	ESTs
2809	8	M55267	Hs.41846	EVI2A PROTEIN PRECURSOR TROPIC VIRAL INTEGRATION SITE 2A PROTEIN)
5620	8	X14885	Hs.2025	Transforming growth factor beta 3
16643	8	AA039325	Hs.47200	ESTs
32051	8	R01450	Hs.91061	ESTs
33550	8	W90617	Hs.50120	ESTs
6177	8	X75535	Hs.118884	33 KD HOUSEKEEPING PROTEIN
33000	8	W45531	Hs.94642	ESTs
20066	8	H98701	Hs.4985	ESTs
4590	8	U50534	Hs.30649	Human infant brain mRNA clone 13cDNA73
37199	8	AA448257	Hs.97127	ESTs
24601	8	Z38844	Hs.25803	ESTs
33589	8	W93074	Hs.59342	ESTs
37389	8	AA453466	Hs.99330	ESTs
5801	8	X55448	Hs.3118	H.sapiens: mRNA for 2.19 gene
28748	8	D25912	Hs.74832	ESTs
40070	8	H72592	Hs.77554	ESTs

FIG. 7Bi

206 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
40367	8	H98857	Hs.75520	Human mRNA for KIAA0041 gene partial cds
33609	8	W93585	Hs.59476	ESTs
24502	8	Z38214	Hs.26946	ESTs
11129	8	AA156873	Hs.15970	ESTs
7144	8	AA033659	Hs.95154	ESTs
28584	8	C21221	Hs.68619	ESTs Highly similar to METALLOTHIONEIN-IA [Equus caballus]
22165	8	R52822	Hs.22003	ESTs
31987	8	N94551	Hs.55060	ESTs
32470	8	T15956	Hs.65289	EST
38642	8	AA599152	Hs.91379	PTB-ASSOCIATED SPLICING FACTOR
40438	8	N21684	Hs.80500	Human mRNA for KIAA0061 gene partial cds
34471	8	AA258843	Hs.111376	ESTs
41571	8	R61005	Hs.115170	Homo sapiens mRNA for GalT4 protein
31417	8	N68435	Hs.49516	ESTs
23951	8	T97318	Hs.18037	ESTs
7832	8	AA249260	Hs.28545	ESTs
27928	8	AA461093	Hs.26799	ESTs Moderately similar to zinc finger protein [R.norvegicus]
2017	8	L34219	Hs.1933	Cellular retinaldehyde-binding protein
25530	8	AA098834	Hs.83428	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)
20556	8	N55189	Hs.34081	ESTs
27036	8	AA400155	Hs.142935	ESTs
22651	7	R85266	Hs.33487	ESTs
33663	7	W95805	Hs.59736	EST
19374	7	H19472	Hs.31653	EST
10275	7	R79356	Hs.19280	ESTs Weakly similar to PROTEIN Q300 [Mus musculus]

FIG. 7Bi

207 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
39471	7	D60265	Hs.107894	ESTs
25100	7	AA019426	Hs.103343	EST
8828	7	AB002316	Hs.65746	Human mRNA for KIAA0318 gene partial cds
17132	7	AA075674		EST - RC_AA075674
15915	7	Y09858	Hs.82577	Human DNA sequence from clone 323P24 on chromosome Xp11.21-11.23 Contains SPIN (spindlin homolog (PROTEIN DXF34) hypothetical prote
8216	7	AA393089	Hs.86723	ESTs
22512	7	R71489	Hs.29196	EST
19097	7	H08171	Hs.30842	ESTs
25048	7	AA011041	Hs.130843	ESTs
35353	7	AA398962	Hs.97699	ESTs
31278	7	N66399	Hs.49193	EST
23149	7	T26893	Hs.7569	EST
11880	7	AA262783	Hs.22057	ESTs
17547	7	AA127595	Hs.71016	ESTs
32854	7	W32094	Hs.55501	ESTs
36822	7	AA435978	Hs.98852	EST
35530	7	AA400893	Hs.41717	Human 3'5' cyclic nucleotide phosphodiesterase (HSPDE1 A3A) mRNA complete cds
3869	7	U14417	Hs.106185	Human Fal guanine nucleotide dissociation stimulator mRNA partial cds
9368	7	H09246	Hs.100739	ESTs
15154	7	U79527	Hs.111075	Human orphan G-protein coupled receptor Dez isoform a mRNA complete cds
21178	7	R06607	Hs.19748	EST-

FIG. 7Bk

208 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
33081	7	W57731	Hs.56213	ESTs
13848	7	AA465664	Hs.21323	ESTs
18659	7	F03220	Hs.13258	ESTs
1979	7	L29339	Hs.1964	Solute carrier family 5 (sodium/glucose cotransporter) member 1
22609	7	R80945	Hs.29978	ESTs
2418	7	M19507	Hs.1817	Myeloperoxidase
28863	7	D80051	Hs.124418	ESTs
26764	7	AA283926	Hs.51501	ESTs
6544	7	X95677		EST - X95677
33524	7	W89188	Hs.59096	ESTs
18374	7	AA226877	Hs.67624	ESTs
10108	7	R25069	Hs.23790	ESTs
26178	7	AA251153	Hs.27910	Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA complete cds
36428	7	AA427605	Hs.98551	Human cardiac myosin binding protein-C (MyBP-C) gene complete cds
29808	7	N21032	Hs.42931	EST
24837	7	Z41186	Hs.27997	ESTs
24909	7	Z98492	Hs.27250	ESTs
26333	7	AA256075	Hs.82280	Homo sapiens regulator of G protein signaling 10 mRNA complete cds
11507	7	AA235465	Hs.29161	ESTs
40387	7	H99460	Hs.108873	ESTs
16112	7	AA004377	Hs.91813	Human butyrophilin (BTF2) mRNA complete cds
25413	7	AA065096		EST - RC_AA065096

FIG. 7BI

209 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
13232	7	AA443844	Hs.20887	ESTs
27236	7	AA417037	Hs.67805	ESTs
21684	7	R38944	Hs.129672	ESTs
9294	7	D82712	Hs.15301	ESTs Weakly similar to weakly similar to ANK repeat region of Fowlpox virus BamHI-orf7 protein [C.elegans]
16886	7	AA057119	Hs.5091	Homo sapiens torsinB (DQ1) mRNA partial cds
20083	7	H99879	Hs.28029	ESTs Highly similar to EPIDERMAL GROWTH FACTOR PRECURSOR [Mus musculus]
30651	7	N51029	Hs.38672	ESTs
22362	7	R62447	Hs.22123	ESTs
21561	7	R33245	Hs.23076	ESTs
21636	7	R37501	Hs.23600	ESTs
21223	7	R08175	Hs.110130	Homo sapiens chromosome 19 cosmid F22329
32218	7	R45654	Hs.1339	Collagen type IV alpha 2
13405	7	AA450118	Hs.25722	ESTs Weakly similar to KRUPPEL-RELATED ZINC FINGER PROTEIN 1 [Homo sapiens]
30627	7	N50740	Hs.47111	ESTs
30117	7	N30824	Hs.44227	ESTs Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
31344	7	N67238		EST - RC_N67238
38119	7	AA485714	Hs.105669	ESTs
33297	7	W73781	Hs.105715	ESTs
6892	7	Z30426	Hs.82401	CD69 antigen (early T cell activation antigen)
9923	7	N44998	Hs.24550	ESTs
27942	7	AA463237	Hs.13021	ESTs

FIG.-7Bm

210 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
34845	7	AA293420	Hs.95464	ESTs Moderately similar to transcription enhancer factor TEF1 [H.sapiens]
29829	7	N21460	Hs.43005	ESTs
15059	7	U53831	Hs.85280	Human interferon regulatory factor 7 (humirf7) mRNA complete cds
40441	7	N22053	Hs.112083	ESTs
25095	7	AA018937	Hs.109558	ESTs
2941	7	M62840	Hs.82542	Acylglycerol hydrolase (neutrophil)
1945	7	L25878	Hs.89649	Epoxide hydrolase 1 microsomal (xenobiotic)
42648	7	W92150	Hs.79310	Human GiAP SH3 binding protein mRNA complete cds
19592	7	H40696	Hs.33790	ESTs
29801	7	N20939	Hs.38759	ESTs
15417	7	W26982	Hs.39330	ESTs
39877	7	H38627	Hs.107696	ESTs
23967	7	T97910	Hs.18184	EST
20041	7	H97012	Hs.11050	ESTs Weakly similar to L8004.7 gene product [S.cerevisiae]
18314	7	AA214510	Hs.86618	ESTs
22452	7	R67370	Hs.28758	ESTs
30496	7	N48294	Hs.46850	EST
26830	7	AA287057	Hs.48820	ESTs
33432	7	W86075	Hs.38715	ESTs
31394	7	N67990	Hs.49421	ESTs
7053	6	Z84721	Hs.75792	Hemoglobin alpha 1
33518	6	W88996	Hs.59134	EST
5355	6	U94320	Hs.123021	Human Y5 receptor mRNA complete cds
41311	6	R38516	Hs.124255	EST

FIG. 7Bn

211 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
12545	6	AA406320	Hs.24702	ESTs
23843	6	T92561	Hs.110422	ESTs
21667	6	R38475	Hs.21408	ESTs
17472	6	AA121704	Hs.69494	ESTs
25648	6	AA126673	Hs.110341	ESTs
32710	6	T87324	Hs.91021	EST
3450	6	S73840	Hs.931	H.sapiens mRNA for fast 2a myosin heavy chain (3' end)
979	6	HG2090-		EST - HG2090-HT2152
8151	6	AA348686		EST - AA348686
35380	6	AA399522	Hs.97671	ESTs Weakly similar to T04A8.9 [C.elegans]
23798	6	T91047	Hs.126785	ESTs
940	6	HG1496-		EST - HG1496-HT1496
35896	6	AA412106	Hs.97349	ESTs
16350	6	AA019034	Hs.94000	ESTs
27547	6	AA436613	Hs.72157	ESTs
22528	6	R73036	Hs.29323	EST
25815	6	AA149889	Hs.96200	ESTs Weakly similar to A-kinase anchor protein 95 AKAP95 [R.norvegicus]
8473	6	AA437346	Hs.2967	SHB adaptor protein (a Src homology 2 protein)
35742	6	AA406058	Hs.97999	EST
36538	6	AA430002	Hs.112044	ESTs
17831	6	AA152323	Hs.71947	ESTs
25072	6	AA015799	Hs.33792	ESTs
15632	6	W56102	Hs.71218	ESTs
20442	6	N50827	Hs.25275	ESTs

FIG.-7Bo

212 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
28357	6	AA609120	Hs.56185	ESTs Weakly similar to The KIAA0147 gene product is related to adenylyl cyclase. [H.sapiens]
25022	6	AA007591	Hs.110227	ESTs
29334	6	H68158	Hs.28310	ESTs
28148	6	AA488875	Hs.6433	Homo sapiens clone 24523 mRNA sequence
30744	6	N52195	Hs.105365	H.sapiens mRNA for arginine methyltransferase
27577	6	AA442090	Hs.119295	ESTs
33472	6	W87469	Hs.58992	ESTs
25687	6	AA130867	Hs.100119	ESTs
10549	6	AA027317	Hs.19136	ESTs Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
32836	6	W23631	Hs.55426	ESTs
17025	6	AA070160		EST - RC_AA070160
22939	6	T10070	Hs.4217	Homo sapiens mRNA for KIAA0667 protein partial cds
15803	6	X52332	Hs.104115	Human Kox1 gene for zinc finger protein
34618	6	AA282143	Hs.58094	H.sapiens mRNA for melanoma growth regulatory protein MIA.
11074	6	AA148983	Hs.29068	ESTs
12212	6	AA297746	Hs.22654	ESTs
16102	6	AA002150	Hs.59872	ESTs
31340	6	N67197	Hs.50125	EST
19459	6	H24317	Hs.6526	ESTs
17533	6	AA127098	Hs.71057	EST
22017	6	R46597	Hs.22703	ESTs
23687	6	T87519	Hs.16075	ESTs Weakly similar to no similarities to reported gene products [H.sapiens]
30298	6	N36130	Hs.44792	EST Weakly similar to hypothetical protein [H.sapiens]

FIG.-7Bb

213 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
28973	6	F04014	Hs.65996	ESTs
17042	6	AA070397		EST - RC_AA070397
20817	6	N68628	Hs.37630	ESTs
18430	6	AA232138	Hs.118898	ESTs
28493	6	C14820	Hs.67186	EST
30497	6	N48302	Hs.46852	EST
32502	6	T16896	Hs.65373	ESTs
41324	6	R38804	Hs.13434	Homo sapiens clone 24418 mRNA sequence
18418	6	AA228096	Hs.60480	ESTs
23622	6	T84046	Hs.15345	ESTs
15342	6	W25781	Hs.8136	Homo sapiens clone 23698 mRNA sequence
15246	6	W01094	Hs.84628	ESTs
2247	6	M10321	Hs.110802	VON WILLEBRAND FACTOR PRECURSOR
31906	6	N92643	Hs.35986	Homo sapiens CASK mRNA complete cds
9062	6	C06238	Hs.95665	Homo sapiens clone 24700 unknown mRNA partial cds
38640	6	AA599142	Hs.112509	EST
42622	6	W87801	Hs.108209	ESTs
27908	6	AA460671	Hs.54837	ESTs
7293	6	AA085354		EST - AA085354
27322	6	AA424325	Hs.40496	ESTs
5774	6	X54199	Hs.82285	Phosphoribosylglycinamide formyltransferase phosphoribosylglycinamide synthetase phosphoribosylaminoimidazole synthetase
33469	6	W87454	Hs.58987	ESTs Highly similar to homogentisate 12-dioxygenase [H.sapiens]
40329	6	H97488	Hs.108802	Human N-ethylmaleimide-sensitive factor mRNA partial cds
26539	6	AA278848	Hs.88522	ESTs

FIG. 7Ba

214 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
23579	6	T81098	Hs.124065	ESTs
22435	6	R66706	Hs.28706	ESTs
19956	6	H80842	Hs.37445	ESTs
18607	6	F02345	Hs.21197	ESTs
18991	6	H02554	Hs.30323	ESTs
7810	6	AA248169	Hs.106709	ESTs Highly similar to LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR [Rattus norvegicus]
30810	6	N53419	Hs.47646	ESTs
17996	6	AA169606	Hs.72815	ESTs
26245	6	AA252357	Hs.87794	ESTs
13348	6	AA449267	Hs.17914	ESTs Weakly similar to HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT [M.musculus]
15034	6	U43701	Hs.75403	60S RIBOSOMAL PROTEIN L23A
33802	6	Z41058	Hs.79248	ESTs
33394	6	W84432	Hs.58670	ESTs
31170	6	N64017	Hs.48911	ESTs
40828	6	N64144	Hs.102749	EST
1789	6	L13258	Hs.936	Solute carrier family 17 (sodium phosphate) member 2
17740	5	AA142922	Hs.9817	Homo sapiens Arg/Abi-interacting protein ArgBP2a (ArgBP2a) mRNA complete cds
9509	5	H58970	Hs.49683	ESTs
15540	5	W30895	Hs.7535	ESTs
27827	5	AA455976	Hs.42355	ESTs
30697	5	N51585	Hs.47049	ESTs
40299	5	H95787	Hs.108745	ESTs

FIG. 7Br

215 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
16627	5	AA036779	Hs.61826	Homo sapiens clone 23928 mRNA sequence
20659	5	N62915	Hs.57672	ESTs Weakly similar to weakly similar to myosin heavy chain [C.elegans]
31009	5	N62272	Hs.48502	ESTs
14877	5	T65508	Hs.14623	Homo sapiens mRNA for KIAA0625 protein partial cds
31102	5	N63178	Hs.48728	ESTs
22830	5	R98421	EST - RC_R98421	EST - RC_R98421
25248	5	AA040507	Hs.92924	ESTs
32145	5	R38910	Hs.66170	Homo sapiens clone 24503 mRNA sequence
27970	5	AA464626	Hs.10247	Activated leucocyte cell adhesion molecule
34509	5	AA262974	Hs.111394	ESTs
29522	5	H88338	Hs.90250	ESTs
32159	5	R40974	Hs.124270	ESTs
35492	5	AA400514	Hs.97505	ESTs
37630	5	AA459649	Hs.99485	ESTs
27103	5	AA404282	Hs.63481	ESTs Weakly similar to kynurenine/alpha-aminoacidipate aminotransferase [R.norvegicus]
17209	5	AA082933	EST - RC_AA082933	EST - RC_AA082933
589	5	D50930	Hs.5084	Human mRNA for KIAA0140 gene complete cds
17489	5	AA122394	Hs.70811	ESTs
6293	5	X80878	Hs.95262	Human R kappa B mRNA complete cds
5067	5	U77845	Hs.21254	Human hTRIP (hTRIP) mRNA complete cds
23060	5	T23513	Hs.7147	ESTs
28902	5	D80990	Hs.45247	ESTs
32328	5	R76401	Hs.92262	ESTs
33218	5	W70259	Hs.48523	ESTs

FIG.-7Bs

216 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
28751	5	D45455	Hs.65524	ESTs
21400	5	R19360	Hs.14651	ESTs
15557	5	W36290	Hs.9115	ESTs
12631	5	AA412293	Hs.21258	ESTs
32282	5	R62579	Hs.62264	ESTs
10416	5	AA009809	Hs.37599	ESTs
40308	5	H96306	Hs.32980	Human mRNA for BST-1 complete cds
11599	5	AA242829	Hs.7508	ESTs
33220	5	W70279	Hs.94811	ESTs Weakly similar to 3-oxoacyl-[acyl-carrier protein] reductase: [E.coli]
23100	5	T23867	Hs.7316	ESTs
15333	5	W24154	Hs.6166	ESTs
8331	5	AA412556	EST - AA412556	
9010	5	C01360	Hs.67364	Homo sapiens clone 23904 mRNA sequence
4660	5	U53225	Hs.75283	Sorting nexin 1
25213	5	AA035444	Hs.100543	Homo sapiens clone 24505 mRNA sequence
25242	5	AA039933	Hs.30941	Myasthenic syndrome antigen B [human fetal brain mRNA 3477 nt]
28708	5	D20538	Hs.90165	EST
7435	5	AA096412	Hs.26236	ESTs
25538	5	AA099580	Hs.101442	ESTs Highly similar to ZINC FINGER PROTEIN 8 [Homo sapiens]
271	5	D14823	EST - D14823	
5490	5	X04571	Hs.2230	Epidermal growth factor
18812	5	F10040	Hs.13251	ESTs
23393	5	T62918	Hs.11110	ESTs Weakly similar to ZINC FINGER PROTEIN 42 [H.sapiens]
23446	5	T66282	Hs.12907	ESTs

FIG. 7Bt

217 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
35204	5	AA398155	Hs.97600	ESTs
31369	5	N67598	Hs.136395	ESTs
5244	5	U85992	Hs.87197	Human clone IMAGE:35527 unknown protein mRNA partial cds
20835	5	N69215	Hs.37456	ESTs
16502	5	AA027059	Hs.61425	EST
23691	5	T87693	Hs.16414	ESTs
31842	5	N90168	Hs.54593	EST
7845	5	AA249611		EST - AA249611
29297	5	H65459	Hs.38323	ESTs
7953	5	AA284403	Hs.74750	Homo sapiens mRNA for KIAA0554 protein partial cds
36412	5	AA426464	Hs.98466	ESTs
19357	5	H18929		EST - RC_H18929
16299	5	AA016258		EST - RC_AA016258
25312	5	AA047078	Hs.95278	ESTs Weakly similar to IIII ALU SUBFAMILY SQ WARNING ENTRY IIII [H.sapiens]
27617	5	AA446114	Hs.55409	ESTs
42432	5	W46403	Hs.107293	ESTs
38432	5	AA496983	Hs.78672	Laminin alpha 4
32215	5	R45175	Hs.117183	ESTs
15214	5	U93553	Hs.91310	Human alpha1-fetoprotein transcription factor (hFTF) mRNA complete cds
15141	5	U78798	Hs.90957	Human TNF receptor associated factor 6 (TRAF6) mRNA complete cds
20052	5	H97922	Hs.5376	Human LAR-interacting protein 1a mRNA complete cds
7551	5	AA156838	Hs.107941	ESTs
26451	5	AA259058	Hs.43616	ESTs

FIG. 7Bu

218 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
42355	5	W20404	Hs.55405	ESTs
39480	5	D60419	Hs.81915	STATHMIN
17369	5	AA101833	Hs.69293	EST
14993	5	U22172	Hs.73046	Human CNA damage repair and recombination protein RAD52 pseudogene mRNA partial cds
23400	5	T63336	Hs.105095	ESTs
21153	5	R05315		EST - RC_R05315
14282	5	AA505141	Hs.11923	ESTs
21104	5	R01081		EST - RC_R01081
32825	5	W20364	Hs.55412	ESTs
35018	5	AA349591		EST - RC_AA349591
25104	5	AA019598	Hs.103351	ESTs
19235	5	H12725	Hs.31181	ESTs
34979	5	AA347209	Hs.7841	Human mRNA for KIAA0324 gene partial cds
21501	5	R26855	Hs.24120	ESTs
18331	5	AA218543	Hs.10881	Homo sapiens mRNA for KIAA0541 protein partial cds
37529	5	AA456112	Hs.99410	ESTs
15532	5	W28944	Hs.5296	ESTs Highly similar to PUTATIVE 2-HYDROXYACID DEHYDROGENASE IN BISC-CSPA INTERGENIC REGION [Escherichia coli]
11858	5	AA262308	Hs.106385	ESTs
29450	5	H80865	Hs.111026	Phosphatidylinositol glycan class F
37294	5	AA450127	Hs.110571	ESTs Highly similar to MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD118 [Mus musculus]
35170	5	AA397830	Hs.98347	ESTs Weakly similar to rtvp-1 [H.sapiens]
23201	5	T40652	Hs.8279	ESTs

FIG. 7Bv

219 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
27012	5	AA398913	Hs.45231	ESTs
28767	5	D45608	Hs.83792	Surfactant pulmonary-associated protein D
17777	5	AA149634	Hs.62788	ESTs Weakly similar to hypothetical L1 protein [H.sapiens]
20588	5	N58009	Hs.36218	ESTs
20356	5	N39453	Hs.27371	ESTs
23375	5	T59670	Hs.10615	EST
17030	5	AA070188		EST - RC_AA070188
30752	5	N52340	Hs.118084	EST
25808	5	AA149226	Hs.95821	Human osteoclast stimulating factor mRNA complete cds
31345	5	N67268	Hs.50139	ESTs
30784	5	N52857	Hs.47558	ESTs
13707	5	AA460281	Hs.14697	ESTs
29199	5	H25761	Hs.57082	EST
39003	4	AA609920	Hs.112785	EST
41529	4	R54458	Hs.2699	Glypican 1 -
3151	4	M83652	Hs.53155	Properdin P factor complement
33134	4	W61264	Hs.57829	ESTs
29196	4	H24456	Hs.85053	Homo sapiens clone 24440 mRNA sequence
12863	4	AA425782	Hs.27973	ESTs
11949	4	AA279827	Hs.125035	ESTs
31925	4	N92924	Hs.125032	ESTs
35258	4	AA398428	Hs.97628	ESTs
39838	4	H27216	Hs.107635	ESTs
30796	4	N53046	Hs.91146	ESTs Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
19464	4	H24458	Hs.32085	EST

FIG.-7Bw

220 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
42486	4	W68410	Hs.106857	Calbindin 2 (29kD calretinin)
34274	4	AA236352	Hs.110821	ESTs
37648	4	AA459917	Hs.99506	EST
3169	4	M85085	Hs.693	Cleavage stimulation factor 3' pre-RNA subunit 2 64kD
10326	4	R96417	Hs.107795	ESTs
15063	4	U56814	Hs.88646	Homo sapiens DNase gamma mRNA complete cds
23571	4	T80628	Hs.108169	ESTs
14377	4	AA599583	Hs.15299	ESTs Weakly similar to HSM-2 [H.sapiens]
22255	4	R56239	Hs.6666	ESTs
36820	4	AA435968	Hs.98849	ESTs Weakly similar to bithoraxoid [D.melanogaster]
35063	4	AA358015	Hs.96998	EST
12376	4	AA399271	Hs.19610	ESTs
31406	4	N68163	Hs.49455	EST
27430	4	AA429028	Hs.42676	ESTs Moderately similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]
30362	4	N40170	Hs.45046	ESTs
30599	4	N50039	Hs.47004	ESTs
27894	4	AA460319	Hs.48469	ESTs
31844	4	N90218	Hs.54607	ESTs
24935	4	AFFX-		AFFX-HLIMGAPDH/M33197_M
40906	4	N68829	Hs.131510	ESTs
35220	4	AA398246	Hs.97594	ESTs
10024	4	N94832	Hs.121699	ESTs
4238	4	U33053	Hs.2499	Human lipid-activated protein kinase PRK1 mRNA complete cds
26358	4	AA256396	Hs.88156	EST
24716	4	Z39734	Hs.22550	ESTs

FIG.-7Bx

221 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
19243	4	H13539	Hs.31222	ESTs
41844	4	T15833	Hs.100227	EST
39774	4	H17948	Hs.106311	Homo sapiens DGS-A mRNA 3' end
20111	4	N21380	Hs.25497	H.sapiens mRNA for ROX protein
24008	4	T99337	Hs.18624	ESTs
8316	4	AA410529	Hs.30732	ESTs
35072	4	AA358738	EST - RC; AA358738	
39794	4	H21819	Hs.14896	Homo sapiens clone 24590 mRNA sequence
1517	4	J04501	Hs.772	Glycogen synthase 1 (muscle)
9164	4	D38081	Hs.89887	Thromboxane A2 receptor
35027	4	AA349996	Hs.96937	ESTs
35185	4	AA398015	Hs.97590	Untitled
26570	4	AA279425	Hs.86428	ESTs Weakly similar to hypothetical L1 protein [H.sapiens]
19759	4	H54352	Hs.36873	ESTs
34310	4	AA243416	Hs.75470	Homo sapiens mRNA expressed in osteoblast complete cds
39961	4	H57317	Hs.108161	ESTs
23249	4	T47919	Hs.8749	ESTs
19119	4	H09077	Hs.30895	EST
14158	4	AA490182	Hs.118598	ESTs
22866	4	R99938	Hs.36189	EST
16935	4	AA059392	Hs.66791	ESTs
41950	4	T33137	Hs.7967	ESTs
20404	4	N48694	Hs.30881	Homo sapiens liprin-alpha2 mRNA complete cds
18406	4	AA227962	Hs.112075	ESTs Weakly similar to reverse transcriptase [M.musculus]
16560	4	AA031308	Hs.24341	ESTs
26098	4	AA242831	Hs.87606	ESTs

FIG..7Bv

222 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
34360	4	AA251547	Hs.104358	EST
16830	4	AA054222	Hs.40400	ESTs
32668	4	T69284	Hs.2314	Mannose-binding lectin soluble (opsonic defect)
32912	4	W38051		EST - RC_W38051
16230	4	AA011549	Hs.47884	ESTs
29696	4	H97909	Hs.42344	ESTs
8232	4	AA397529		EST - AA397529
25584	4	AA112320	Hs.16704	ESTs
30878	4	N56882	Hs.46761	EST
40579	4	N34524	Hs.102516	ESTs
8026	4	AA301842	Hs.105189	ESTs Weakly similar to reverse transcriptase homolog [H.sapiens]
3094	4	M77481	Hs.72879	Human antigen (MAGE-1) gene complete cds
17480	4	AA121974		EST - RC_AA121974
15766	4	W95777	Hs.90804	ESTs
34865	4	AA299903	Hs.111498	EST
29779	4	N20290	Hs.42836	ESTs
6547	4	X95808	Hs.9568	Human mRNA for KIAA0385 gene complete cds
24479	4	W96222	Hs.34192	ESTs
16135	4	AA004805	Hs.63668	Human Toll-like receptor 2 (TLR2) mRNA complete cds
11098	4	AA151243	Hs.38163	ESTs
14388	4	AA599742	Hs.21600	ESTs
36078	4	AA417275	Hs.98214	ESTs
23440	4	T65566	Hs.12859	ESTs
20863	4	N69989	Hs.19167	ESTs
20347	4	N39117	Hs.12250	ESTs
7795	4	AA247455	Hs.15220	ESTs

FIG._7Bz

223 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
10729	4	AA054087	Hs.18858	ESTs
12734	4	AA419200	Hs.5737	ESTs
24446	4	W93119	Hs.19512	ESTs
30734	4	N52083	Hs.47418	EST
20641	4	N62353	Hs.109685	ESTs
21183	4	R06769	Hs.19795	ESTs
18138	4	AA192757	Hs.131687	ESTs
35310	4	AA398662	Hs.97302	ESTs
39497	4	D80154	Hs.56340	ESTs
29866	4	N22343	Hs.43145	ESTs
8707	4	AA479995	Hs.76982	Homo sapiens mRNA for KIAA0583 protein partial cds
18472	4	AA233299	Hs.72158	ESTs
24720	4	Z39754	Hs.23236	ESTs
40825	4	N63923	Hs.102746	ESTs
15375	4	W26395	Hs.56876	ESTs
32869	4	W35211	Hs.54801	ESTs
4641	4	U52426	Hs.74597	Homo sapiens GOK (STIM1) mRNA complete cds
11786	4	AA256616	Hs.31707	ESTs
21571	4	R33841	Hs.24709	ESTs Highly similar to NUCLEOLYSIN TIA-1 [Homo sapiens]
1600	4	K03474		EST - K03474
21103	4	R01068	Hs.14603	ESTs
22993	4	T16358	Hs.106443	ESTs
38666	4	AA599661	Hs.103849	ESTs
27148	4	AA406231	Hs.100113	Human mRNA for KIAA0381 gene partial cds
28680	4	D20261	Hs.80067	ESTs
36397	4	AA426372	Hs.109804	Human mRNA for histone H1x complete cds

FIG. 7Ca

224 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
26915	4	AA330634		EST - RC_AA330634
6912	4	Z35278	Hs.2536	H.sapiens PEBP2aC1 acute myeloid leukaemia mRNA
31825	4	N89848	Hs.54543	ESTs
10763	4	AA057620	Hs.30807	ESTs
17007	4	AA069696	Hs.67317	ESTs
33439	4	W86445	Hs.58844	ESTs
27657	4	AA447612	Hs.60435	ESTs
26288	4	AA253393	Hs.87734	ESTs
8235	4	AA397616	Hs.107245	ESTs Moderately similar to potassium channel protein Raw3 [R.norvegicus]
12114	4	AA287097	Hs.25114	ESTs
879	4	D88155	Hs.97196	Human steroidogenic factor 1 mRNA complete cds
30793	4	N52979	Hs.51919	Plasminogen-like protein
13522	4	AA454115	Hs.6000	ESTs
20819	4	N68730	Hs.12160	ESTs
20019	4	H94266	Hs.9451	ESTs
32396	4	R95778	Hs.93008	EST
38162	4	AA487165	Hs.105706	EST
8487	4	AA442669		EST - AA442669
18444	4	AA232646	Hs.68061	ESTs
16183	4	AA010070	Hs.60339	EST
33047	4	W49755	Hs.89359	ESTs Moderately similar to type Ia hair keratin a3 [H.sapiens]
14797	4	S82769	Hs.104133	GABAA receptor gamma 3 subunit [human fetal brain mRNA Partial 1536 nt]
26107	3	AA243172	Hs.87619	ESTs
24421	3	W92001	Hs.120969	ESTs

FIG. 7Cb

225 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
27665	3	AA447759	Hs.134724	ESTs
19154	3	H10047	Hs.22515	ESTs
10933	3	AA121360	Hs.27567	ESTs Weakly similar to similar to alpha-13-mannosyl-glycoprotein beta-1 2-N-acetylglucosaminyltransferase [C.elegans]
7254	3	AA074897		EST - AA074897
18684	3	F04262	Hs.22137	ESTs
40997	3	N77904	Hs.44380	ESTs
14971	3	U10493	Hs.438	Human Mox1 protein (MOX1) mRNA complete cds
11217	3	AA180487	Hs.62440	ESTs
16782	3	AA047265	Hs.82582	Homo sapiens mRNA for osteoblast specific cysteine-rich protein complete cds
21477	3	R26094	Hs.23531	ESTs
21382	3	R16896	Hs.89615	PROTEIN KINASE C THETA TYPE
19508	3	H28966		EST - RC_H28966
30301	3	N36174	Hs.2507	5-HYDROXYTRYPTAMINE 2B RECEPTOR
21553	3	R33005	Hs.23153	ESTs Weakly similar to ETX1 {alternatively spliced} [H.sapiens]
6102	3	X70340	Hs.2023	Transforming growth factor alpha
23502	3	T70580	Hs.13759	ESTs
8333	3	AA412620	Hs.4248	ESTs
30500	3	N48329	Hs.30490	ESTs Highly similar to HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III [Caenorhabditis elegans]
21431	3	R22057	Hs.23336	ESTs
35920	3	AA412290	Hs.98124	ESTs
12065	3	AA283907	Hs.110480	Homo sapiens clone 23837 mRNA sequence
19156	3	H10068	Hs.25924	Homo sapiens clone 24466 mRNA sequence
24844	3	Z41301	Hs.23539	ESTs

FIG.-7Cc

226 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
33178	3	W68846	Hs.141719	EST
2052	3	L36818	Hs.75339	Inositol polyphosphate phosphatase-like protein 1 (51C protein)
15327	3	W23474	Hs.23352	ESTs
18874	3	F10565	Hs.12345	ESTs
9039	3	C02049	Hs.106291	ESTs
37470	3	AA454935	Hs.99566	ESTs
19167	3	H10641	Hs.22928	ESTs
34888	3	AA303078	Hs.94479	Human GT334 protein (GT334) gene mRNA complete cds
30591	3	N49952	Hs.138717	ESTs
26997	3	AA398488	Hs.93090	ESTs
18647	3	F03004	Hs.27109	ESTs
17867	3	AA157291	Hs.72163	ESTs
15280	3	W07019	Hs.35088	ESTs
20465	3	N51599	Hs.14633	ESTs
11047	3	AA142849	Hs.22660	ESTs
19451	3	H23747	Hs.31697	ESTs
41621	3	R69233	Hs.101504	ESTs
2822	3	M55621	Hs.117946	N-acetylglucosaminyltransferase I
28675	3	D20188	Hs.74876	ESTs
13928	3	AA478441	Hs.11590	ESTs
29473	3	H83694	Hs.40478	ESTs
25829	3	AA151621	Hs.110964	ESTs
28532	3	C20680	Hs.68513	EST
32376	3	R91391	Hs.64391	ESTs
12064	3	AA283848	Hs.11367	ESTs Weakly similar to KIAA0009 [H.sapiens]
15547	3	W32012	Hs.29353	ESTs

FIG..7Cd

227 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
40284	3	H95073	Hs.108734	ESTs Highly similar to HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION [Saccharomyces cerevisiae]
22861	3	R99595	Hs.36152	ESTs
15525	3	W28763	Hs.16349	Homo sapiens KIAA0431 mRNA partial cds
17968	3	AA167496	Hs.72695	EST
3836	3	U12707	Hs.2157	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)
4528	3	U48251	Hs.75871	Homo sapiens protein kinase C-binding protein RACK7 mRNA partial cds
29784	3	N20468	Hs.42849	ESTs Weakly similar to line-1 protein ORF2 [H.sapiens]
7892	3	AA262100		EST - AA262100
15279	3	W05746	Hs.133302	ESTs
42064	3	T63364	Hs.9225	ESTs Highly similar to FIBRINOGEN-LIKE PROTEIN A PRECURSOR [Parastichopus parvimensis]
17943	3	AA165117	Hs.20509	ESTs
4596	3	U50743	Hs.19520	Sodium/potassium ATPase gamma subunit
16421	3	AA022541	Hs.61146	ESTs
4914	3	U67611		EST - U67611
38171	3	AA487301	Hs.105713	EST
20168	3	N24106	Hs.2799	Cartilage linking protein 1
18791	3	F09892	Hs.12575	ESTs
24281	3	W79773	Hs.16511	ESTs
13996	3	AA480907	Hs.15769	ESTs
20583	3	N57797	Hs.34421	ESTs
37181	3	AA448158	Hs.99152	EST
21450	3	R23146	Hs.23466	ESTs
19634	3	H44866	Hs.31597	ESTs

FIG. 7Ce

228 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
10163	3	R54534	Hs.7898	Homo sapiens clone 23938 mRNA sequence
7059	3	Z96810		EST - Z96810
25762	3	AA136066	Hs.91797	Retinoblastoma-binding protein 1{alternative products}
27426	3	AA428900	Hs.92897	ESTs
29023	3	F09302		EST - RC_F09302
10989	3	AA132366	Hs.8023	Homo sapiens mRNA for SPOP
6587	3	X97748		EST - X97748
8722	3	AA481309	Hs.30204	ESTs
21476	3	R26065	Hs.23523	ESTs
14096	3	AA487558	Hs.8135	ESTs
35392	3	AA399562	Hs.97566	ESTs
28608	3	C21509	Hs.112774	ESTs
13350	3	AA449297	Hs.8944	ESTs Weakly similar to type 1 procollagen C-proteinase enhancer protein precursor [H.sapiens]
41202	3	R12808	Hs.113619	ESTs
15612	3	W51955	Hs.73372	ESTs
33930	3	AA169539	Hs.95870	ESTs
34215	3	AA233855	Hs.104252	UTROPHIN
19208	3	H11734	Hs.110454	ESTs Weakly similar to coded for by C. elegans cDNA cm10e3 [C.elegans]
24047	3	W15386	Hs.26750	ESTs
14852	3	T52099	Hs.100383	ESTs Highly similar to C-1-TETRAHYDROFOLATE SYNTHASE CYTOPLASMIC [Rattus norvegicus]
27815	3	AA455370	Hs.59729	ESTs
22610	3	R81173	Hs.11482	ESTs Highly similar to F11 antigen [H.sapiens]
37510	3	AA455896	Hs.2699	Glypican 1

FIG.-7Cf

229 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
37825	3	AA470073	Hs.104836	ESTs
13321	3	AA448238	Hs.16714	ESTs
25999	3	AA235375	Hs.87421	EST
9738	3	M13150	Hs.99900	MAS1 oncogene
16248	3	AA013125	Hs.40871	ESTs
27582	3	AA442856	Hs.61979	ESTs Moderately similar to THREONYL-TRNA SYNTHETASE CYTOPLASMIC [H.sapiens]
16546	3	AA029452	Hs.95162	ESTs
16981	3	AA064859		EST - RC_AA064859
22128	3	R51021	Hs.23161	Homo sapiens retinoic acid hydroxylase mRNA complete cds
23312	3	T54617		EST - RC_T54617
18783	3	F09741	Hs.124205	ESTs
10308	3	R86920	Hs.127585	ESTs
22518	3	R71892	Hs.25996	ESTs Highly similar to 40S RIBOSOMAL PROTEIN S27A [Homo sapiens Cavia porcellus]
8255	3	AA400226	Hs.25024	ESTs Weakly similar to estrogen-responsive finger protein efp [H.sapiens]
16361	3	AA019218	Hs.40550	ESTs Moderately similar to proto-cadherin 3 [R.norvegicus]
5453	3	X02910	Hs.2037	Tumor necrosis factor
22509	3	R71393	Hs.29190	ESTs
20065	3	H98657	Hs.27291	ESTs
31091	3	N63076	Hs.138746	EST
39050	3	AA610112	Hs.124849	ESTs
2493	3	M22919	Hs.77385	MYOSIN LIGHT CHAIN ALKALI SMOOTH-MUSCLE ISOFORM
30159	3	N32623	Hs.44069	ESTs
28913	3	F01560	Hs.22583	ESTs Highly similar to co-repressor protein [M.musculus]

FIG.-7Ca

230 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
12257	3	AA350030	Hs.4221	ESTs
359	3	D26350	Hs.75119	Human mRNA for type 2 inositol 145-trisphosphate receptor complete cds
23587	3	T81358	Hs.14906	ESTs
14323	3	AA598575	Hs.12851	ESTs
27231	3	AA416936	Hs.7491	Homo sapiens methionine synthase reductase (MTRR) mRNA complete cds
34914	3	AA338729	Hs.133096	ESTs
21233	3	R08359	Hs.19308	ESTs
23660	3	T86475	Hs.16193	ESTs
14236	3	AA496891	Hs.5011	ESTs Weakly similar to The ha1237 gene product is related to S.pombe rad21 gene product. [H.sapiens]
17617	3	AA131394	Hs.44672	ESTs Weakly similar to The KIAA0147 gene product is related to adenyl cyclase. [H.sapiens]
24594	3	Z38804	Hs.22555	ESTs Highly similar to OPIOID BINDING PROTEIN/CELL ADHESION MOLECULE PRECURSOR [Bos taurus]
7426	3	AA095885	Hs.111818	Homo sapiens heat shock factor binding protein 1 HSBP1 mRNA complete cds
34871	3	AA300151	Hs.125146	ESTs
17962	3	AA167051	Hs.83525	Human brain mRNA homologous to 3'UTR of human CD24 gene partial sequence
24337	3	W86007	Hs.8876	ESTs
22589	3	R79580	Hs.29874	ESTs
24554	3	Z38522	Hs.27082	EST
22348	3	R61750	Hs.6136	ESTs
30217	3	N34288	Hs.44554	EST

FIG.-7Ch

231 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
10210	3	R67468	Hs.131828	ESTs
22156	3	R52145	Hs.25894	ESTs
16404	3	AA021284	Hs.60554	ESTs Moderately similar to sodium-calcium exchanger form 3 [R.norvegicus]
29310	3	H66642	Hs.88729	ESTs
15956	3	Z21217	Hs.77695	Human mRNA for KIAA0008 gene complete cds
9758	3	M26393	Hs.127610	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
20917	3	N72295	Hs.18004	ESTs
4847	3	U64573		EST - U64573
22964	3	T10362	Hs.57958	ESTs
9806	2	M79462	Hs.89633	Probable transcription factor PML {alternative products}
29807	2	N21031	Hs.42930	ESTs
39646	2	H02255	Hs.7268	Homo sapiens clone 23872 mRNA sequence
22733	2	R92181	Hs.34558	EST
23233	2	T41177	Hs.8410	Homo sapiens retinoic acid-inducible endogenous retroviral DNA
18549	2	F01360	Hs.6092	ESTs Highly similar to HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III [Caenorhabditis elegans]
31892	2	N91968	Hs.39635	ESTs
18861	2	F10452	Hs.12254	ESTs
24553	2	Z38521	Hs.9428	ESTs
19289	2	H16568	Hs.23748	ESTs
14185	2	AA490911	Hs.22393	Homo sapiens drp1 mRNA complete cds
30723	2	N51935	Hs.47374	EST
34031	2	AA192614	Hs.83577	Human LIM protein MLP mRNA complete cds
18434	2	AA232206	Hs.50743	ESTs
14647	2	D20378	Hs.30731	EST

FIG.-7Ci

232 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
41048	2	N92734	Hs.115985	ESTs
38157	2	AA486858	Hs.105702	EST
33299	2	W73790	Hs.73803	IMMUNOGLOBULIN-RELATED 14.1 PROTEIN PRECURSOR
16616	2	AA035446	Hs.61783	ESTs
3276	2	M93718	Hs.76983	Nitric oxide synthase 3 (endothelial cell)
33022	2	W46976	Hs.94667	EST
31704	2	N75055	Hs.14632	ESTs
38713	2	AA608577	Hs.112575	ESTs
20396	2	N48293	Hs.12296	ESTs
10310	2	R87373	Hs.75429	ESTs
22388	2	R63695	Hs.1432	Protein Kinase C substrate 80K-H
15936	2	Z11737	Hs.2664	Flavin-containing monooxygenase 4
23667	2	T86826	Hs.142528	ESTs
30903	2	N57730	Hs.48058	EST
20938	2	N73988	Hs.37477	ESTs Weakly similar to No definition line found [C.elegans]
5935	2	X62466	Hs.108338	CDW52 antigen (CAMPATH-1 antigen)
19304	2	H16976	Hs.7973	ESTs
8804	2	AB000463	Hs.16227	Homo sapiens mRNA for SH3 binding protein complete cds clone:RE:S4-23A
41485	2	R49689	Hs.5260	ESTs Weakly similar to C06G8.3 [C.elegans]
24685	2	Z39406	Hs.11797	ESTs Moderately similar to retinoid X receptor interacting protein [M.musculus]
25403	2	AA063316		EST - RC_AA063316
35773	2	AA406219	Hs.104747	ESTs
27965	2	AA464267	Hs.24912	Homo sapiens bicaudal-D (BICD) mRNA complete cds
16911	2	AA058659	Hs.60669	ESTs

FIG. 7Cj

233 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
42315	2	T97353		EST - RC_T97353
40632	2	N45221		EST - RC_N45221
15722	2	W79046	Hs.15250	Homo sapiens DBI-related protein mRNA complete cds
14842	2	T47519		EST - T47519
36088	2	AA417344	Hs.98220	ESTs Moderately similar to located at OATL1 [H.sapiens]
15527	2	W28798	Hs.63260	Phosphodiesterase 6A cGMP-specific rod alpha
10302	2	R84933	Hs.133217	ESTs
21243	2	R08773	Hs.20231	ESTs
7759	2	AA234687	Hs.64147	ESTs Weakly similar to F59C6.4 [C.elegans]
31672	2	N74336	Hs.91681	ESTs
26799	2	AA284722	Hs.89121	ESTs
25857	2	AA156504	Hs.95875	EST
16695	2	AA043115	Hs.9452	ESTs Weakly similar to ORF YDL077c [S.cerevisiae]
964	2	HG1804-		EST - HG1804-HT1829
12439	2	AA401452	Hs.32060	ESTs
19599	2	H41235	Hs.109968	ESTs
24223	2	W70158	Hs.29696	ESTs
21052	2	N93764	Hs.10175	ESTs Weakly similar to hypothetical protein [H.sapiens]
17463	2	AA121338		EST - RC_AA121338
28949	2	F03032	Hs.65826	ESTs Weakly similar to reverse transcriptase homolog [H.sapiens]
34140	2	AA215637	Hs.104186	ESTs
7465	2	AA120886		EST - AA120886
17376	2	AA102425		EST - RC_AA102425
5130	2	U79288	Hs.85053	Homo sapiens clone 24440 mRNA sequence
30041	2	N27628	Hs.132744	Homo sapiens clone 24525 mRNA sequence
19684	2	H48488	Hs.143798	ESTs

FIG.-7Ck

234 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
8166	2	AA359093		EST - AA359093
19202	2	H11509	Hs.22482	ESTs
20439	2	N50785	Hs.13269	ESTs
10431	2	AA011310	Hs.3757	ESTs
29707	2	H98244	Hs.42519	ESTs
39868	2	H37909	Hs.107680	ESTs
8988	2	C00185	Hs.10444	ESTs
41350	2	R40442	Hs.75652	Glutathione S-transferase M5
13121	2	AA436156	Hs.110837	ESTs
15747	2	W88550	Hs.132188	ESTs
18674	2	F03989	Hs.18995	ESTs Weakly similar to KIAA0412 [H.sapiens]
914	2	HG1019-		EST - HG1019-HT1019
23804	2	T91086		EST - RC_T91086
26556	2	AA279089	Hs.88550	ESTs
8567	2	AA453381	Hs.104900	ESTs
30457	2	N47686	Hs.64607	Human RACH1 (RACH1) mRNA complete cds
21975	2	R45441	Hs.23710	ESTs
17452	2	AA120766	Hs.70724	ESTs
31958	2	N93495	Hs.54960	ESTs
31495	2	N69850	Hs.49759	ESTs
32490	2	T16389	Hs.81248	Human RNA-binding protein CUG-BP/hNab50 (NAB50) mRNA complete cds
39174	2	AA621067	Hs.112944	ESTs
21572	2	R34073	Hs.69740	Zinc finger protein 136 (clone pHZ-20)
15914	2	Y09846	Hs.81972	V-ski avian sarcoma viral oncogene homolog
12014	2	AA281769	Hs.7214	Human Hpast (HPAST) mRNA complete cds

FIG.-7C1

235 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
39777	2	H18412	Hs.75253	Human clone ID 193225 NAD (H)-specific isocitrate dehydrogenase gamma subunit mRNA alternatively spliced partial cds
9484	2	H50178	Hs.108081	ESTs Highly similar to PROTEIN PHOSPHATASE PP2A 55 KD REGULATORY SUBUNIT NEURONAL ISOFORM [Oryctolagus cuniculus]
19147	2	H09751	Hs.117619	ESTs
36276	2	AA424179	Hs.124027	ESTs
16475	2	AA025903	Hs.57911	ESTs
21304	2	R11208	Hs.20755	ESTs
11199	2	AA176446	Hs.10024	ESTs
18093	2	AA187955	Hs.85564	ESTs
19190	2	H11274	Hs.31040	EST
15710	2	W76399		EST - W76399
18707	2	F04627	Hs.23540	ESTs
6477	2	X91504	Hs.64904	Transcription factor COUP 2 (a.k.a. ARP1)
20823	2	N68869	Hs.15119	ESTs
16336	2	AA018601	Hs.75649	EXTRACELLULAR SIGNAL-REGULATED KINASE 3
19680	2	H48457	Hs.35104	ESTs
24833	2	Z41087	Hs.19066	ESTs
24058	2	W23709	Hs.109047	ESTs
26180	2	AA251230	Hs.112272	ESTs
37177	2	AA447988	Hs.7765	ESTs
14047	2	AA482597	Hs.26054	ESTs
10770	2	AA058683	Hs.22552	ESTs
41994	2	T47601	Hs.138805	ESTs

FIG.-7Cm

236 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
19217	2	H12243		EST - RC_H12243
36532	2	AA429889	Hs.68882	Acrosin
23378	2	T60072	Hs.10688	ESTs
1450	2	J03071	Hs.115352	Growth hormone 1
8007	2	AA293072	Hs.97283	ESTs Moderately similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]
17266	2	AA084723		EST - RC_AA084723
24819	2	Z40923	Hs.24812	ESTs
6532	2	X95325	Hs.89491	DNA-BINDING PROTEIN A
26850	2	AA287651	Hs.86641	ESTs
34175	2	AA227523	Hs.108788	ESTs
34620	2	AA282169		EST - RC_AA282169
27085	2	AA402495	Hs.77978	ESTs
20173	2	N24730	Hs.15420	ESTs
17574	2	AA129060		EST - RC_AA129060
22330	2	R60920	Hs.26419	Homo sapiens clone 24510 mRNA sequence
30070	2	N29696	Hs.44076	EST
20487	2	N52322	Hs.19978	ESTs
724	2	D83703	Hs.30729	Peroxisomal biogenesis factor 6
4132	2	U27655	Hs.82294	Human FGP3 mRNA complete cds
8557	2	AA452705	Hs.23954	ESTs Weakly similar to D2045.9 [C.elegans]
33659	2	W95626	Hs.59718	EST
13375	2	AA449716	Hs.5723	ESTs
30891	2	N57007	Hs.94074	EST
13988	2	AA480045	Hs.7934	ESTs
22306	2	R59906	Hs.100530	ESTs

FIG.-7Cn

237 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
23167	2	T33164	Hs.12840	Homo sapiens germline mRNA sequence
20873	2	N70134	Hs.31476	ESTs
7231	2	AA059327	Hs.6580	Homo sapiens clone 23718 mRNA sequence
24582	2	Z38752	Hs.26330	ESTs
11320	2	AA213667	Hs.22222	ESTs
16388	2	AA020781	Hs.60847	ESTs
24608	2	Z38888	Hs.25046	ESTs
7809	2	AA248085	Hs.12469	Homo sapiens clone 23930 mRNA sequence
13163	2	AA437225	Hs.22410	ESTs
20549	2	N54991	Hs.37991	ESTs Weakly similar to transposon LRE2.reverse transcriptase homolog [H.sapiens]
1139	2	HG3227-		EST - HG3227-HT3404
35572	2	AA401489		EST - RC_AA401489
6964	2	Z49105	Hs.137591	H.sapiens HD21 mRNA
27704	2	AA449704	Hs.77637	Homeo box A4
33196	2	W69725	Hs.10711	ESTs
30963	2	N59373	Hs.26812	ESTs
13886	2	AA476937	Hs.24441	ESTs
16164	2	AA007509	Hs.75395	Human mRNA for TPRD complete cds
18083	2	AA181926	Hs.70954	Homo sapiens mRNA for hoxA7 protein
20107	2	N21207	Hs.129942	ESTs Moderately similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]
23004	2	T16556	Hs.6653	ESTs
16238	2	AA011678	Hs.40470	ESTs
18189	2	AA195042	Hs.85978	ESTs
37567	2	AA457377		EST - RC_AA457377

FIG.-7Co

238 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
2174	2	L42611	Hs.111758	KERATIN TYPE II CYTOSKELETAL 6D
38958	2	AA609707	Hs.112751	ESTs
37919	2	AA478162	Hs.104965	ESTs
28905	2	D81123	Hs.57475	ESTs
33315	2	W74418	Hs.55410	ESTs
7421	2	AA095600	EST - AA095600	EST - AA095600
3745	2	U09117	Hs.80776	Human phospholipase c delta 1 mRNA complete cds
19545	2	H37834	Hs.32699	ESTs
21204	2	R07632	Hs.17949	ESTs
8416	2	AA428531	EST - AA428531	EST - AA428531
17569	2	AA128926	EST - RC_AA128926	EST - RC_AA128926
19572	2	H39195	Hs.22223	ESTs
22760	2	R93714	Hs.33833	ESTs Highly similar to ALPHA-2-MACROGLOBULIN PRECURSOR [Homo sapiens]
19354	2	H18829	Hs.121515	ESTs
40618	2	N39565	Hs.108540	ESTs
29913	2	N23708	Hs.43429	ESTs
22571	2	R78565	Hs.138395	EST
7598	2	AA174185	Hs.3354	Homo sapiens ezrin-radixin-moesin binding phosphoprotein-50 mRNA complete cds
25385	2	AA059099	Hs.109727	ESTs
14176	2	AA490620	Hs.11809	ESTs
37400	2	AA453578	Hs.120994	ESTs Weakly similar to T20D3.5 [C.elegans]
29487	2	H85120	Hs.80881	N-ACETYLGLYCOSAMINE SYNTHASE
10197	2	R64199	Hs.50785	Homo sapiens vesicle trafficking protein sec22b mRNA complete cds

FIG.-7Cp

239 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
322	2	D21241		EST - D21241_xpt1
22224	2	R55192	Hs.25689	ESTs
19488	2	H27675	Hs.25604	ESTs
10568	2	AA029703	Hs.36574	ESTs
10872	2	AA099357	Hs.15780	ESTs Moderately similar to ATP-BINDING CASSETTE TRANSPORTER 2 [Mus musculus]
29987	2	N26172	Hs.43760	ESTs
30799	2	N53143	Hs.64001	ESTs
9638	2	L07592	Hs.106415	Human peroxisome proliferator activated receptor mRNA complete cds
21069	2	N98461	Hs.17706	ESTs
27195	2	AA411473	Hs.65311	ESTs
9241	2	D79565		EST - D79565
9218	2	D61469	Hs.56896	ESTs
22238	2	R55763	Hs.107287	ESTs
7512	2	AA136369		EST - AA136369
17438	2	AA115508	Hs.2780	Jun D proto-oncogene
24932	2	AFFX-		AFFX-HISAC07/X00351_M
28911	2	F01525	Hs.3786	Glutamate receptor metabotropic 3
10944	2	AA125969	Hs.34769	ESTs Weakly similar to F35G12.9 [C.elegans]
42324	2	T98199	Hs.142702	ESTs
34756	2	AA287665	Hs.8245	ESTs
12743	2	AA421050	Hs.24545	ESTs
21275	2	R10075	Hs.14890	ESTs
13676	2	AA459389	Hs.26350	Homo sapiens mRNA for tyrosyl sulfotransferase-2
13009	2	AA430474	Hs.16466	ESTs

FIG.-7Cq

240 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
7403	2	AA094921	Hs.79788	ESTs
11151	2	AA159961	Hs.25819	ESTs
35669	2	AA404707	Hs.54865	ESTs
17701	2	AA135941	Hs.71626	ESTs
18713	2	F04686	Hs.21782	ESTs
24144	2	W52312	Hs.30303	ESTs Highly similar to ZINC FINGER PROTEIN 45 [Homo sapiens]
30741	2	N52175	Hs.22222	ESTs
23042	2	T23433	Hs.7105	ESTs
18479	2	AA233483	Hs.87159	ESTs
8314	2	AA410355	Hs.103081	ESTs Highly similar to RIBOSOMAL PROTEIN S6 KINASE [Homo sapiens]
7990	2	AA291786	Hs.32822	ESTs Weakly similar to HYPOTHETICAL PROTEIN KIAA0168 [H.sapiens]
10388	2	AA005355		EST - RC_AA005355
9407	2	H20086		EST - H20086
42791	2	AFFX-		AFFX-HUMGAPDH/M33197_M
26302	2	AA255470	Hs.88040	ESTs
30722	1	N51924	Hs.47370	ESTs
24965	1	AFFX-		AFFX-LysX-5
38850	1	AA609262		EST - RC_AA609262
13746	1	AA461300	Hs.30643	ESTs
6893	1	Z30643	Hs.123123	H.sapiens mRNA for chloride channel (putative) 2139bp
31403	1	N68117	Hs.41119	ESTs
17830	1	AA152312	Hs.72047	ESTs
10583	1	AA033874	Hs.12035	ESTs

FIG.-7Cr

241 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
20913	1	N72116	Hs.57435	Natural resistance-associated macrophage protein 2
35607	1	AA402267	Hs.133475	ESTs Weakly similar to zinc finger protein [H.sapiens]
9920	1	N44756	Hs.141935	ESTs Weakly similar to transformation-related protein [H.sapiens]
9468	1	H46074	Hs.31562	ESTs
29469	1	H82929		EST - RC_H82929
18121	1	AA191310	Hs.89608	Protein phosphatase 2 (formerly 2A) regulatory subunit A (PR 65) beta isoform
14705	1	D59362		EST - RC_D59362
18692	1	F04444	Hs.6217	ESTs
16543	1	AA029430	Hs.61557	EST
16359	1	AA019197	Hs.40763	ESTs
40818	1	N63772	Hs.144550	Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydroge
35205	1	AA398161	Hs.97602	ESTs
7831	1	AA249175	Hs.96334	ESTs Weakly similar to GOLIATH PROTEIN [Drosophila melanogaster]
17794	1	AA150260	Hs.72062	EST
11347	1	AA224245	Hs.26612	ESTs
17919	1	AA161125	Hs.72384	EST
22184	1	R53520	Hs.102755	ESTs
14827	1	T35288	Hs.90421	ESTs
28091	1	AA481788	Hs.87593	ESTs
28815	1	D59267	Hs.56782	ESTs
17813	1	AA151480	Hs.91202	ESTs
24655	1	Z39191	Hs.27262	ESTs Weakly similar to Lph17p [S.cerevisiae]

FIG.-7Cs

242 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
15611	1	W51743	Hs.35096	ESTs
39998	1	H62865	Hs.38132	ESTs
15700	1	W73859	Hs.78061	Homo sapiens mesoderm-specific basic-helix-loop-helix protein (POD1) mRNA complete cds
22045	1	R48965	Hs.24796	EST
36770	1	AA435753		EST - RC: AA435753
9877	1	N31127	Hs.40098	ESTs
22467	1	R68284	Hs.28399	ESTs
32400	1	R97176	Hs.110783	ESTs
10802	1	AA069425	Hs.20573	ESTs
23033	1	T17353	Hs.108894	Homo sapiens clone 23918 mRNA sequence
17593	1	AA129856		EST - RC: AA129856
14867	1	T58588	Hs.100419	ESTs
20266	1	N32118	Hs.107365	ESTs Highly similar to THREONYL-TRNA SYNTHETASE CYTOPLASMIC [Homo sapiens]
14447	1	AA609045	Hs.11759	ESTs
37994	1	AA479919		EST - RC: AA479919
12892	1	AA426521	Hs.18528	Homo sapiens mRNA for NA14 protein
11970	1	AA280687	Hs.4069	ESTs
19738	1	H53059	Hs.15548	ESTs
14471	1	AA609346	Hs.20102	ESTs
14855	1	T54762	Hs.9786	ESTs
24725	1	Z39781	Hs.8004	Homo sapiens Duo mRNA complete cds
5796	1	X55019	Hs.99975	Cholinergic receptor nicotinic delta polypeptide
20259	1	N31598	Hs.12727	ESTs
18441	1	AA232508	Hs.77480	ESTs

FIG. 7Ct

243 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
18468	1	AA233177	Hs.87134	ESTs
10164	1	R54743	Hs.19400	ESTs Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisiae]
8830	1	AB002319	Hs.8663	Human rRNA for KIAA0321 gene partial cds
15287	1	W07461	Hs.121559	ESTs Highly similar to DIPHTHINE SYNTHASE [Saccharomyces cerevisiae]
16477	1	AA026031	Hs.61312	ESTs
21969	1	R45334	Hs.21175	ESTs
22340	1	R61522	Hs.26892	ESTs
12884	1	AA426259		EST - RC_AA426259
8682	1	AA477891	Hs.104476	ESTs
22594	1	R79793	Hs.29900	ESTs
19131	1	H09331	Hs.122791	ESTs
17103	1	AA074997		EST - RC_AA074997
35620	1	AA402493	Hs.10552	ESTs Highly similar to c-Jun leucine zipper interactive [M.musculus]
35401	1	AA399593	Hs.97682	EST
10901	1	AA112307	Hs.25224	ESTs
19546	1	H37901	Hs.32706	ESTs
15378	1	W26448	Hs.15071	ESTs Highly similar to VACUOLAR ATP SYNTHASE SUBUNIT D [Bos taurus]
30292	1	N35978	Hs.82364	ESTs
39087	1	AA620607	Hs.111591	ESTs
37896	1	AA477463	Hs.77039	Ribosomal protein S28
8836	1	AB002325	Hs.105917	Human rRNA for KIAA0327 protein complete cds
16150	1	AA005428	Hs.60140	ESTs

FIG._7Cu

244 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
23955	1	T97467	Hs.18065	ESTs Weakly similar to alternatively spliced product using exon 13A [H.sapiens]
37812	1	AA469939	Hs.105323	ESTs
14782	1	S72370	Hs.89890	Pyruvate carboxylase
23540	1	T79178	Hs.14463	ESTs
41552	1	R59352	Hs.101253	Human mRNA for KIAA0296 gene complete cds
21836	1	R42569	Hs.22444	EST
11467	1	AA234089	Hs.14593	ESTs
18347	1	AA219230	Hs.86815	ESTs
8215	1	AA389673	Hs.84344	ESTs Weakly similar to No definition line found [C.elegans]
15505	1	W28366	Hs.7252	Homo sapiens clone 24800 mRNA sequence
22764	1	R93802	Hs.33687	ESTs
14966	1	U07620	Hs.89661	Human MAP kinase mRNA complete cds
24213	1	W69184	Hs.23973	ESTs
8165	1	AA358888	Hs.104135	Homo sapiens mRNA for DRIM protein
32724	1	T90750	Hs.15230	ESTs Weakly similar to F25H2.2 [C.elegans]
8212	1	AA386236	Hs.96757	Homo sapiens transcription factor SUPT3H (SUPT3H) mRNA complete cds
9834	1	M92299	Hs.22554	Homeo box B5 (2.1 protein)
7229	1	AA059213	Hs.91898	ESTs
15649	1	W58725	Hs.75074	H.sapiens mRNA for MAP kinase activated protein kinase
42306	1	T96538	Hs.45090	Human K ⁺ channel beta 1a subunit mRNA alternatively spliced complete cds
9159	1	D31483	Hs.90062	Homo sapiens clone 23565 unknown mRNA partial cds
20040	1	H96712	Hs.125198	ESTs
42218	1	T86444	Hs.110095	ESTs

FIG..7Cv

245 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
15526	1	W28790	Hs.8124	ESTs
17790	1	AA150182	Hs.42262	ESTs Weakly similar to HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOME III [C.elegans]
17595	1	AA129929	Hs.71166	EST
31314	1	N66866	Hs.49278	EST
9777	1	M57888	Hs.95946	GRANZYM E H PRECURSOR
15373	1	W26376	Hs.74563	THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR
23547	1	T79448	Hs.14577	EST
12076	1	AA284362	Hs.6448	ESTs Weakly similar to No definition line found [C.elegans]
11956	1	AA279991	Hs.124691	ESTs
15391	1	W26651	Hs.15961	ESTs
9287	1	D82557	Hs.18104	ESTs
16419	1	AA022466	Hs.61141	EST
21713	1	R39930	Hs.21034	ESTs
12905	1	AA427537	Hs.32419	ESTs
30257	1	N34961	Hs.75873	H.sapiens mRNA for Zyxin
28134	1	AA487622	Hs.64095	ESTs
16380	1	AA019750	Hs.40797	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]
10553	1	AA028904	Hs.33215	ESTs
18063	1	AA180054	Hs.73677	ESTs
39820	1	H24085	Hs.25443	ESTs
7374	1	AA093378	Hs.101810	ESTs
13109	1	AA435838	Hs.7985	ESTs
19378	1	H19673	Hs.31670	ESTs
24325	1	W84733	Hs.3978	ESTs

FIG.-7Cw

246 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
22318	1	R60224	Hs.7065	ESTs
24249	1	W73069	Hs.12600	ESTs
16514	1	AA027946	Hs.44608	ESTs
21421	1	R21741	Hs.23258	EST
8397	1	AA426178	Hs.71725	ESTs Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]
8412	1	AA428090	Hs.26102	ESTs
10072	1	R14782	Hs.31931	ESTs
10349	1	AA001908	Hs.18160	ESTs
14492	1	AA609635	Hs.27497	ESTs
14930	1	T92512		EST - T92512
15861	1	X81001	Hs.141503	Small inducible cytokine A5 (RANTES)
16706	1	AA043800	Hs.62645	ESTs
16744	1	AA045643	Hs.62866	EST
16950	1	AA062980	Hs.66960	ESTs
17836	1	AA155779	Hs.29759	ESTs Weakly similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]
18834	1	F10207	Hs.13269	ESTs
19178	1	H10992	Hs.100910	EST
19767	1	H54720	Hs.36941	ESTs
21341	1	R14959	Hs.21871	EST Moderately similar to ninein [M.musculus]
21466	1	R24518	Hs.23674	EST
21602	1	R36624	Hs.135137	ESTs
21748	1	R40697	Hs.21290	EST
21860	1	R43089		EST - RC_R43089
21891	1	R43590	Hs.13290	ESTs

FIG.-7Cx

247 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
21937	1	R44508	Hs.22653	ESTs
22006	1	R46244	Hs.23110	ESTs
22054	1	R49116	Hs.25067	EST
22222	1	R55042	Hs.106645	ESTs
22292	1	R59385	Hs.141053	Homo sapiens bestrophin (VMD2) mRNA alternatively spliced product complete cds
22383	1	R63463	Hs.23282	ESTs
22446	1	R67259	Hs.25968	EST
23103	1	T23939	Hs.7344	ESTs
23872	1	T94562	Hs.17338	EST
24291	1	W80642	Hs.16951	ESTs
24640	1	Z39086	Hs.21403	ESTs
27519	1	AA435835	Hs.90695	ESTs
32067	1	R06424	Hs.64896	ESTs
32204	1	R44210	Hs.91440	EST
32692	1	T79942	Hs.90930	ESTs
33714	1	Z39430	Hs.65749	ESTs
33733	1	Z39668	Hs.65792	ESTs
33873	1	AFFX-	AFFX-DapX-3	
35434	1	AA400034	Hs.97769	EST
35950	1	AA412498	Hs.104778	ESTs
36483	1	AA428865	Hs.98563	EST
36615	1	AA431469	Hs.98737	ESTs
37329	1	AA452138	Hs.3781	Homo sapiens BAC clone RG118D07 from 7q31
37700	1	AA461090	Hs.124826	EST
38285	1	AA489840	Hs.105302	ESTs

FIG.-7Cy

248 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
38887	1	AA609422	Hs.112705	EST
38933	1	AA609606	Hs.112732	ESTs
39894	1	H42037	Hs.144150	ESTs
40244	1	H91660	Hs.30250	Homo sapiens short form transcription factor C-MAF (c-maf) mRNA complete cds
40645	1	N47952	Hs.102624	EST
40819	1	N63787	Hs.109304	ESTs
41445	1	R45611	Hs.137696	ESTs Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]
41700	1	R85829	Hs.101883	EST
41776	1	T03170	Hs.100165	EST
13254	1	AA446587	Hs.6775	ESTs Highly similar to ALANINE AMINOTRANSFERASE [Homo sapiens]
8171	1	AA362708	Hs.5009	ESTs Weakly similar to mTERF [H.sapiens]
23030	1	T17291	Hs.6995	ESTs
8406	1	AA427510	Hs.104287	ESTs
16767	1	AA046650	Hs.40342	ESTs
25010	1	AA005315	Hs.51262	ESTs
14829	1	T35529	EST - T35529	EST - T35529
34584	1	AA280934	Hs.132872	ESTs Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]
15909	1	Y07868	Hs.38842	H.sapiens mRNA for Pirin isolate 1
9922	1	N44971	Hs.107164	Spectrin beta non-erythrocytic 1
15381	1	W26496	Hs.107725	ESTs Weakly similar to LIS-1 protein [H.sapiens]
22168	1	R53024	Hs.25985	ESTs
11690	1	AA252762	Hs.31235	ESTs

FIG..7Cz

249 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
22999	1	T16510	Hs.6624	ESTs
24490	1	Z38153	Hs.26921	ESTs
19993	1	H91255	Hs.15227	ESTs
19689	1	H48825	Hs.36291	ESTs
12450	1	AA401809	Hs.19865	ESTs
24368	1	W87280	Hs.124800	ESTs
22565	1	R77631	Hs.29126	ESTs
18872	1	F10542	Hs.12292	ESTs
15358	1	W26105	Hs.8961	ESTs
24186	1	W61319	Hs.37482	ESTs Highly similar to COATOMER ZETA SUBUNIT [Bos taurus]
23863	1	T93870	Hs.17265	ESTs
23846	1	T93078	Hs.17117	EST
15143	1	U79257	Hs.86921	Human clone 23932 mRNA sequence
9711	1	L44334	Hs.10432	ESTs Weakly similar to BENOMYL/METHOTREXATE RESISTANCE PROTEIN [Candida albicans]
22544	1	R74235	Hs.80844	Homo sapiens mRNA for KIAA0573 protein partial cds
41506	1	R52088		EST - RC_R52088
39345	1	C21105	Hs.7768	Homo sapiens FGF-1 intracellular binding protein (FIBP) mRNA complete cds
22272	1	R58922	Hs.26590	ESTs
16434	1	AA024494	Hs.61199	ESTs
17255	1	AA084412		EST - RC_AA084412
22692	1	R88711	Hs.34183	ESTs
38830	1	AA609189	Hs.116415	ESTs
9179	1	D50312	Hs.102308	Human mRNA for uKATP-1 complete cds
42547	1	W73946		EST - RC_W73946

FIG.-7Da

250 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
36195	1	AA421144		EST - RC_AA421144
29355	1	H70121	Hs.79592	ESTs
34608	1	AA281765	Hs.104441	ESTs
20779	1	N67553	Hs.16917	ESTs
11081	1	AA149826	Hs.34274	ESTs
12151	1	AA291269	Hs.24642	ESTs
39935	1	H52379		EST - RC_H52379
7157	1	AA037199	Hs.9899	ESTs
17858	1	AA156596	Hs.72146	ESTs
34885	1	AA302831	Hs.57732	Homo sapiens p38beta2 MAP kinase mRNA complete cds
18445	1	AA232648	Hs.87068	ESTs
22524	1	R72597		EST - RC_R72597
19224	1	H12448	Hs.124570	ESTs Weakly similar to unknown protein [H.sapiens]
18803	1	F09988	Hs.5244	ESTs
13810	1	AA464689	Hs.23294	ESTs Weakly similar to weak similarity to HSP90 [C.elegans]
18070	1	AA180352	Hs.72733	ESTs
17937	1	AA164750	Hs.72499	ESTs
39115	1	AA620736	Hs.112893	EST
22517	1	R71892	Hs.25996	ESTs Highly similar to 40S RIBOSOMAL PROTEIN S27A [Homo sapiens Cavia porcellus]
16906	1	AA058555	Hs.63392	EST
14251	1	AA497049	Hs.32501	ESTs
23923	1	T96407	Hs.17812	ESTs
21177	1	R06569	Hs.19721	ESTs
25705	1	AA131921	Hs.71030	ESTs
19805	1	H57725	Hs.124031	ESTs

FIG._7Db

251 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
19668	1	H47656	Hs.33991	EST
36693	1	AA432389	Hs.98702	ESTs
14036	1	AA482107	Hs.5473	ESTs
20859	1	N69825	Hs.16762	ESTs
23849	1	T93113		EST - RC_T93113
18265	1	AA207122	Hs.86316	ESTs
35275	1	AA398530	Hs.97363	ESTs
10262	1	R77869	Hs.110493	ESTs
21757	1	R40789	Hs.21299	ESTs
21541	1	R31607	Hs.24420	ESTs
16873	1	AA056258	Hs.63264	EST
19646	1	H46006	Hs.31677	ESTs
23719	1	T89160	Hs.138506	ESTs
19608	1	H41581	Hs.31582	ESTs Moderately similar to HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III [Caenorhabditis elegans]
17382	1	AA102731	Hs.109072	ESTs
16864	1	AA055971	Hs.63238	ESTs
10897	1	AA111881	Hs.9192	ESTs
17028	1	AA070178		EST - RC_AA070178
19220	1	H12318	Hs.24324	ESTs
9726	1	L44574	Hs.125235	ESTs
24570	0	Z38681	Hs.27150	ESTs
22167	0	R53021	Hs.25873	ESTs
42537	0	W73417	Hs.103183	EST
18806	0	F10005	Hs.12599	ESTs
16585	0	AA033948	Hs.4236	ESTs

FIG.-7Dc

252 / 454

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
17309	0	AA086232	Hs.68717	EST Moderately similar to mariner transposase [H.sapiens]
22813	0	R97419	Hs.35718	ESTs
16429	0	AA022953	Hs.61172	EST
22013	0	R46526	Hs.25377	EST
8439	0	AA431277	Hs.32419	ESTs
22934	0	T10042	Hs.4205	ESTs
13063	0	AA432386	Hs.1191	Human mRNA for KIAA0073 gene partial cds
10122	0	R31745		EST - R31745
18195	0	AA195263	Hs.86001	EST
33249	0	W72557	Hs.57836	ESTs
16966	0	AA063378	Hs.144270	ESTs
18363	0	AA223929	Hs.86902	EST
34154	0	AA219304	Hs.74561	ALPHA-2-MACROGLOBULIN PRECURSOR
16222	0	AA011210	Hs.95044	ESTs
17174	0	AA079306		EST - RC_AA079306

FIG._7Dd

253 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
16074	>10	AA001507	ESTs	other
25047	>10	AA011031	ESTs	other
25082	>10	AA017257	ESTs	other
16490	>10	AA026418	ESTs	other
25179	>10	AA031268	H.sapiens mRNA for kinesin-2	other
25215	>10	AA035540	APOLIPOPROTEIN AI REGULATORY PROTEIN-1	other
25282	>10	AA044825	ESTs	other
16810	>10	AA053636	ESTs	other
16835	>10	AA054438	ESTs	SS,
10747	>10	AA055841	ESTs	other
10748	>10	AA055892	ESTs	other
16993	>10	AA065300	Human mRNA for KIAA0035 gene partial cds	other
17051	>10	AA070801	ESTs	TM
10840	>10	AA084104	ESTs	other
7296	>10	AA085661	ESTs	other
7325	>10	AA090842	ESTs Weakly similar to HYPOTHETICAL 36.7 KD PROTEIN C2F7.02C IN CHROMOSOME I [Schizosaccharomyces pombe]	other
17419	>10	AA113349	EST	?
17541	>10	AA127459	ESTs	other
17559	>10	AA128407	ESTs	other
25669	>10	AA128978	ESTs	?
17600	>10	AA130596	ESTs	other
10992	>10	AA132523	Homo sapiens BAC clone RG119C02 from 7p15	other
17654	>10	AA133250	ESTs	TM
17734	>10	AA137246	ESTs	other
25801	>10	AA148530	EST - RC_AA148530	TM
25806	>10	AA149007	EST	?

FIG._8Aa

254 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
11121	>10	AA156359	Human TAR DNA-binding protein-43 mRNA complete cds	?
11160	>10	AA164289	ESTs	other
25925	>10	AA164494	ESTs Weakly similar to C/CLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 [H.sapiens]	other
25934	>10	AA165355	Human clone iota unknown protein mRNA complete cds	?
17987	>10	AA169379	ESTs	other
18008	>10	AA171895	Homo sapiens clone 24749 and 24750 mRNA sequences	TM
33953	>10	AA173290	Human HOXA1 mRNA long transcript and alternatively spliced forms complete cds	other
33980	>10	AA180223	CAMP-DEPENDENT PROTEIN KINASE TYPE II-ALPHA REGULATORY CHAIN	other
34013	>10	AA190888	EST - RC_AA190888	other
34014	>10	AA191348	ESTs	other
34015	>10	AA191353	ESTs	TM
34070	>10	AA196549	ESTs	other
18260	>10	AA206801	ESTs	?
34105	>10	AA207123	ESTs	SS,
34107	>10	AA209469	ESTs	other
18330	>10	AA216722	Human mRNA for apolipoprotein E receptor 2 complete cds	TM
18362	>10	AA223912	Ribonuclease L (2'5'-oligoadenylate synthetase-dependent) inhibitor	other
18392	>10	AA227751	ESTs	SS,
34188	>10	AA228030	ESTs	TM
34197	>10	AA232315	Homo sapiens clone 23797 and 23917 mRNA partial cds	other
25948	>10	AA234365	Homo sapiens survival of motor neuron protein interacting protein 1 (SIP1) mRNA complete cds	?
25951	>10	AA234556	EST	?

FIG.-8Ab

255 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
11561	>10	AA236533	Evi-1	other
26059	>10	AA236685	ESTs	other
26100	>10	AA242835	Human mRNA for KIAA0391 gene complete cds	other
11603	>10	AA243052	ESTs Highly similar to GONADOTROPIN-RELEASING HORMONE RECEPTOR [Rattus norvegicus]	other
7785	>10	AA243375	EST - AA243375	other
34372	>10	AA251973	ESTs	?
26240	>10	AA252282	Human mRNA for KIAA0152 gene complete cds	TM
34382	>10	AA252512	ESTs	other
34391	>10	AA252703	EST - RC_AA252703	other
26274	>10	AA253011	ESTs	?
34400	>10	AA253400	ESTs	other
26291	>10	AA253422	ESTs	other
26355	>10	AA256379	ESTs	?
11813	>10	AA258158	ESTs	other
34518	>10	AA278721	ESTs	?
26545	>10	AA278979	ESTs	other
26574	>10	AA279504	ESTs	other
34554	>10	AA280016	DNA polymerase gamma	other
34561	>10	AA280298	ESTs	TM
26628	>10	AA280641	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L39 [Rattus norvegicus]	TM
11969	>10	AA280670	ESTs	SS,
34575	>10	AA280738	ESTs	TM
26677	>10	AA281636	ESTs	?
26700	>10	AA282197	EST	?
34672	>10	AA284372	ESTs	other

FIG..8Ac

256 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
34692	>10	AA285079	ESTs	other
12143	>10	AA290991	ESTs	other
8092	>10	AA316272	ESTs	TM
34904	>10	AA321746	EST	other
8111	>10	AA323787	ESTs	other
8125	>10	AA330771	Human protein-tyrosine phosphatase (HU-PP-1) mRNA partial sequence	TM
26916	>10	AA331393	ESTs	other
26926	>10	AA342402	ESTs	other
26935	>10	AA347193	ESTs Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 [Caenorhabditis elegans]	TM
35038	>10	AA350541	ESTs Moderately similar to URACIL-DNA GLYCOSYLASE 1 PRECURSOR [H.sapiens]	TM
35049	>10	AA350857	ESTs	other
35106	>10	AA371561	EST Weakly similar to putative p150 [H.sapiens]	?
35197	>10	AA398120	ESTs	other
35277	>10	AA398536	ESTs	other
35309	>10	AA398660	EST	other
35322	>10	AA398710	H. sapiens RNA for CLCN3	TM
27037	>10	AA400198	ESTs	TM
35495	>10	AA400527	ESTs	?
27046	>10	AA400670	Homo sapiens mRNA for KIAA0582 protein partial cds	other
35500	>10	AA400715	ESTs	other
12480	>10	AA403116	Homo sapiens U-snRNP-associated cyclophilin (USA-CyP) mRNA complete cds	other
35693	>10	AA405485	ESTs Weakly similar to similar to t complex testis-specific protein [C.elegans]	other

FIG..8Ad

257 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
35697	>10	AA405512	ESTs	other
35766	>10	AA406169	Homo sapiens KIAA0431 mRNA partial cds	other
35769	>10	AA406206	ESTs	other
35798	>10	AA410231	ESTs	other
35801	>10	AA410291	ESTs	other
35803	>10	AA410295	ESTs	other
35822	>10	AA411144	ESTs	TM
35874	>10	AA412024	EST	?
35958	>10	AA412550	ESTs	other
36052	>10	AA417027	EST	TM
36258	>10	AA423962	ESTs Weakly similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII [H.sapiens]	other
36288	>10	AA424502	ESTs	other
36307	>10	AA424803	EST	?
36371	>10	AA426017	ESTs	TM
36395	>10	AA426353	ESTs	other
36405	>10	AA426406	Homo sapiens mRNA for KIAA0530 protein partial cds	other
36506	>10	AA429610	ESTs	other
36571	>10	AA430726	EST - RC_AA430726	SS,
36695	>10	AA433910	ESTs	other
36739	>10	AA435610	EST - RC_AA435610	?
36753	>10	AA435686	ESTs	other
36845	>10	AA436198	ESTs	?
13136	>10	AA436560	ESTs	SS, TM
13143	>10	AA436619	ESTs	SS,
36958	>10	AA442060	ESTs	other
36962	>10	AA442082	ESTs	?

FIG. 8Ae

258 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
36981	>10	AA442845	EST	?
13237	>10	AA443971	ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	?
13242	>10	AA445994	ESTs	other
37057	>10	AA446131	ESTs	other
37068	>10	AA446312	ESTs Weakly similar to !!! ALU CLASS C WARNING ENTRY !!!! [H.sapiens]	other
37074	>10	AA446344	ESTs	SS,
37084	>10	AA446486	Homo sapiens Ran binding protein 2 (RanBP2alpha) mRNA partial cds	?
37135	>10	AA447540	EST	?
37159	>10	AA447714	EST - RC_AA447714	other
37168	>10	AA447772	ESTs	?
37246	>10	AA449311	Homo sapiens mitotic checkpoint protein kinase (BUB1) mRNA complete cds	other
37310	>10	AA451707	ESTs	other
37453	>10	AA454610	ESTs	?
37456	>10	AA454632	ESTs	TM
27787	>10	AA454660	ESTs	?
37492	>10	AA455248	EST - RC_AA455248	other
37546	>10	AA456641	ESTs	TM
37601	>10	AA458864	ESTs	other
37611	>10	AA458996	Human signaling lymphocytic activation molecule (SLAM) mRNA complete cds	other
37615	>10	AA459101	Human serine/threonine kinase mRNA partial cds	SS, TM
37653	>10	AA460017	ESTs	other

FIG._8A1

259 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
37677	>10	AA460530	Homo sapiens orphan G protein-coupled receptor HG38 mRNA complete cds	other
37777	>10	AA464860	Homo sapiens Jak2 kinase mRNA complete cds	other
8648	>10	AA465016	Homo sapiens serine protease-like protease (nest1) mRNA complete cds	?
37816	>10	AA469954	EST	?
37829	>10	AA470084	ESTs	other
28015	>10	AA477421	ESTs	other
37978	>10	AA479294	EST - RC_AA479294	other
37979	>10	AA479295	ESTs Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]	other
37983	>10	AA479348	H.sapiens mRNA for SYT	other
14054	>10	AA485223	ESTs	TM
38121	>10	AA485724	EST - RC_AA485724	other
28122	>10	AA485928	ESTs Weakly similar to LOK [M.musculus]	other
38167	>10	AA487207	EST - RC_AA487207	other
38172	>10	AA487424	EST - RC_AA487424	other
38179	>10	AA487492	Homo sapiens clone 23592 mRNA sequence	other
38182	>10	AA487501	ESTs	other
38194	>10	AA487969	ESTs	other
28141	>10	AA488432	ESTs	?
38211	>10	AA488687	ESTs	other
38235	>10	AA489030	ESTs	other
38280	>10	AA489791	EST - RC_AA489791	other
38316	>10	AA490500	Homo sapiens ribonuclease P protein subunit p20 (RPP20) mRNA complete cds	other
38330	>10	AA490882	ESTs	other

FIG. 8Ag

260 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
38456	>10	AA504343	ESTs	SS,
38460	>10	AA504462	ESTs	other
38553	>10	AA521471	ESTs	other
38580	>10	AA598545	ESTs	?
38590	>10	AA598648	Human mRNA for transcriptional activator hSNF2b complete cds	other
38601	>10	AA598738	ESTs	?
28323	>10	AA599639	ESTs	other
38828	>10	AA609177	ESTs	TM
38838	>10	AA609215	EST - RC_AA609215	?
38867	>10	AA609318	Human cbl-b mRNA complete cds	TM
38871	>10	AA609333	EST	?
38970	>10	AA609749	ESTs	other
38984	>10	AA609839	ESTs Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	?
39045	>10	AA610077	ESTs	other
39062	>10	AA620333	EST	?
39080	>10	AA620552	EST - RC_AA620552_r	?
39110	>10	AA620709	ESTs Weakly similar to HYPOTHETICAL 90.8 KD PROTEIN T05H10.7 IN CHROMOSOME II [C.elegans]	other
39176	>10	AA621091	ESTs	other
39218	>10	AA621330	ESTs	other
39221	>10	AA621346	Homo sapiens protein phosphatase with EF-hands-1 (PPEF-1) mRNA complete cds	other
39232	>10	AA621409	ESTs	other
21	>10	AB000905	H.sapiens histone H4 gene	?

FIG._8Ah

261 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
8963	>10	AFFX-HUMTFRR/M11507_M		?
33890	>10	AFFX-HUMTFRR/M11507_5		?
39302	>10	ESTs		other
39329	>10	EST		?
28644	>10	ESTs		other
218	>10	PROTEIN-TYROSINE PHOSPHATASE 2C		other
236	>10	Human mRNA for KIAA0020 gene complete cds		other
9127	>10	PHOSPHATIDYLINOSITOL		other
459	>10	Human mRNA for clathrin-like protein complete cds		TM
39405	>10	ESTs		other
39433	>10	Human thymidine kinase 2 (TK2) mRNA complete cds		other
39436	>10	Human Ca ²⁺ -dependent activator protein for secretion mRNA complete cds		TM
14708	>10	EST		?
39488	>10	ESTs		other
39504	>10	ESTs		other
765	>10	Prostaglandin E receptor 3 (subtype EP3) (alternative products)		?
787	>10	Human mRNA for KIAA0215 gene complete cds		other
789	>10	Human mRNA for KIAA0217 gene partial cds		other
39529	>10	ESTs		?
39535	>10	ESTs Moderately similar to unknown protein [H.sapiens]		TM
18676	>10	ESTs		other
18718	>10	ESTs		other

FIG. 8A

262 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
18762	>10	F09458	ESTs	other
18782	>10	F09739	ESTs	other
29080	>10	F13655	ESTs Moderately similar to !!! ALU SUBFAMILY SB1 ₂ WARNING ENTRY !!!! [H.sapiens]	other
19001	>10	H02890	ESTs	other
19164	>10	H10395	EST	?
39725	>10	H11323	ESTs	other
19203	>10	H11593	ESTs	other
19328	>10	H17808	ESTs	other
19387	>10	H20128	ESTs	?
39787	>10	H20131	ESTs	SS,
19389	>10	H20165	EST	?
39832	>10	H26279	EST - RC_H26279	other
19591	>10	H40688	ESTs	other
29229	>10	H48459	Human mRNA for KIAA0186 gene complete cds	other
19727	>10	H52702	ESTs	?
19787	>10	H56679	ESTs	other
39995	>10	H62474	EST	SS, TM
29331	>10	H68116	ESTs	TM
29344	>10	H68839	EST	?
40064	>10	H72283	Human mRNA for KIAA0265 gene partial cds	other
40083	>10	H73466	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3	other
19949	>10	H78263	ESTs	TM
40204	>10	H88296	EST - RC_H88296	other
29523	>10	H88353	ESTs Weakly similar to lin-1 protein ORF2 [H.sapiens]	?
29551	>10	H90134	ESTs	?
29645	>10	H95840	ESTs	?

FIG. 8A_j

263 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
20057	>10	H98079	ESTs	other
976	>10	HG2036-	EST - HG2036-HT2090	?
		HT2090		
1158	>10	HG3344-	EST - HG3344-HT3521	?
		HT3521		
1210	>10	HG37-HT37	EST - HG37-HT37	?
1346	>10	HG4716-	EST - HG4716-HT5158	?
		HT5158		
1349	>10	HG4747-	EST - HG4747-HT5195	?
		HT5195		
1445	>10	J03027	MHC class I protein HLA-A3	?
1570	>10	K01383	EST - K01383	?
1684	>10	L07541	Replication factor C (activator 1) 3 (38kD)	other
1852	>10	L17328	Human FEZ2 mRNA partial cds	TM
1856	>10	L18920	MELANOMA-ASSOCIATED ANTIGEN 2	?
1863	>10	L19161	TRANSLATIONAL INITIATION FACTOR 2 GAMMA SUBUNIT	other
2070	>10	L37378	Homo sapiens guanylyl cyclase (RetGC-2) mRNA complete cds	SS, TM
2123	>10	L40396	Homo sapiens (clone s2271) mRNA fragment	other
2144	>10	L41349	Homo sapiens (clone s2271) mRNA fragment	SS,
9723	>10	L44542	Phospholipase C beta 4	other
2188	>10	L47276	ESTs	other
2343	>10	M15353	EST - L47276	other
2627	>10	M29610	Eukaryotic translation initiation factor 4E	TM
2857	>10	M58597	Glycophorin E	TM
			Fucosyltransferase 4 (alpha (13) fucosyltransferase myeloid-specific)	
3021	>10	M68941	Protein tyrosine phosphatase non-receptor type 4	other
3163	>10	M84424	Cathepsin E	?

FIG..8Ak

264 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
3196	>10	M86917	Oxysterol binding protein	other
20088	>10	N20054	ESTs Weakly similar to putative p150 [H.sapiens]	?
29795	>10	N20641	ESTs Highly similar to HYPOTHETICAL MYELOID CELL LINE	other
40427	>10	N21147	PROTEIN 3 [Homo sapiens]	other
40444	>10	N22140	ESTs	other
29893	>10	N23003	ESTs Highly similar to TUEULIN GAMMA CHAIN	TM
40498	>10	N26086	[Euplotes octocarinatus]	SS,
40559	>10	N33024	ESTs	SS,
30190	>10	N33264	EST	?
30207	>10	N33920	H.sapiens mRNA for diubiquitin	other
20304	>10	N34686	Homo sapiens clone 23915 mRNA sequence	?
20307	>10	N34830	ESTs	other
30265	>10	N35115	ESTs	other
40594	>10	N35388	ESTs	other
40604	>10	N38893	Homo sapiens KIAA0428 mRNA complete cds	other
40631	>10	N45124	ESTs	other
40660	>10	N49104	NUCLEAR FACTOR RIP140	?
30610	>10	N50138	EST	other
30617	>10	N50646	ESTs	?
30631	>10	N50807	EST	?
30790	>10	N52935	EST	?
20564	>10	N55443	ESTs	TM
40760	>10	N57927	ESTs Weakly similar to ELL [M.musculus]	other
30938	>10	N58561	Cathepsin B	other
20614	>10	N59230	ESTs	SS,

FIG. 8A

265 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE: DESCRIPTOR	ORF STRUCTURAL INFO
20657	>10	N62889	ESTs	other
31136	>10	N63512	ESTs Weakly similar to MC1F1.4 [C.elegans]	TM
40827	>10	N64051	Homo sapiens Werner syndrome gene complete cds	other
31310	>10	N66831	EST	?
40876	>10	N67607	Human Rho-associated coiled-coil containing protein kinase p160ROCK mRNA complete cds	other
20791	>10	N68057	Homo sapiens telomeric repeat binding factor (TRF1) mRNA complete cds	?
40905	>10	N68738	ESTs	other
40911	>10	N69114	H.sapiens mRNA for orphan nuclear hormone receptor	other
40913	>10	N69218	ESTs	other
31484	>10	N69466	ESTs	other
31619	>10	N73449	ESTs	other
41005	>10	N79516	ESTs	TM
31818	>10	N89774	Homo sapiens mRNA for KIAA0292 gene partial cds	other
31872	>10	N91109	EST	other
41040	>10	N91948	ESTs	other
31944	>10	N93193	ESTs	other
41065	>10	N93618	ESTs	other
32034	>10	N98926	ESTs Moderately similar to DMR-N9 PROTEIN [H.sapiens]	other
41107	>10	R01634	ESTs	other
41163	>10	R08176	ESTs	other
21238	>10	R08564	Plasminogen-like protein	other
21240	>10	R08613	ESTs	other
21412	>10	R20670	ESTs	other
21519	>10	R27975	EST - RC_R27975	other
41381	>10	R42278	H.sapiens mRNA for TRE15	?

FIG. 8Am

266 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENI: DESCRIPTOR	ORF STRUCTURAL INFO
32189	>10	R43183	ESTs	TM
32195	>10	R43471	ESTs Weakly similar to ORF YOR258w [S.cerevisiae]	other
21902	>10	R43822	EST	?
21946	>10	R44707	ESTs	TM
22072	>10	R49406	ESTs	?
32240	>10	R50976	Ribonuclease L (2'5'-oligoadenylate synthetase-dependent) inhibitor	other
32258	>10	R55623	ESTs	other
22258	>10	R56432	ESTs	other
22282	>10	R59197	ESTs	other
32277	>10	R61493	Human mRNA for rod photoreceptor protein complete cds	other
22372	>10	R62831	EST	?
22400	>10	R64109	ESTs	other
41593	>10	R64129	ESTs	other
10233	>10	R71427	ESTs Highly similar to PHENYLALANYL-TRNA SYNTHETASE ALPHA CHAIN CYTOPLASMIC [Saccharomyces cerevisiae]	other
41654	>10	R76437	THROMBOXANE-A SYNTHASE	TM
22557	>10	R76722	ESTs	other
22576	>10	R79111	ESTs	other
22593	>10	R79777	EST	?
41678	>10	R80675	EST	?
41719	>10	R89260	EST - RC_R89260	other
22793	>10	R96208	ESTs	other
41752	>10	R97063	ESTs	other
3375	>10	S50223	HKR-T1	other
3406	>10	S66896	SQUAMOUS CELL CARCINOMA ANTIGEN 1	other
3522	>10	S80267	Spleen tyrosine kinase	other

FIG.-8An

267 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
41793	>10	T03887	ESTs	?
23198	>10	T40530	ESTs Weakly similar to B0035.14 [C.elegans]	other
23360	>10	T58531	ESTs	other
32635	>10	T61116	ESTs	other
42177	>10	T79786	ESTs	?
23623	>10	T84047	ESTs	?
23662	>10	T86674	ESTs	other
42242	>10	T89579	Homo sapiens E2F-related transcription factor (DP-1) mRNA complete cds	other
23759	>10	T90313	ESTs	other
23832	>10	T92018	ESTs	other
32740	>10	T92950	ESTs	other
42290	>10	T95105	ESTs	?
3598	>10	U01157	Glucagon-like peptide-1 receptor	SS, TM
3659	>10	U04313	Protease inhibitor 5 (maspin)	other
3799	>10	U10690	Human MAGE-5a antigen (MAGE5a) gene complete cds	?
3870	>10	U14518	Centromere protein A (17kD)	other
3913	>10	U16261	Human MDA-7 (mda-7) r RNA complete cds	SS,
4029	>10	U21090	Human DNA polymerase delta small subunit mRNA complete cds	other
4157	>10	U28811	Human cysteine-rich fibroblast growth factor receptor (CFR-1) mRNA complete cds	other
4178	>10	U30246	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds	TM
15006	>10	U30246	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds	TM
4193	>10	U31116	Human beta-sarcoglycan A3b mRNA complete cds	TM
4306	>10	U36798	Homo sapiens platelet cG1-PDE mRNA complete cds	TM

FIG. 8A

268 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
4362	>10	U39817	Bloom syndrome	other
4386	>10	U40622	DNA repair protein XRCC4	other
4388	>10	U40714	Human tyrosyl-tRNA synthetase mRNA complete cds	other
4455	>10	U43944	MALATE OXIDOREDUCTASE	other
4477	>10	U45880	Human IAP-like protein ILP mRNA complete cds	other
4680	>10	U55766	Human Rev interacting protein Rip-1 mRNA complete cds	TM
4702	>10	U57341	EST - U57341	other
4713	>10	U57721	Human L-kynurenine hydrolase mRNA complete cds	other
4787	>10	U61145	Human enhancer of zeste homolog 2 (EZH2) mRNA complete cds	other
4862	>10	U65437	Human homeodomain-containing protein (HANF) mRNA complete cds	?
4945	>10	U69108	Homo sapiens mRNA for TRAF5 complete cds	other
4975	>10	U71088	Human MEK5 mRNA complete cds	other
4994	>10	U72514	Human C2f mRNA complete cds	other
5002	>10	U72761	Human karyopherin beta 3 mRNA complete cds	other
5021	>10	U73524	Human putative ATP/GTP-binding protein (HEAB) mRNA complete cds	TM
5149	>10	U79716	Human reelin (RELN) mRNA complete cds	SS,
5214	>10	U83303	H.sapiens mRNA for granulocyte chemotactic protein	?
5243	>10	U85946	Human brain secretory protein hSec10p (HSEC10) mRNA complete cds	other
32789	>10	W02779	ESTs Moderately similar to kinesin-73 [D.melanogaster]	other
42354	>10	W19346	ESTs	other
42390	>10	W40150	Homo sapiens chromosome-associated polypeptide (HCAP) mRNA complete cds	other
33006	>10	W46286	ESTs Weakly similar to Zk1058.5 [C.elegans]	TM

FIG..8Ap

269 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
33020	>10	W46891	ESTs Weakly similar to polypeptide	other
33109	>10	W59961	N-acetylgalactosaminyltransferase [H.sapiens]	other
24197	>10	W67277	Human mRNA for KIAA0389 gene complete cds	other
24215	>10	W69425	ESTs	other
33301	>10	W73883	ESTs	other
33343	>10	W79834	ESTs Weakly similar to rho-kin [M.musculus]	other
33377	>10	W81219	ESTs Weakly similar to F46B6.7 [C.elegans]	other
42602	>10	W86423	ESTs	TM
33556	>10	W90705	Murine leukemia viral (bmi-1) oncogene homolog	other
33616	>10	W93726	Protease inhibitor 5 (maspin)	other
33666	>10	W95876	ESTs	TM
5510	>10	X05360	Cell division cycle 2 G1 to S and G2 to M	?
5558	>10	X07876	Wingless-type MMTV integration site 2 human homolog	SS, TM
5603	>10	X14253	Teratocarcinoma-derived growth factor 1	SS, TM
5619	>10	X14850	HISTONE H2A.X	?
5623	>10	X14975	T-CELL SURFACE GLYCOPROTEIN CD1E PRECURSOR	other
5692	>10	X17644	G1 to S phase transition 1	other
5789	>10	X54925	Matrix metalloproteinase 1 (interstitial collagenase)	SS, TM
5799	>10	X55330	Aspartylglucosaminidase	?
5802	>10	X55544	CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-1	other
5857	>10	X58377	Human mRNA for adipogenesis inhibitory factor	TM
5960	>10	X63575	ATPase Ca++ transporting plasma membrane 2 (NOTE: redefinition of symbol)	SS, TM
5963	>10	X63629	Cadherin 3 (P-cadherin)	?
5986	>10	X64810	Protein kinase convertase subunit kexin type 1	other
6041	>10	X67155	MITOTIC KINESIN-LIKE PROTEIN-1	

FIG. 8Aq

270 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
6095	>10	X69962	Fragile X mental retardation 1	other
6106	>10	X70683	SRY (sex determining region Y)-box 4	TM
6155	>10	X74331	DNA primase polypeptide 2A (58kD)	other
6167	>10	X74987	Ribonuclease L (2'5'-oligoadenylate synthetase-dependent) inhibitor	other
6188	>10	X76029	NEUROMEDIN U-25 PRECURSOR	TM
6315	>10	X81889	H.sapiens mRNA for p0071 protein	other
6382	>10	X85133	H.sapiens RBQ-1 mRNA	other
6384	>10	X85137	Human kinesin-like spindle protein HKSP (HKSP) mRNA complete cds	other
6438	>10	X89398	URACIL-DNA GLYCOSYLASE 1 PRECURSOR	?
6449	>10	X89986	H.sapiens mRNA for NBK apoptotic inducer protein	TM
6478	>10	X91648	H.sapiens mRNA for pur alpha extended 3'untranslated region	SS, TM
6479	>10	X91653	EST - X91653	?
6494	>10	X92689	H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylglucosaminyl transferase	TM
6713	>10	Y08564	EST - Y08564	?
6790	>10	Y12394	Homo sapiens importin-alpha homolog (SRP1gamma) mRNA complete cds	other
24915	>10	YEL003w/	EST - YEL003w/	?
42773	>10	YEL019c/	EST - YEL019c/MMS21	?
		MMS21		
24545	>10	Z38462	ESTs	other
33713	>10	Z39427	ESTs	other
33791	>10	Z40883	ESTs	other
42766	>10	Z99394	ESTs Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]	other

FIG. 8A

271 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
21558	>10	R33112	Human AF-6 mRNA complete cds	other
26718	>10	AA282576	ESTs	?
40113	9.9955090946	H78003	ESTs	?
10801	9.9879448276	AA069285	ESTs Weakly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 [C.elegans]	other
37491	9.9513600842	AA455239	ESTs Highly similar to CHROMOSOME CONDENSATION PROTEIN DPY-27 [Caenorhabditis elegans]	other
23900	9.9272347693	T95789	ESTs	other
254	9.9198395324	D14657	Human mRNA for KIAA0101 gene complete cds	other
6885	9.8970927914	Z29331	Ubiquitin-conjugating enzyme E2H (homologous to yeast UBC8)	other
29693	9.8850766398	H97819	ESTs	SS,
26482	9.8765189024	AA262491	ESTs	other
23123	9.8699502035	T25306	EST	?
26525	9.8160399123	AA278392	ESTs	other
13110	9.7643356605	AA435840	Homo sapiens mRNA for high mobility group protein HMG2a	other
34863	9.7087597628	AA299784	EST	other
39432	9.7034550083	D51691	Phosphoribosylglycinamide-formyltransferase	?
			phosphoribosylglycinamide synthetase	
			phosphoribosylaminoimidazole synthetase	
31312	9.6513325388	N66845	ESTs Weakly similar to !!! ALU CLASS B WARNING ENTRY !!! [H.sapiens]	?
21112	9.6358446349	R01179	ESTs	?
31572	9.6254820695	N71294	ESTs	other
17903	9.6221229759	AA160259	EST	?
20747	9.6094813734	N66842	ESTs	other
4676	9.589223908	U55206	Homo sapiens human gamma-glutamyl hydrolase (hGH) mRNA complete cds	TM

FIG.-8As

272 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
34363	9.5627081023	AA251587	Homo sapiens mRNA for KIAA0530 protein partial cds	other
39094	9.540768988	AA620636	ESTs	other
3888	9.5372000133	U15128	Human beta-12-N-acetylglucosaminyltransferase II (MGAT2) gene complete cds	?
39386	9.506250529	D12184	ESTs	TM
7674	9.4458059039	AA203742	ESTs	other
4192	9.4329744134	U31099	Human DP prostanoid receptor (PTGDR) mRNA partial cds	TM
4507	9.422674945	U47050	Human putative calcium influx channel (htrp3) mRNA complete cds	TM
35606	9.412026255	AA402227	ESTs Moderately similar to N-tropomodulin [R.norvegicus]	other
4970	9.3649551013	U70862	Human nuclear factor I-B2 (NFIB2) mRNA complete cds	?
19829	9.3432151573	H58813	EST	?
14837	9.2878584141	T40145	ESTs	TM
17336	9.2822148675	AA099585	ESTs	other
40541	9.2532836505	N30160	ESTs	other
29496	9.2487643833	H85434	EST	?
29943	9.1797074262	N24786	ESTs Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	TM
17997	9.1629681314	AA169633	EST	other
21320	9.1243463318	R11673	ESTs	other
13883	9.1178796537	AA476917	ESTs Weakly similar to No definition line found [C.elegans]	other
30539	9.0886887776	N49072	ESTs	other
32778	9.0877919549	W02063	EST	?
26380	9.0809559378	AA257012	EST	?
15888	9.0595893607	X95632	Human Abl interactor 2 (Abl-2) mRNA complete cds	other
40812	9.0012874244	N63419	ESTs	other
903	8.9640387908	D90070	ATL-derived PMA-responsive (APR) peptide	other

FIG._8At

273 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE: DESCRIPTOR	ORF STRUCTURAL INFO
22674	8.9515777733	R87160	ESTs	TM
40807	8.9510132281	N62995	TRANSCRIPTION INITIATION FACTOR IIF BETA SUBUNIT	other
15244	8.9195644974	W00904	ESTs	TM
32296	8.8658776567	R67075	Zinc finger protein X-linked	other
18269	8.8575656769	AA209467	ESTs	other
19662	8.8507626284	H47391	ESTs	other
41607	8.833925517	R67868	CLEAVAGE SIGNAL-1 PFOTEIN	other
2548	8.8299864699	M25897	Platelet factor 4	TM
7736	8.8279341243	AA232121	Human tyrosyl-tRNA synthetase mRNA complete cds	other
34490	8.7844537272	AA262354	ESTs	other
38658	8.7669313482	AA599477	ESTs	other
7528	8.765157554	AA149543	ESTs	other
39939	8.7555031142	H53454	EST - RC_H53454	other
25111	8.7232692309	AA020787	ESTs	other
21655	8.716167279	R38239	EST	other
39663	8.665982852	H04756	ESTs Highly similar to NADH-UBIQUINONE OXIDO REDUCTASE B17 SUBUNIT [Bos taurus]	?
1042	8.652112324	HG2510-HT2606	EST - HG2510-HT2606	?
32330	8.6361115426	HT2606	ESTs	other
25382	8.6239456487	R77776	ESTs	other
27074	8.5900813076	AA059007	ESTs Weakly similar to C36B1.3 [C.elegans]	SS,
3955	8.5298909183	AA401475	MHC class II transactivator	other
4959	8.52646827	U18259	Human transportin (TRN) mRNA complete cds	other
2315	8.5259185808	U70322	EST - M14123_xpt1	?
37253	8.4896914632	M14123	ESTs	other
39624	8.471316877	AA449357	ESTs	?
		F10836	ESTs	

FIG.-8Au

274 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
23213	8.4569920887	T40891	ESTs	?
2798	8.455596435	M54995	Connective tissue activation peptide III	TM
41154	8.4413390141	R07499	ESTs	?
32479	8.4093689549	T16282	WEE1-LIKE PROTEIN KINASE	other
41251	8.3587565415	R28279	Human clone 23548 mRNA sequence	other
19081	8.3583603183	H06701	ESTs Weakly similar to RHOMBOTIN-1 [H.sapiens]	other
21098	8.3105927559	R00545	ESTs	other
14723	8.3061679053	D59894	ESTs	other
37154	8.2994822341	AA447666	Human CENP-F kinetochore protein mRNA complete cds	other
8068	8.2835586361	AA313387	ESTs Highly similar to HYPOTHETICAL 84.7 KD PROTEIN ZK1098.1 IN CHROMOSOME III [Caenorhabditis elegans]	other
7485	8.281679348	AA129547	ESTs	other
16501	8.2517969834	AA026969	ESTs	other
34527	8.2419163754	AA279091	ESTs	other
6700	8.1948675662	Y07867	H.sapiens mRNA for Pirin isolate 1	other
2852	8.1928816537	M58460	Human 75-kD autoantigen: (PM-Sc1) mRNA complete cds	other
11188	8.1862492468	AA172372	ESTs	TM
42293	8.183311064	T95333	ESTs Weakly similar to coded for by C. elegans cDNA yk110g8.3 [C.elegans]	TM
5443	8.1763317544	X02530	Interferon (gamma)-induced cell line protein 10 from	SS, TM
40937	8.1534810594	N70607	ESTs	?
23371	8.1499496068	T59505	EST - RC_T59505	?
26272	8.1339974519	AA252981	ESTs Weakly similar to K07C11.10 gene product [C.elegans]	other
17306	8.1332403762	AA086201	ESTs	other
18497	8.1192326373	AA233795	ESTs	other
235	8.0944363901	D13644	Human mRNA for KIAA0019 gene complete cds	other
24525	8.0860187097	Z38347	ESTs	TM

FIG..8Av

275 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
7826	8.0750029554	AA248884	EST - AA248884	TM
32142	8.0739258775	R38715	Homo sapiens clone 24540 mRNA sequence	other
39067	8.0557768803	AA620405	ESTs	other
6235	8.0448957236	X78416	Casein alpha S1	TM
29517	8.0017588725	H88261	ESTs	other
28570	7.9852455973	C21104	Homo sapiens STAT-induced STAT inhibitor-2 mRNA complete cds	other
39344	7.9162087762	C21034	ESTs Moderately similar to initiation factor eIF-2B gamma subunit [R.norvegicus]	other
18951	7.9002189759	H00580	ESTs	other
18953	7.8709160227	H00615	ESTs	other
18376	7.8564099916	AA226925	ESTs	other
19830	7.847878447	H58911	ESTs	other
36023	7.840835828	AA416881	ESTs	other
13347	7.8344414518	AA449238	ESTs	other
36614	7.8284591351	AA431466	ESTs	other
2192	7.8254072032	L48211	ESTs	?
33016	7.8006574068	W46577	Homo Sapiens angiotensin II receptor gene complete cds	other
17215	7.7941954038	AA083044	H.sapiens mRNA for ESM-1 protein	other
34894	7.7659738105	AA311881	ESTs	?
40614	7.695001222	N39257	EST	other
36295	7.6834749899	AA424534	ESTs	other
19564	7.6744302788	H38833	ESTs	TM
16914	7.6686405336	AA058665	ESTs	SS,
35967	7.6378079107	AA412694	Human splicing factor SRp55-2 (SRp55) mRNA complete cds	other
21672	7.6364823402	R38635	ESTs	other
19918	7.6303275831	H69787	ESTs	?

FIG._8Aw

276 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE: DESCRIPTOR	ORF STRUCTURAL INFO
10511	7.6297744492	AA024482	ESTs Highly similar to KERATIN TYPE I CYTOSKELETAL 14 [Homo sapiens]	other
17721	7.6057911016	AA136590	ESTs	?
42302	7.6031859697	T96130	EST	SS,
26134	7.6000619383	AA243763	ESTs	other
18766	7.5621799008	F09497	ESTs	other
34492	7.501590494	AA262439	ATL-derived PMA-responsive (APR) peptide	other
270	7.4512152125	D14822	EST - D14822	other
35975	7.4177746986	AA412738	ESTs	other
29842	7.4095809671	N21688	ESTs	?
35389	7.3913043319	AA399555	ESTs	other
19979	7.3868157166	H88477	ESTs	other
5793	7.3865864025	X54942	CDC28 protein kinase 2	other
19978	7.380969715	H87770	EST - RC_H87770	other
1280	7.3691089318	HG4126-HT4396	EST - HG4126-HT4396	?
31571	7.3676263454	HT4396	ESTs	other
23765	7.3541191734	N71250	ESTs Weakly similar to KIAA0376 [H.sapiens]	?
35123	7.3397933455	T90443	EST	?
38252	7.3341119467	AA380927	EST	other
38216	7.3282021037	AA489247	ESTs	other
29418	7.2489407005	AA488861	ESTs	?
4834	7.1980951054	H77915	EST - RC_H77915	other
42504	7.1913036522	U63541	Human mRNA expressed in HC/HCC livers and MolT-4 proliferating cells partial sequence	other
6111	7.158000198	W69803	ESTs	other
41773	7.154479618	X71125	H.sapiens mRNA for glutamine cyclotransferase	TM
		T03024	ESTs Weakly similar to ribosomal protein L7 [H.sapiens]	other

FIG.-8Ax

277 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE: DESCRIPTOR	ORF STRUCTURAL INFO
9951	7.1363626365	N71513	ESTs	other
28109	7.0941968224	AA485212	ESTs	other
988	7.0783044659	HG2160- HT2230	EST - HG2160-HT2230	?
29848	7.0610668511	N22107	ESTs	other
30628	7.0607950168	N50744	ESTs	other
22567	7.0225726353	R77771	ESTs	TM
9347	7.006323071	H03686	ESTs	TM
11696	7.0026773299	AA252894	ESTs	other
40584	7.0010096333	N34870	EST	?
193	6.9767029188	D10923	PROBABLE G PROTEIN-COUPLED RECEPTOR HM74	TM
18305	6.9740536051	AA214048	Collagen type IV alpha 4	other
6078	6.9699682397	X69141	FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE	other
26741	6.902658703	AA283198	ESTs	other
35069	6.8992865685	AA358397	EST	?
23504	6.8977135983	T71042	ESTs	other
299	6.8824513029	D16815	Homo sapiens orphan nuclear hormone receptor BD73 mRNA 3' end	other
40583	6.8689903023	N34855	ESTs	other
31428	6.8623762224	N68594	ESTs	other
6169	6.8606959727	X75091	SET PROTEIN	other
39524	6.8567355171	F01905	MALATE OXIDOREDUCTASE	other
34578	6.8430689439	AA280837	ESTs	other
38678	6.837527995	AA599920	Small inducible cytokine A5 (RANTES)	other
23936	6.8251471804	T96930	ESTs	other
9326	6.8181321394	D89377	Msh (Drosophila) homeo box homolog 2	other
19188	6.8067351968	H11255	ESTs Highly similar to ACTIN-LIKE PROTEIN [Bos taurus]	TM

FIG.-8Ay

278 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
18185	6.7882148811	AA194983	Homo sapiens mRNA for osteoclastogenesis inhibitory factor (OCIF) complete cds	other
27028	6.757529124	AA399630	ESTs Weakly similar to KIAA0371 [H.sapiens]	other
41289	6.7519531681	R37265	EST	other
34511	6.7364448798	AA278298	EST - RC_AA278298	other
1566	6.7056207716	J05614	EST - J05614	?
25675	6.6692299748	AA129757	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L22 [Rattus norvegicus]	other
5814	6.6584342828	X56088	CYTOCHROME P450 VII	SS,
13861	6.6236291607	AA470145	ESTs	other
29794	6.6026313352	N20598	ESTs	other
39333	6.5902382643	C20910	Cyclin B1	other
3770	6.5835303599	U09609	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	other
31831	6.5829933764	N89894	ESTs	?
33063	6.5808125026	W53000	Homo sapiens clone 24431 mRNA sequence	other
20326	6.5640084836	N35583	ESTs Weakly similar to PFI0ABLE E5 PROTEIN [Human papillomavirus type 58]	?
34384	6.5535703492	AA252537	ESTs	other
25599	6.5490481991	AA114091	Human (clone 8B1) Br-cadherin mRNA complete cds	other
39749	6.5369363254	H14988	ESTs	other
42596	6.5200567072	W85900	ESTs	?
39606	6.5119482185	F10243	ESTs Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]	?
14617	6.5105504748	C14983	ESTs	other
27831	6.45670814	AA456044	ESTs	?
34896	6.4496517783	AA312551	EST	?

FIG._8Az

279 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
27360	6.4434305006	AA425356	ESTs	other
20126	6.4326610424	N22015	ESTs	TM
6663	6.4324809977	Y00291	RETINOIC ACID RECEPTOR BETA-2	TM
30692	6.4196636207	N51563	ESTs	other
36472	6.4189542265	AA428633	EST	?
9578	6.3961788753	H87652	Homo sapiens bicaudal-D (BICD) mRNA complete cds	other
39670	6.3818496159	H05626	ESTs	other
22697	6.3652792447	R89218	ESTs	other
37308	6.3647804993	AA451694	EST	TM
16101	6.3517262802	AA002147	EST	?
20629	6.3486854401	N59798	ESTs	other
36100	6.3364146287	AA417740	ESTs	?
15488	6.3252590241	W28097	Homo sapiens clone 23711 unknown mRNA partial cds	other
36667	6.3131273544	AA432136	ESTs	other
30766	6.3115037924	N52627	EST - RC_N52627	?
32882	6.2745311453	W37683	ESTs	TM
18072	6.2675797205	AA180448	EST	?
18231	6.2652604863	AA199747	Human mRNA for KIAA0096 gene partial cds	other
38282	6.2514165678	AA489814	EST	?
28125	6.250317021	AA486073	ESTs	other
37464	6.2484456382	AA454747	ESTs	?
36618	6.1946328223	AA431478	ESTs	other
5082	6.1931116815	U78524	Human Gu binding protein mRNA partial cds	other
1441	6.1777287039	J02963	Integrin alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex antigen CD41B)	other
42105	6.14875944	T67710	ESTs	?
6061	6.1394863141	X68314	Glutathione peroxidase 2 gastrointestinal	SS,

FIG..8Ba

280 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
32570	6.1156028796	T30222	ESTs Weakly similar to telracycline transporter-like protein [M.musculus]	TM
32504	6.1019612076	T17063	EST	?
23335	6.0977927504	T56804	EST	?
10867	6.0970991075	AA088458	ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	other
30883	6.0911993489	N56923	EST	?
14528	6.0859008453	AA620295	ESTs	TM
29454	6.0685955036	H81308	EST	?
6798	6.0539173278	Y13153	Homo sapiens mRNA for lynurenine 3-monooxygenase	TM
21248	6.0525426545	R08871	ESTs	?
21940	6.0499964138	R44538	ESTs	?
29066	6.0455247653	F10927	Homo sapiens clone 23636 mRNA sequence	other
18774	6.0446826953	F09609	ESTs	?
36722	6.0172343991	AA435512	ESTs	SS,
18062	6.0034342969	AA179845	ESTs Moderately similar to rabkinesin-6 [M.musculus]	other
22989	5.9992817406	T16305	ESTs	other
41745	5.9905623898	R95895	ESTs	?
8787	5.9894877658	AA504307	X-LINKED HELICASE II	other
20550	5.984861795	N55013	ESTs	other
26470	5.9417764101	AA262179	ESTs	other
16574	5.9356497569	AA031926	EST	other
693	5.9169537385	D80007	Human mRNA for KIAA0135 gene partial cds	other
4093	5.914830973	U25182	Human antioxidant enzyme AOE37-2 mRNA complete cds	TM
1192	5.9086264407	HG3546-HT3744	EST - HG3546-HT3744	?
22956	5.8954735623	HT3744	ESTs	other
		T10248		

FIG._8Bb

281 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
36723	5.891606409	AA435524	EST	?
2114	5.8844986595	L40384	EST - L40384	other
26872	5.868238789	AA291137	ESTs	other
6602	5.8663883018	X98266	EST - X98266_cds2	other
42701	5.8594493433	Z38612	ESTs	other
28573	5.84591116	C21118	ESTs	other
18290	5.8189427595	AA211901	ESTs	other
732	5.8043917941	D83781	Human mRNA for KIAA0197 gene partial cds	other
5330	5.8014145611	U91327	EST - U91327	?
33503	5.7990715189	W88720	EST	?
2553	5.7797505864	M26167	Human platelet factor 4 variation 1 (PF4var1) gene complete cds	?
34705	5.7658806254	AA286907	ESTs Weakly similar to putative p150 [H.sapiens]	other
42665	5.7594091043	W93659	ESTs	other
38180	5.7539310793	AA487495	EST - RC_AA487495	other
4244	5.7476738809	U33286	Human chromosome segregation gene homolog CAS mRNA complete cds	other
32822	5.7418957453	W16834	ESTs	TM
3977	5.7245885557	U18991	Retinal pigment epithelium-specific protein (65kD)	?
24673	5.7202366155	Z39301	ESTs	TM
6928	5.7120261128	Z46629	SRY (sex-determining region Y)-box 9 (campomelic dysplasia autosomal sex-reversal)	other
38726	5.7030796258	AA608733	ESTs	?
39290	5.6892372058	C14573	Human mRNA for KIAA0029 gene partial cds	other
11405	5.6818873796	AA232231	ESTs	other
22538	5.6792006591	R73567	Homo sapiens meltrin-L precursor (ADAM12) mRNA complete cds	TM

FIG. 8Bc

282 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
40747	5.6605393208	N56872	Homo sapiens clone 22 mRNA alternative splice variant alpha-1 complete cds	TM
31596	5.6554024604	N72094	ESTs	other
6329	5.6415652518	X82279	EST - X82279	?
31578	5.6273323661	N71361	ESTs	other
33207	5.6271818482	W70051	H.sapiens mRNA for M-phase phosphoprotein mpp9	other
2545	5.6105860146	M25753	Cyclin B1	other
22580	5.5988402647	R79156	ESTs	other
33592	5.5935314518	W93127	ESTs	other
28843	5.5734698755	D60252	ESTs	other
6160	5.5689050619	X74794	CDC21 HOMOLOG	other
37987	5.561345667	AA479666	ESTs	other
42515	5.5217868611	W72116	Homo sapiens clone 23622 mRNA sequence	other
4732	5.5130668527	U58522	Human huntingtin interacting protein (HIP2) mRNA complete cds	other
3299	5.5099850678	M95623	Hydroxymethylbilane synthase	?
28320	5.473406981	AA599574	ESTs	?
746	5.471260899	D84454	Human mRNA for UDP-galactose translocator complete cds	TM
39373	5.4635804954	C21517	ESTs	other
3117	5.4398413537	M81182	Peroxisomal membrane protein 1 (70kD Zellweger syndrome)	other
21257	5.4343612441	R09196	ESTs Moderately similar to M-phase phosphoprotein 11 [H.sapiens]	other
31487	5.4318648859	N69507	ESTs	other
28954	5.4137130511	F03153	ESTs	other
38928	5.389782721	AA609595	ESTs	other
29903	5.3722320622	N23366	EST	?
30925	5.3437432315	N58295	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE - HOMOLOG [H.sapiens]	?

FIG..8Bd

283 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
19091	5.3344615669	H07864	ESTs	TM
28209	5.3138951918	AA491250	ESTs	other
9470	5.3118897984	H46617	EST - H46617	other
9435	5.3070056656	H30201	EST - H30201	?
28552	5.2954432572	C20914	ESTs	other
27411	5.2940164267	AA428137	ESTs	other
30615	5.2924125264	N50556	ESTs	other
28313	5.2657977167	AA599309	ESTs	TM
39321	5.2649035384	C20632	ESTs	?
29934	5.2531047395	N24194	ESTs	other
1094	5.2496703122	HG2846- HT2983	EST - HG2846-HT2983	?
39578	5.2481126384	F08925	ESTs	TM
11232	5.2466798424	AA186804	ESTs Weakly similar to unknown [S.cerevisiae]	other
2466	5.2426349328	M21539	Human small proline rich protein (sprl) mRNA clone 1292	other
26843	5.2387758661	AA287450	ESTs	?
40331	5.2353385567	H97562	ESTs Weakly similar to SPERMATID-SPECIFIC PROTEIN T2 [Sepia officinalis]	other
8035	5.205798365	AA305116	EST - AA305116	other
29793	5.1955425722	N20593	ESTs Weakly similar to weak similarity to procollagen alpha chain 1(V) chain [C.elegans]	other
34109	5.1481590107	AA210722	EST	?
26408	5.1432577257	AA258177	ESTs Weakly similar to R(0)SA26AS [M.musculus]	other
19263	5.1427029807	H15054	ESTs	TM
24596	5.1416089352	Z38810	ESTs	other
28589	5.1365059753	C21245	H.sapiens mRNA for apoptosis specific protein	other
5684	5.1121931412	X17098	Pregnancy-specific beta-1 glycoprotein 6	other

FIG..8Be

284 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
30710	5.1079347344	N51761	EST	?
35765	5.0973514948	AA406167	EST	?
26360	5.0863127861	AA256460	ESTs	?
2351	5.0849612092	M15796	Proliferating cell nuclear antigen	?
30262	5.0836877534	N35065	Homo sapiens clone 24739 mRNA sequence	other
41792	5.0737512465	T03886	ESTs	?
36710	5.0703839864	AA434411	ESTs	other
39090	5.0546885407	AA620628	ESTs	TM
42185	5.0539926381	T79951	ESTs	?
18745	5.0460321557	F09134	ESTs	other
35746	5.0396841996	AA406063	ESTs	other
35356	5.0354809581	AA399053	EST	?
36769	5.0312706878	AA435750	EST	?
36900	5.0279911548	AA436866	H.sapiens mRNA for M-phase phosphoprotein mpp9	other
27595	5.0244757301	AA443328	ESTs	TM
16290	5.0056611904	AA016145	ESTs	?
27117	5.0016146599	AA405098	ESTs Weakly similar to MOESIN/EZRIN/RADIXIN HOMOLOG [D.melanogaster]	other
4304	4.9951954397	U36764	Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit	other
33458	4.9907402071	W86835	Homo sapiens mRNA for KIAA0636 protein complete cds	other
26693	4.9800090679	AA282120	EST	?
12669	4.9758138651	AA417030	Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds	other
29701	4.9708526387	H97970	EST	?
20480	4.9557253636	N52168	ESTs	TM
8720	4.9439110602	AA481218	EST - AA481218	other
34828	4.9431269475	AA292436	Homo sapiens semaphorin F homolog mRNA complete cds	SS, TM

FIG..8Bf

285 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
14985	4.941621032	U15128	Human beta-12-N-acetylglucosaminyltransferase II (MGAT2) gene complete cds	?
16115	4.9377553522	AA004420	ESTs	?
42506	4.9348587118	W70074	EST	other
34761	4.9316837445	AA287833	ESTs	other
11870	4.9281056201	AA262587	ESTs	TM
23211	4.9258391854	T40889	ESTs	other
40611	4.9160502275	N39138	Homo sapiens mRNA for KIAA0584 protein partial cds	other
42611	4.9128605354	W87006	Homo sapiens putative RNA binding protein KOC (koc) mRNA complete cds	other
39652	4.9045174605	H03099	ESTs	other
17581	4.889674751	AA129395	EST	?
37239	4.8704375389	AA449121	ESTs	?
18712	4.8703618781	F04677	ESTs	other
30709	4.8611171953	N51752	ESTs Weakly similar to synapse-associated protein sap47-1 [D.melanogaster]	other
34179	4.8503613948	AA227903	ESTs Highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluoresceris]	other
21433	4.825670988	R22183	EST	?
39731	4.8186142741	H11760	ESTs	other
31295	4.8116614607	N66653	ESTs	other
24647	4.804163055	Z39108	EST	?
31292	4.8008871817	N66615	ESTs	other
1285	4.7997542393	HG4157- HT4427	EST - HG4157-HT4427	?
1106	4.7932425858	HG2981- HT3127	EST - HG2981-HT3127	?

FIG..8Bg

286 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
18212	4.7912262565	AA196506	ESTs	other
34367	4.782207045	AA251758	Homo sapiens spleen mitotic checkpoint BUB3 (BUB3) mRNA complete cds	other
34802	4.7797760205	AA291468	ESTs	TM
34762	4.7775301546	AA287834	ESTs	other
11595	4.7696612848	AA242819	ESTs	other
8295	4.7639839111	AA405082	ESTs	?
17622	4.758635576	AA131584	ESTs Weakly similar to SOF1 PROTEIN [Saccharomyces cerevisiae]	other
35781	4.7572463523	AA406335	ESTs	other
34754	4.7483874972	AA287642	Human mRNA for KIAA00178 gene complete cds	other
23237	4.7444854356	T47291	EST	?
37667	4.7280445357	AA460318	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L26 [Rattus norvegicus]	other
11568	4.7257189975	AA236786	ESTs	other
38622	4.7190695733	AA598967	ESTs	?
5137	4.7057359474	U79296	Dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	other
25038	4.7002244728	AA010065	CDC28 protein kinase 2	other
19288	4.7000147312	H16567	ESTs	other
32503	4.6979488292	T17045	Collagen type I alpha-2	other
3278	4.6953739298	M94055	SODIUM CHANNEL PROTEIN BRAIN II ALPHA SUBUNIT	TM
9696	4.6942061018	L38961	Integral transmembrane protein 1	TM
35400	4.6901390898	AA399591	Homo sapiens putative DNA methyltransferase (DNMT2) mRNA complete cds	other
35246	4.6862691303	AA398367	EST Weakly similar to HSP60 protein [M.musculus]	?
36387	4.6822499271	AA426270	ESTs	other

FIG.-8Bh

287 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
21509	4.6730072542	R27314	ESTs	other
31381	4.6729672124	N67889	ESTs	other
26723	4.6727894925	AA282781	ESTs Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP28 [Saccharomyces cerevisiae]	other
36326	4.6703621086	AA425151	Human GAP SH3 binding protein mRNA complete cds	other
17409	4.6688418667	AA113136	EST - RC_AA113136	other
4908	4.6552339935	U67156	Human mitogen-activated kinase kinase kinase 5 (MAPKKK5) mRNA complete cds	other
30594	4.6496238328	N49967	ESTs	other
38286	4.64639735	AA489847	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Nycticebus coucang]	?
13073	4.6426509459	AA433950	ESTs	other
40435	4.6240181066	N21614	Homo sapiens basic-leucine zipper transcription factor MafG (MAFG) mRNA complete cds	other
14474	4.6228694379	AA609427	ESTs Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]	other
38213	4.615309907	AA488847	ESTs Weakly similar to putative p150 [H.sapiens]	?
5312	4.606644198	U90716	Human cell surface protein HCAR mRNA complete cds	SS,TM
24225	4.6041550359	W70326	ESTs	?
35588	4.5868982366	AA401750	EST	?
29739	4.5863199051	H99626	EST	?
7203	4.5792992577	AA053096	EST - AA053096	other
2157	4.5772055869	L41939	Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA complete cds	SS,TM
32086	4.5661024279	R11510	ESTs	?
8085	4.5648114738	AA314779	ESTs Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]	SS,

FIG. 8Bi

288 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
224	4.5622018989	D13633	Human mRNA for KIAA0008 gene complete cds	other
34006	4.5609980241	AA188761	DNA polymerase gamma	other
33656	4.5557384389	W95477	ESTs	other
34065	4.5537335124	AA195517	ESTs Weakly similar to III ALU SUBFAMILY J WARNING ENTRY III [H.sapiens]	TM
6028	4.5357922097	X66503	Adenylosuccinate synthase	other
4166	4.5032930671	U29463	Cytochrome B561	?
40262	4.5024727522	H93562	ESTs	TM
22687	4.5018672549	R88209	ESTs	TM
41069	4.4977510482	N93969	H.sapiens mRNA for hFat protein	SS,
8264	4.4793100575	AA401334	ESTs	other
27588	4.472017297	AA443187	ESTs	other
35882	4.4717597552	AA412047	ESTs	?
34479	4.465519191	AA262080	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds	TM
15921	4.4548516436	Y12065	Homo sapiens mRNA for nucleolar protein hNop56	?
11279	4.4380038671	AA195399	ESTs	other
39222	4.4367650786	AA621348	ESTs Highly similar to DCILICHL-PHOSPHATE BETA-GLUCOSYLTRANSFERASE [Saccharomyces cerevisiae]	other
34428	4.4364736766	AA256526	ESTs	other
8771	4.432067373	AA491188	ESTs	other
22193	4.4189610024	R53891	Homo sapiens mRNA from chromosome 5q21-22 clone A3-A	other
7898	4.4066170674	AA263032	ESTs	other
19902	4.3886145805	H66736	ESTs	other
9276	4.3868095209	D82374	ESTs	other
10716	4.3794529068	AA053319	ESTs	TM

FIG..8Bj

289 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
13193	4.3751913512	AA442763	ESTs Highly similar to G2/MITOTIC-SPECIFIC CYCLIN B2 [Mesocricetus auratus]	other
5690	4.3723059417	X17620	NUCLEOSIDE DIPHOSPHATE KINASE A	other
35102	4.37147138	AA371509	EST - RC_AA371509	TM
17983	4.3612985467	AA169226	ESTs	other
24962	4.3497206925	AFFX- HUMTFRR/ M11507	AFFX-HUMTFRR/M11507_5	?
31680	4.3416539669	N74438	ESTs	other
27168	4.330306894	AA410258	ESTs	other
28731	4.3231846659	D20981	EST	?
28348	4.3212284906	AA608752	ESTs	other
16335	4.3019961487	AA018587	ESTs Weakly similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]	?
33036	4.2915644973	W48580	ESTs Weakly similar to transposon LRE2 reverse transcriptase homolog [H.sapiens]	other
30180	4.2897721925	N33144	ESTs	other
35591	4.2895541242	AA401758	ESTs Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	SS,
25340	4.2721717135	AA054554	EST	?
28106	4.2659103748	AA485084	ESTs	other
38690	4.2649184307	AA600121	ESTs	other
20203	4.2626499431	N26855	ESTs Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	other
10251	4.2608760694	R76185	ESTs Weakly similar to Cc1H6.7 [C.elegans]	SS,
12684	4.2604192389	AA417558	ESTs	SS,
31636	4.2509469427	N73680	Natural resistance-associated macrophage protein 2	TM

FIG.-8Bk

290 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
20769	4.2479765348	N67277	ESTs	other
1572	4.2353281083	K01884	EST - K01884	?
10923	4.2292322072	AA116036	ESTs	other
34380	4.2283792392	AA252414	ESTs	other
10132	4.2222816115	R35733	EST - R35733	other
16629	4.2161752119	AA036811	ESTs	other
25146	4.1969683794	AA026356	ESTs	?
28730	4.1965943098	D20959	ESTs Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	other
10200	4.1874912391	R64521	ESTs	other
38695	4.1545794663	AA600176	ESTs	other
31365	4.150549979	N67550	ESTs	other
42379	4.1496120668	W37999	ESTs	other
28050	4.1428703354	AA479139	Acid phosphatase 1 soluble	other
2620	4.1386565707	M29474	Human recombination activating protein (RAG-1) gene complete cds	?
8927	4.1340593744	AF008442	Homo sapiens RNA polymerase I subunit hRPA39 mRNA complete cds	other
13379	4.1269549188	AA449741	ESTs Weakly similar to AF-9 PROTEIN [H.sapiens]	other
5134	4.1218251808	U79293	Human clone 23948 mRNA sequence	other
2626	4.1213948	M29581	Zinc finger protein 8 (clone HF.18)	other
38005	4.1160483666	AA479969	ESTs	other
36575	4.1127196584	AA431085	EST	?
18296	4.1121837207	AA213620	ESTs Weakly similar to putative p150 [H.sapiens]	?
29531	4.1111459313	H88953	EST - RC_H88953	TM

FIG..8BI

291 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
143	4.1095880506	AFFX-HUMTFRR/M11507_5		?
10970	4.0967613396	AA129390	ESTs	other
25836	4.0952825397	AA152305	Interferon (gamma)-induced cell line protein 10 from	SS,
19735	4.0937927853	H53038	EST	?
40711	4.0909709431	N53564	ESTs	other
4149	4.0901471427	U28386	RAG (recombination activating gene) cohort 1	TM
5767	4.0862784557	X53793	MULTIFUNCTIONAL PROTEIN ADE2	other
5503	4.0861035825	X05232	Stromelysin	SS,
20310	4.0641711656	N34893	ESTs Highly similar to HYPOTHETICAL 47.8 KD PROTEIN B0280.9 IN CHROMOSOME III [Caenorhabditis elegans]	other
456	4.0599824566	D38145	Prostaglandin I2 (prostaglandin) synthase	SS,
7814	4.0559685576	AA248406	ESTs	other
40230	4.0447282719	H90161	ESTs	SS,
33651	4.039204804	W95409	ESTs	other
16777	4.0231657929	AA046968	EST	?
19110	4.0094905222	H08778	ESTs	other
34442	4.0077010365	AA258093	HKR-T1	other
5099	4.004992433	U79247	Human clone 23599 mRNA sequence	TM
8209	3.9990473163	AA384220	ESTs	other
24408	3.9976586074	W90146	ESTs	other
26596	3.9974919787	AA279943	ESTs	other
16485	3.9811264008	AA026269	Spleen focus forming virus (SFFV) proviral integration oncogene spi1	other
32969	3.9804901745	W42451	ESTs	TM
27006	3.9799768093	AA398695	ESTs Weakly similar to E04F6.2 gene product [C.elegans]	other

FIG..8Bm

292 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
29809	3.9526765967	N21043	EST	?
9596	3.9440163451	H91564	ESTs	TM
29024	3.9377933938	F09315	Homo sapiens mRNA for KIAA0583 protein partial cds	other
21694	3.9356365584	R39317	Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA complete cds	other
13207	3.9299998104	AA443321	ESTs	other
37865	3.9143752629	AA476623	ESTs Highly similar to PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C13A11.04C [Schizosaccharomyces pombe]	other
36201	3.9129828172	AA421164	ESTs	?
8961	3.8981160269	AFFX-HUMTFRR/M11507_3	AFFX-HUMTFRR/M11507_3	?
17444	3.8927133917	HUMTFRR/M11507	ESTs	other
25869	3.8919834527	AA115933	ESTs Highly similar to HYPOTHETICAL 37.7 KD PROTEIN ZK686.3 IN CHROMOSOME III [Caenorhabditis elegans]	TM
24862	3.89042252	AA157267	ESTs Highly similar to BCINE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]	other
26685	3.889363206	Z41415	ESTs	?
42300	3.8850230366	AA281950	ESTs	?
6495	3.8830844863	T95850	Zinc finger protein 74 (Cos52)	other
38604	3.8828045942	X92715	ESTs	TM
36358	3.8826713718	AA598803	ESTs	other
30560	3.873276445	AA425756	MYB PROTO-ONCOGENE PROTEIN	other
14413	3.8724466158	N49284	ESTs	other
23823	3.8574824967	AA600150	Homo sapiens mRNA for ST1C2 complete cds	other
38158	3.853096838	T91805	EST	?
		AA487021		

FIG._8Bn

293 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
2572	3.8519747554	M27281	Vascular endothelial growth factor	other
40100	3.8464168967	H75933	Laminin receptor (2H5 epitope)	other
40258	3.8462992993	H93340	ESTs	TM
20944	3.8461621525	N74443	ESTs	other
20411	3.8459400966	N48963	Homo sapiens mRNA for KIAA0689 protein partial cds	other
10345	3.8457714481	AA001663	ESTs	other
31261	3.8451974374	N66248	EST	other
8513	3.8378410994	AA446990	ESTs	other
13877	3.8363409835	AA476604	ESTs	other
40748	3.8253562321	N56879	EST	?
14509	3.8152852193	AA609943	ESTs	other
10281	3.8065567331	R80333	ESTs	other
25284	3.8044158642	AA045074	ESTs Weakly similar to 52-kD SS-A/Ro autoantigen [H.sapiens]	other
6730	3.7900025129	Y09305	H.sapiens mRNA for protein kinase Dyrk4 partial	other
16033	3.7884592402	AFFX- HUMISGF3A/ M97935	AFFX-HUMISGF3A/M97935_MB	?
39242	3.7827164808	AA621523	ESTs	other
27354	3.7794760435	AA425221	ESTs	?
4552	3.777263605	U49188	Human placenta (Diff33) mRNA complete cds	SS, TM
18385	3.7756199108	AA227219	Homo sapiens CAGF9 mRNA partial cds	other
16754	3.7677416053	AA046067	EST - RC_AA046067	other
12752	3.7671137403	AA421250	ESTs	other
42463	3.7601033106	W60180	ESTs	?
10614	3.7581669016	AA037357	ESTs	other
867	3.7459337969	D87716	Human mRNA for KIAA0007 gene partial cds	other
7608	3.7336047135	AA180967	ESTs	other

FIG.-8Bo

294 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
31795	3.732738742	N80703	ESTs	other
35377	3.7273784603	AA399453	EST - RC_AA399453	?
22828	3.7243928524	R98192	ESTs	other
25240	3.7243198336	AA039713	ESTs	other
11008	3.7197361366	AA134289	ESTs Weakly similar to A5I1 [D.melanogaster]	?
4341	3.7162349944	U38545	Human ARF-activated phosphatidylcholine-specific phospholipase D1a (hPLD-1) mRNA complete cds	other
28833	3.7147818393	D59787	EST - RC_D59787_f	?
3750	3.7121007154	U09279	Collagen type XIX alpha 1	SS, TM
17483	3.6943413512	AA122147	ESTs	TM
16854	3.6915208471	AA055552	ESTs Weakly similar to KIAA0319 [H.sapiens]	other
3709	3.6891656771	U07550	Heat shock 10 kD protein 1 (chaperonin 10)	?
1608	3.6652978422	L00205	KERATIN TYPE II CYTOSKELETAL 6D	TM
24577	3.6617721053	Z38727	Homo sapiens mRNA for KIAA0555 protein complete cds	other
31032	3.6570916386	N62508	ESTs	other
4951	3.6536195433	U69546	Human RNA binding protein Etr-3 mRNA complete cds	other
37660	3.6523275307	AA460225	ESTs	other
20418	3.6495357091	N49209	ESTs	?
27995	3.6485167436	AA470155	Homo sapiens coatomer protein (COPA) mRNA complete cds	other
7971	3.6434397185	AA287423	ESTs	other
27606	3.64303453	AA443793	ESTs	other
24677	3.6427250633	Z39338	ESTs Highly similar to PCLOVIRUS RECEPTOR HOMOLOG PRECURSOR [Mus musculus]	other
11070	3.6406198277	AA148521	ESTs Weakly similar to putative p150 [H.sapiens]	TM
9328	3.6356048599	D89618	Homo sapiens importin-alpha homolog (SRP1gamma) mRNA complete cds	other
36826	3.634689802	AA435996	ESTs	other

FIG.-8Bp

295 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
17678	3.6300045795	AA134275	Human HIV1 tata element modulatory factor mRNA sequence from chromosome 3	other
36209	3.6274694477	AA421266	ESTs Weakly similar to LKs-1 protein [H.sapiens]	other
34120	3.6258090412	AA211615	EST	?
38152	3.6246442011	AA486737	H.sapiens mRNA for Sm protein F	TM
38463	3.6184693268	AA504491	ESTs Weakly similar to contains similarity to C3HC4-class zinc finger [C.elegans]	TM
20064	3.6183699978	H98653	ESTs	TM
31256	3.5992620732	N66152	EST	?
9713	3.5985228843	L44338	Homo sapiens mRNA for KIAA0525 protein partial cds	other
28622	3.5768056147	D11837	ESTs	?
38057	3.5736105703	AA481549	EST - RC_AA481549	other
28763	3.5688723791	D45568	EST	?
16996	3.5680705709	AA069038	EST - RC_AA069038	TM
28628	3.5604144617	D11888	ESTs Moderately similar to PROHIBITIN [H.sapiens]	?
25804	3.5442954572	AA148885	ESTs	?
2492	3.5423964239	M22898	Tumor protein p53 (Li-Fraumeni syndrome)	?
14904	3.5411970737	T83389	ESTs Highly similar to GEPHYRIN [Rattus norvegicus]	other
25265	3.5347588502	AA043765	H.sapiens RY-1 mRNA for putative nucleic acid binding protein	other
13606	3.5327912417	AA456437	ESTs Weakly similar to CLEAVAGE STIMULATION FACTOR 64 KD SUBUNIT [H.sapiens]	other
42307	3.5318436465	T96595	EST - RC_T96595	TM
1544	3.526202414	J05068	TRANSCOBALAMIN I PRECURSOR	SS,
42339	3.5195061035	W02072	ESTs Weakly similar to Nc definition line found [C.elegans]	other
42311	3.5183719631	T97257	ESTs	other
2023	3.5040279423	L34600	INITIATION FACTOR IF-2 MITOCHONDRIAL PRECURSOR	other
4540	3.4955308569	U48807	Human MAP kinase phosphatase (MKP-2) mRNA complete cds	other

FIG. 8Bq

296 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE: DESCRIPTOR	ORF STRUCTURAL INFO
33707	3.4888534277	Z39297	Neuronal pentraxin II	other
17220	3.4755763461	AA083070	EST - RC_AA083070_s	SS,
24332	3.4725273806	W85782	ESTs	other
35887	3.4668063718	AA412067	ESTs	other
20158	3.4538150055	N23638	ESTs Weakly similar to coded for by C. elegans cDNA yk52e10.5 [C.elegans]	other
8338	3.4465832071	AA417152	Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds	other
387	3.4421427234	D28589	EST - D28589	other
12319	3.4356289717	AA398109	ESTs	SS, TM
38276	3.4313139432	AA489711	ESTs	TM
15643	3.4312194246	W58247	ESTs Highly similar to KINESIN-LIKE PROTEIN KIF4 [Mus musculus]	other
11218	3.4232932843	AA180488	ESTs	TM
16539	3.417886379	AA029328	Human mRNA for KIAA0073 gene partial cds	?
29203	3.4162847487	H28581	ESTs	other
13838	3.4162403464	AA465342	ESTs	other
25585	3.4160353003	AA112389	H4(D10S170)	SS,
34018	3.4145338583	AA191488	Human high-affinity copper uptake protein (hCTR1) mRNA complete cds	TM
251	3.4006042851	D14520	Basic transcription element binding protein 2	other
3778	3.4004516201	U09848	Zinc finger protein 139 (clone pHZ-37)	other
24535	3.3964397637	Z38409	ESTs	other
16858	3.3925194041	AA055759	Human mRNA for KIAA0128 gene partial cds	TM
16127	3.3921645927	AA004669	ESTs	other
36683	3.3841316491	AA432268	ESTs	other
26149	3.3809497785	AA250824	ESTs Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]	other

FIG..8Br

297 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
4011	3.3798093471	U20536	Human cysteine protease Mch2 isoform alpha (Mch2) mRNA complete cds	other
41001	3.3794250205	N78844	ESTs	other
5660	3.3789336731	X16396	NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE	SS,
19204	3.3776332343	H11629	ESTs	other
42323	3.3768515979	T98152	Fibrillin 2	SS,
26928	3.3725378868	AA342580	ESTs	SS,
20497	3.369285912	N52565	ESTs	other
19226	3.36674249	H12455	ESTs	other
36267	3.3606641838	AA424046	ESTs	other
32257	3.3559796018	R54726	DNA-REPAIR PROTEIN XRCC1	other
17365	3.3522214732	AA101551	ESTs	other
15296	3.3491193196	W16684	ESTs Moderately similar to Similar to S.cerevisiae hypothetical protein L3111 [H.sapiens]	other
17675	3.3485870272	AA134064	ESTs	TM
40332	3.3456469589	H97565	Homo sapiens mRNA from chromosome 5q21-22 clone:A3-A	other
7219	3.3385684843	AA056319	Homo sapiens protein phosphatase 2A B56-epsilon (PP2A) mRNA complete cds	other
10006	3.3322827922	N81193	Homo sapiens mRNA for KIAA0628 protein complete cds	?
33985	3.3276877441	AA181580	Homo sapiens importin beta subunit mRNA complete cds	other
9570	3.3263855302	H85169	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene complete cds	other
37551	3.3155406577	AA456679	ESTs	other
886	3.3111782759	D88613	Human mRNA for hGCMa complete cds	other
23650	3.3069426629	T86293	ESTs	other
18367	3.3007433533	AA224180	ESTs Moderately similar to ovarian-specific protein [R.norvegicus]	?

FIG..8Bs

298 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
42494	3.2908070546	W69385	H.sapiens NuMA gene (Clone T33)	other
14310	3.2753564661	AA598412	ESTs Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN PMT6-PCT1 INTERGENIC REGION [Saccharomyces cerevisiae]	SS, TM
19233	3.274416299	H12634	ESTs	other
42283	3.2731086284	T94343	Homo sapiens M962 protein spliced isoform 2 mRNA complete cds	other
12809	3.271352097	AA424406	ESTs	other
36285	3.2696023617	AA424469	ESTs	other
21555	3.2666296446	R33073	EST	?
13767	3.2665695616	AA463234	ESTs	TM
4738	3.2661591937	U58766	Human FX protein mRNA complete cds	other
7258	3.263106866	AA075427	ESTs	other
17041	3.2629042076	AA070364	EST - RC_AA070364	?
15504	3.2616745245	W28362	ESTs	other
23793	3.2611829896	T90971	EST - RC_T90971	other
18214	3.2572346955	AA196635	ESTs	TM
7401	3.257164123	AA094800	Human translation initiation factor eIF3 p66 subunit mRNA complete cds	other
18912	3.2553600001	F10913	complete cds	other
36317	3.2509495347	AA425089	Homo sapiens clone 23617 unknown mRNA partial cds	?
9410	3.2507279851	H20443	Human mRNA for KIAA0334 gene complete cds	other
2146	3.2464307696	L41390	H.sapiens mRNA for TRE5	?
18683	3.240814336	F04258	EST - L41390	?
			ESTs Highly similar to INORGANIC PYROPHOSPHATASE [Bos taurus]	

FIG._8Bt

299 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
33891	3.2392191408	AFFX-HUMTFRR HUMTFRR /M11507	AFFX-HUMTFRR/M11507_M	?
14435	3.2372161315	AA608730	ESTs Weakly similar to ELONGATION FACTOR 1-ALPHA [Giardia intestinalis]	other
9584	3.2363829855	H88128	ESTs Highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluorescens]	other
22061	3.2340098572	R49216	ESTs	TM
35796	3.233287605	AA410223	EST - RC_AA410223	?
37403	3.2261852043	AA453613	ESTs	other
15796	3.2260359988	X16889	ALPHA-GALACTOSIDASE A PRECURSOR	SS,
15840	3.2257932439	X70944	PTB-ASSOCIATED SPLICING FACTOR	other
7518	3.2252170427	AA147144	EST - AA147144	other
32335	3.2228388982	R78248	ESTs	other
3256	3.2180538038	M92439	130 KD LEUCINE-RICH PROTEIN	other
4400	3.2173898081	U41387	Human Gu protein mRNA partial cds	other
7681	3.2074414299	AA206983	Homo sapiens mRNA for DRIM protein	other
15676	3.2041299443	W68649	ESTs	TM
39590	3.2038953621	F09281	ESTs	other
26883	3.1980022253	AA291921	ESTs Weakly similar to putative p150 [H.sapiens]	?
9808	3.1920380384	M80627	Transcription factor 12 (H1F4 helix-loop-helix transcription factors 4)	other
27755	3.1900699454	AA453444	ESTs	other
29983	3.1882280623	N26011	ESTs	?
21350	3.1876957756	R15846	ESTs	other
11981	3.1870525747	AA280928	ESTs	other

FIG..8Bu

300 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
23930	3.1817500097	T96690	ESTs Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	other
30399	3.1792054412	N45226	EST	?
22286	3.1781990049	R59312	ESTs	other
13494	3.1673900969	AA453431	ESTs	TM
12908	3.1530533441	AA427579	ESTs	other
22319	3.1469419301	R60567	ESTs	TM
31309	3.1466750623	N66818	ESTs	TM
31192	3.1458779823	N64406	ESTs	other
11288	3.144853134	AA196512	ESTs	TM
170	3.1430726349	D00596	Thymidylate synthase	?
5307	3.1347905628	U90549	Human non-histone chromosomal protein (NHC) mRNA complete cds	other
26105	3.1311103325	AA243133	Homo sapiens serine/threonine kinase (BTAK) mRNA complete cds	other
11659	3.1281786108	AA251909	Homo sapiens MAD3-like protein kinase mRNA complete cds	other
19177	3.124408565	H10984	ESTs	TM
8389	3.1241545824	AA425230	ESTs	TM
34087	3.1216555797	AA205125	Protein serine/threonine kinase stk2	other
25001	3.1209327466	AA004718	ESTs Weakly similar to BAP31 protein [H.sapiens]	other
14149	3.1198500308	AA489665	ESTs	other
10167	3.1191986923	R55076	ESTs	other
17380	3.1071055868	AA102566	ESTs	other
42397	3.1044680628	W42928	ESTs	other
14935	3.1042015743	T94828	ESTs Weakly similar to GAB BINDING PROTEIN BETA-2 CHAIN [H.sapiens]	other
41673	3.1030349819	R78618	ESTs Weakly similar to GTP-binding protein rab10 [R.norvegicus]	other

FIG..8Bv

301 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
2750	3.1026223619	M35999	Integrin beta 3 (platelet glycoprotein IIIa antigen CD61)	?
3190	3.1026223619	M86808	PYRUVATE DEHYDROGENASE E1 COMPONENT ALPHA SUBUNIT TESTIS-SPECIFIC FORM PRECURSOR	?
17406	3.0999394188	AA112979	Homo sapiens mRNA for V/RK1 complete cds	other
598	3.0912414004	D59253	Homo sapiens mRNA for low molecular mass ubiquinone-binding protein complete cds	other
29348	3.0802365759	H69021	ESTs	other
14130	3.0744457534	AA489041	ESTs	other
14134	3.069660341	AA489080	ESTs Highly similar to phosphorylation regulatory protein HP-10 [H.sapiens]	other
42421	3.0684159011	W45491	ESTs Weakly similar to T23G11.7 [C.elegans]	other
15723	3.0660746209	W79060	ESTs Highly similar to ribosome-binding protein p34 [R.norvegicus]	other
11140	3.0650815198	AA158132	ESTs Highly similar to YSA1 PROTEIN [Saccharomyces cerevisiae]	other
28531	3.0649767987	C20679	ESTs	other
2021	3.0628707497	L34409	Homo Sapiens (clone B3E13E13) chromosome 4p16.3 DNA fragment	?
14522	3.058260163	AA610108	ESTs Highly similar to PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C21E11.05C [Schizosaccharomyces pombe]	SS,
29853	3.0545821815	N22162	ESTs	other
15962	3.0521475703	Z21420	ESTs	other
6541	3.0509806038	X95632	Human Abl interactor 2 (Aoi-2) mRNA complete cds	other
13229	3.0485366337	AA443811	ESTs	other
27315	3.046622812	AA424038	ESTs	other
13621	3.0302305369	AA456821	ESTs Highly similar to BCNE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]	other

FIG._8Bw

302 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
35929	3.0269182409	AA12429	ESTs	other
17925	3.0253428426	AA164209	Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA complete cds	other
5053	3.0249536782	U76992	Human Tat-SF1 mRNA complete cds	other
15060	3.0213293848	U54999	Human LGN protein mRNA complete cds	other
17757	3.0205801351	AA147224	EST	?
19050	3.0192379314	H05509	ESTs	other
26530	3.0176823278	AA278650	ESTs	other
16806	3.0158779932	AA053258	Homo sapiens mRNA for KIAA0648 protein partial cds	TM
29088	3.0149440394	F13700	Homo sapiens ribonuclease P protein subunit p40 (RPP40) gene complete cds	other
22960	3.0141662421	T10272	ESTs	other
33585	3.0121672451	W93000	ESTs	other
220	3.0109180714	D13627	Human mRNA for KIAA0002 gene complete cds	TM
4298	3.0024671064	U36448	Human Ca2+-dependent activator protein for secretion mRNA complete cds	TM
7445	2.9995643641	AA104023	ESTs	?
40903	2.9990347068	N68670	ESTs	?
18055	2.9973386648	AA179387	ESTs	other
7282	2.9962792596	AA083339	ESTs	other
9348	2.9949017671	H03686	ESTs	TM
806	2.9877476515	D87009	Human (lambda) DNA for immunoglobulin light chain	?
38447	2.9876031644	AA504255	Human protein kinase ATF1 mRNA complete cds	other
41464	2.9870604981	R46837	ESTs	?
9662	2.9869352306	L19161	TRANSLATIONAL INITIATION FACTOR 2 GAMMA SUBUNIT	other
16976	2.9801154057	AA063625	EST	?
37426	2.9756408909	AA454016	ESTs	other

FIG..8Bx

303 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
2588	2.9725898298	M27878	Zinc finger protein 84 (H1P2)	other
15174	2.9695024379	U82987	Human Bcl-2 binding component 3 (bbc3) mRNA partial cds	other
33620	2.9657446567	W93943	ESTs	other
6784	2.9655506112	Y11681	Homo sapiens ribosomal protein S12 gene nuclear gene encoding mitochondrial protein complete cds	?
41077	2.9642389716	N95028	ESTs	TM
1932	2.9609985996	L24804	Human (p23) mRNA complete cds	other
39556	2.9588964022	F03738	ESTs	other
16108	2.9574232912	AA002258	ESTs	SS,
32156	2.9574232912	R40381	ESTs	?
13617	2.9552305838	AA456646	ESTs	other
11989	2.955203991	AA281251	ESTs Weakly similar to trithorax protein trxl [D.melanogaster]	other
6056	2.947654132	X68194	Pantophysin [human keratinocyte line HaCaT mRNA 2106 nt]	TM
15446	2.9445456286	W27374	Homo sapiens 10kD protein (BC10) mRNA complete cds	other
38086	2.9445277634	AA482557	EST	?
13878	2.9444133384	AA476604	ESTs	other
6209	2.9422425032	X76770	H.sapiens PAP mRNA	other
388	2.9357591919	D28791	Phosphatidylinositol glycan class A (paroxysmal nocturnal hemoglobinuria)	?
1351	2.9266145582	HG4755-HT5203	EST - HG4755-HT5203	?
42624	2.9266145582	W87804	ESTs	other
34895	2.9242794509	AA311972	ESTs	other
20157	2.9214162976	N23393	ESTs	other
29248	2.9188102156	H52918	ESTs	?
4893	2.9178533564	U66615	Human SWI/SNF complex 155 KDa subunit (BAF155) mRNA complete cds	other

FIG.-8By

304 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
10104	2.9150324884	R23855	ESTs	TM
15039	2.9147218324	U46116	Protein tyrosine phosphatase receptor type gamma polypeptide	?
1605	2.9141775797	L00058	V-myc avian myelocytomatosis viral oncogene homolog	?
4536	2.907560336	U48705	Receptor protein-tyrosine kinase EDDR1	?
10173	2.905710598	R56678	ESTs Weakly similar to cell division control protein CDC21 [H.sapiens]	?
26555	2.9056210172	AA279071	ESTs Weakly similar to T08A11.2 [C.elegans]	other
4401	2.9047655582	U41515	Human deleted in split hand/split foot 1 (DSS1) mRNA complete cds	other
21009	2.8995011918	N90401	ESTs	TM
3602	2.894817322	U01317	HEMOGLOBIN EPSILON CHAIN	?
4833	2.8919254016	U63455	Sulfonylurea receptor (hyperinsulinemia)	?
36200	2.8912301426	AA421164	ESTs	?
26645	2.8898309441	AA281076	ESTs	other
35299	2.8887661574	AA398622	Transcription factor 6-like 1 (mitochondrial transcription factor 1-like)	other
9804	2.8880347344	M74558	Human SIL mRNA complete cds	other
5216	2.8877977515	U83410	Human CUL-2 (cul-2) mRNA complete cds	other
12313	2.8847621603	AA397916	ESTs	other
5928	2.8836060438	X62048	WEE1-LIKE PROTEIN KINASE	?
39586	2.8818258313	F09155	ESTs	TM
34758	2.8775214637	AA287680	EST	?
18199	2.8753649024	AA195318	ESTs	other
19867	2.8720974689	H61476	ESTs	?
6081	2.8679372936	X69398	CD47 antigen (Rh-related antigen integrin-associated signal transducer)	SS, TM

FIG.-8Bz

305 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
5254	2.862087239	U86782	Human 26S proteasome-associated pad1 homolog (POH1) mRNA complete cds	other
13579	2.8570620494	AA455967	Human neuronal PAS2 (NPAS2) mRNA complete cds	?
1117	2.8568053461	HG3075-HT3236	EST - HG3075-HT3236	?
20533	2.8564678641	N54407	ESTs	TM
38495	2.8562453397	AA505118	Human nucleoporin 98 (NUP98) mRNA complete cds	other
33729	2.8548155651	Z39654	EST	?
2028	2.8532776139	L35035	RIBOSE 5-PHOSPHATE ISOMERASE	other
27374	2.8520674335	AA425816	ESTs Weakly similar to Y53C12A.3 [C.elegans]	other
19404	2.8518690748	H20568	ESTs	other
26108	2.8504706329	AA243189	ESTs	SS,
4189	2.8439972255	U30930	UDP glycosyltransferase 3 (UDP-galactose ceramide galactosyltransferase)	TM
16708	2.8427388072	AA043944	ESTs	other
357	2.8350474214	D26156	Human mRNA for transcriptional activator hSNF2b complete cds	other
26045	2.8315740098	AA236276	ESTs	other
17796	2.8312342777	AA150435	ESTs	other
8059	2.8288722809	AA310967	ESTs Weakly similar to T04A8.11 [C.elegans]	other
40914	2.827999584	N69220	ESTs	other
27169	2.8263163852	AA410287	H.sapiens mRNA for basic transcription factor 2 34 kD subunit	other
21358	2.8262413945	R16079	ESTs	other
3572	2.8261469131	S87759	Protein phosphatase 2C alpha [human teratocarcinoma mRNA 2346 nt]	other
11877	2.8259099942	AA262727	ESTs	other
1653	2.8234017508	L05424	CD44 antigen (cell adhesion molecule)	?
24645	2.8131264428	Z39106	ESTs	other

FIG.-8Ca

306 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
35830	2.8126257031	AA411448	ESTs	TM
4433	2.8114422177	U43279	EST - U43279	?
20151	2.8109454503	N22895	Homo sapiens clone 1400 unknown protein mRNA partial cds	other
38648	2.8084431065	AA599267	EST - RC_AA599267	other
7777	2.8071817929	AA236820	ESTs	other
32845	2.80583194	W31566	EST	?
28258	2.8043934182	AA505133	ESTs	other
6853	2.798263202	Z22951	TRANSCRIPTION FACTOR P65	?
35944	2.7913872996	AA412488	ESTs	?
30648	2.7866523676	N50971	ESTs	?
18965	2.7857482775	H01411	ESTs	TM
8616	2.785444221	AA460077	ESTs	other
14945	2.7838257917	T99606	ESTs Weakly similar to F35G2.2 [C.elegans]	other
8375	2.7805657722	AA422160	H.sapiens NAP (nucleosome assembly protein) mRNA complete cds	other
34929	2.7792111121	AA342084	EST - RC_AA342084	other
326	2.7786978435	D21262	Human mRNA for KIAA00135 gene partial cds	other
27057	2.7781218063	AA400998	ESTs	SS,
36292	2.7746002184	AA424513	EST - RC_AA424513	other
6480	2.7735431318	X91788	H.sapiens mRNA for Icln protein	other
15424	2.7731675808	W27054	APOLIPOPROTEIN AI REGULATORY PROTEIN-1	other
11602	2.7730818255	AA243007	ESTs	?
18175	2.77056686	AA194730	ESTs	?
25202	2.7698585996	AA034527	EST	?
1681	2.7697545972	L07493	Replication protein A (E coli RecA homolog RAD51 homolog)	other
14566	2.767984858	AA621122	ESTs	other
25614	2.7633374335	AA115769	ESTs	other

FIG.-8Cb

307 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
14182	2.7606048934	AA490885	ESTs	other
31599	2.7591187958	N72196	EST	other
18253	2.7471964081	AA206370	ESTs	other
6193	2.7442487702	X76092	Regulatory factor (trans-acting) 3	other
22911	2.7433449859	T03865	ESTs	other
35549	2.743246906	AA401274	Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA complete cds	other
35955	2.7389431758	AA412528	ESTs Weakly similar to ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH [R.norvegicus]	other
17642	2.7377607284	AA132983	ESTs Moderately similar to C-1-TETRAHYDROFOLATE SYNTHASE CYTOPLASMIC [H.sapiens]	other
6131	2.7371784571	X72841	Human retinoblastoma-binding protein (RbAp46) mRNA complete cds	other
41429	2.7347564467	R44994	ESTs	other
17052	2.7323944161	AA070815	EST - RC_AA070815	other
34243	2.7294147034	AA235050	ESTs	?
22937	2.7284347248	T10065	Homo sapiens TLS-associated protein TASR-2 mRNA complete cds	other
5183	2.7243199196	U82130	Human tumor susceptibility protein (TSG101) mRNA complete cds	other
30837	2.7231409239	N54416	ESTs	other
16243	2.7228028265	AA012902	ESTs	TM
19954	2.7215193495	H80100	ESTs	other
6444	2.720441384	X89750	H.sapiens mRNA for TGII ⁺ protein	other
5916	2.7192579481	X61072	Human mRNA for T cell receptor clone IGRA17	SS,
6240	2.7168544194	X78627	H.sapiens mRNA for translin	?

FIG.-8Cc

308 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
42116	2.7144176166	T69924	EST - RC_T69924	other
7701	2.7107230468	AA215333	ESTs	TM
17568	2.7096978968	AA128905	ESTs	TM
42534	2.7086014274	W73189	Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA complete cds	SS, TM
29813	2.708372123	N21111	ESTs	other
38898	2.7067394943	AA609458	ESTs	other
10316	2.7055636457	R88880	ESTs Moderately similar to zinc finger protein [M.musculus]	other
14769	2.7040821985	S54641	HZF-16	other
32961	2.7012196407	W38366	Human mRNA for KIAA0105 gene complete cds	other
35273	2.6975345483	AA398507	ESTs	other
10180	2.6960696303	R60100	ESTs	?
32563	2.6955462902	T27697	Human mRNA for KIAA0136 gene complete cds	other
34502	2.6948574449	AA262768	ESTs	TM
13223	2.6912995353	AA443720	ESTs	other
8494	2.6908515739	AA443460	ESTs	other
7776	2.6900717525	AA236771	ESTs	other
10400	2.6898958951	AA007234	ESTs	other
1130	2.6897527619	HG3132- HT3308	EST - HG3132-HT3308	?
2379	2.6874247447	M16937	Human homeo box c1 protein mRNA complete cds	TM
18906	2.6861450774	F10868	Human SH3 domain-containing protein SH3P18 mRNA complete cds	?
34796	2.6853510115	AA291259	ESTs	TM
41955	2.6821406177	T33311	Neuronal pentraxin II	other
2009	2.6791061739	L33881	Protein kinase C iota	?

FIG.-8Cd

309 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
33688	2.6775081286	Z38501	ESTs Weakly similar to PROBABLE E5 PROTEIN [Human papillomavirus type 58]	other
1385	2.6771402807	HG884-HT884	EST - HG884-HT884	?
24758	2.6756080868	Z40075	ESTs	other
7620	2.6742248913	AA192484	ESTs Weakly similar to MITOCHONDRIAL INNER MEMBRANE PROTEASE SUBUNIT 2 [S.cerevisiae]	other
30733	2.6739544496	N52078	Homo sapiens mRNA for KIAA0637 protein complete cds	other
21256	2.6723253055	R09195	Homo sapiens mRNA for KIAA0564 protein partial cds	other
40528	2.669020458	N29325	ESTs Highly similar to 47 KD PROTEIN [Pseudomonas chlororaphis]	other
25285	2.6685455408	AA045083	VITAMIN K-DEPENDENT GAMMA-CARBOXYLASE	other
9296	2.667949532	D82775	ESTs Weakly similar to unknown [S.cerevisiae]	SS,
12174	2.6669305328	AA292128	ESTs	other
38357	2.6652770538	AA491265	EST	TM
3154	2.6619596806	M83712	Cholinergic receptor nicotinic alpha polypeptide 5	TM
7383	2.6554440738	AA093834	ESTs Weakly similar to HYPOTHETICAL 16.8 KD PROTEIN IN SMY2-RPS101 INTERGENIC REGION [S.cerevisiae]	other
1923	2.6530372325	L23808	Matrix metalloproteinase 12 (macrophage elastase)	SS,
24906	2.6527048053	Z41840	ESTs	other
34726	2.6495430564	AA287278	ESTs	SS,
30407	2.6495430564	N45983	ESTs	TM
20408	2.6459891347	N48787	ESTs Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]	other
7158	2.6455059455	AA037206	ESTs	TM
26286	2.6445109706	AA253351	ESTs	?
19822	2.6431968212	H58684	ESTs	?

FIG.-8Ce

310 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
12379	2.6428192941	AA399418	Homo sapiens mRNA for JM23 protein complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc1101133Q7 (RZPD Berlin))	other
22698	2.6396306055	R89287	ESTs	other
24161	2.6394502284	W58015	ESTs	other
9558	2.6370149706	H81497	ESTs	TM
18104	2.6358767288	AA188801	ESTs	other
24882	2.6357248889	Z41563	ESTs	other
40038	2.6347974764	H69485	ESTs	other
8865	2.6344845492	AB002359	Human mRNA for KIAA0361 gene KIAA0361 protein	other
22148	2.6288326966	R51831	ESTs	other
4627	2.6277060831	U51990	Human hPrp18 mRNA complete cds	other
8394	2.6275394634	AA426156	ESTs	TM
20422	2.6272599716	N49300	ESTs	other
41602	2.6258613824	R67258	ESTs Moderately similar to rhotekin [M.musculus]	other
612	2.6257836682	D63480	Human mRNA for KIAA0146 gene partial cds	TM
4821	2.619521444	U62801	Human protease M mRNA complete cds	SS, TM
16807	2.617722928	AA053296	ESTs	other
15288	2.6173997018	W07562	ESTs Moderately similar to rA8 [R.norvegicus]	other
38023	2.6135617291	AA481066	ESTs	other
23822	2.6120077647	T91715	ESTs Highly similar to HYPOTHETICAL 103.6 KD PROTEIN IN COX5B-PFK26 INTERGENIC REGION [Saccharomyces cerevisiae]	TM
10951	2.6116018519	AA126719	ESTs	other
6150	2.6113980879	X74262	RETINOBLASTOMA BINDING PROTEIN P48	other

FIG._8Cf

311 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
39336	2.6109987712	C20945	ESTs Highly similar to HYPOTHETICAL 54.2 KD PROTEIN IN CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae]	other
17793	2.6102158178	AA150242	ESTs Highly similar to modulator recognition factor 2 [H.sapiens]	other
26891	2.6085107387	AA292659	ESTs	other
2175	2.607468576	L42621	Homo sapiens Ly-9 mRNA complete cds	TM
10642	2.6048724507	AA040149	Human Chromosome 16 BAC clone CIT987SK-A-270G1	other
15026	2.6031453592	U41816	Human C-1 mRNA complete cds	other
7699	2.6019047419	AA215299	Homo sapiens chromosome 19 cosmid R30783	other
6543	2.6011828937	X95654	Homo sapiens mRNA for SCP-1 complete cds	other
20636	2.5993684878	N62122	ESTs	other
11308	2.5993311375	AA207114	ESTs	other
4086	2.5966362866	U24704	Human antisecretory factor-1 mRNA complete cds	other
38615	2.5963996726	AA598938	EST - RC_AA598938	other
11819	2.5961501969	AA258189	ESTs	other
37433	2.5957446266	AA454103	ESTs	other
28270	2.5939657529	AA521186	ESTs	TM
5587	2.5932338399	X13482	U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A'	other
19841	2.5930132063	H59617	ESTs Highly similar to UEIQUITIN-CONJUGATING ENZYME E2-17 KD [Drosophila melanogaster]	other
10655	2.5925442731	AA040882	ESTs	?
14053	2.5899324577	AA485147	ESTs Highly similar to HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III [Caenorhabditis elegans]	other
31574	2.5883094453	N71303	EST	?
7614	2.5870699315	AA187579	ESTs Weakly similar to Ye1007c-ap [S.cerevisiae]	other
37971	2.5847445397	AA479195	EST	?

FIG..8Cg

312 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
7090	2.5845365105	AA009913	Homo sapiens diphthamide biosynthesis protein-2 (DPH2) mRNA complete cds	other
17852	2.5841100415	AA156360	ESTs	other
24219	2.5823376094	W69960	ESTs	other
19070	2.5813645258	H05970	Human clone 23960 mRNA sequence	other
17719	2.5803606155	AA136569	EST	?
38669	2.579196791	AA599694	Human mRNA for KIAA0133 gene complete cds	TM
20982	2.5763957078	N79565	ESTs	TM
9158	2.5731838907	D31446	Homo sapiens breakpoint cluster region protein 1 (BCRG1) mRNA complete cds	other
11362	2.5731137778	AA227261	ESTs	other
8613	2.5723119462	AA459555	Homo sapiens mRNA for KIAA0648 protein partial cds	TM
13866	2.5715997844	AA476319	ESTs	SS,
10303	2.5712815907	R86178	Ataxia telangiectasia mutated (includes complementation groups A C and D)	?
22299	2.567916035	R59601	EST	?
18257	2.5673459608	AA206591	EST - RC_AA206591	other
20555	2.5654242568	N55168	ESTs	other
39552	2.5645918108	F03605	PUTATIVE 60S RIBOSOMAL PROTEIN	other
27530	2.5631130948	AA435999	ESTs	other
1795	2.5608471476	L13434	Human chromosome 3p21.1 gene sequence complete cds	?
14746	2.5603154966	D60354	Human mRNA for KIAA0007 gene partial cds	other
2993	2.5587815672	M64929	Protein phosphatase 2 (formerly 2A) regulatory subunit B (PR 52) alpha isoform	other
19191	2.5545260975	H11297	ESTs	other
12986	2.5507999853	AA430032	ESTs Moderately similar to PTTG gene product [R.norvegicus]	?
15452	2.5488533884	W27451	Human Cdc5-related protein (PCDC5RP) mRNA complete cds	other

FIG..8Ch

313 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
18003	2.5465671712	AA171692	ESTs	other
24198	2.5461854497	W67524	Human protein-tyrosine phosphatase (HU-PP-1) mRNA partial sequence	TM
42653	2.5447526627	W92703	ESTs	other
26446	2.544106171	AA258796	EST Weakly similar to putative p150 [H.sapiens]	?
30438	2.5368548574	N47204	ESTs Weakly similar to C50F4.12 [C.elegans]	other
36365	2.5362912735	AA425893	ESTs Weakly similar to probable CBP3 protein homolog [C.elegans]	other
26135	2.535658968	AA243765	ESTs	other
41885	2.5349932888	T23449	ESTs Moderately similar to ZNF127-Xp [H.sapiens]	SS,
15457	2.5343495968	W27560	ESTs	other
27748	2.5320767519	AA453159	Human kinesin-like spindlin protein HKSP (HKSP) mRNA complete cds	other
32315	2.5302979959	R69840	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Nycticebus coucang]	?
25310	2.5274401579	AA046745	ESTs	other
42720	2.5222453766	Z39436	ESTs	other
12939	2.5200945911	AA428204	ESTs	other
30746	2.5198420998	N52243	ESTs	other
2222	2.5193624578	L76703	Homo sapiens protein phosphatase 2A B56-epsilon (PP2A) mRNA complete cds	?
11609	2.5191765545	AA243303	ESTs	TM
9658	2.5185814336	L16991	Deoxythymidylate kinase	other
12210	2.5172044681	AA293774	ESTs Weakly similar to PFI0BABLE TRYPTOPHANYL-TRNA SYNTHETASE MITOCHONDRIAL [C.elegans]	other
3563	2.5169918533	S83364	EST - S83364	other
42407	2.5128230047	W44768	Homo sapiens nephrocystin (NPHP1) mRNA partial cds	?

FIG.-8Ci

314 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
32826	2.5128052161	W20391	Human mRNA for kinesin-related protein partial cds	other
9692	2.5119977118	L37747	LAMIN B1	?
27862	2.5094571267	AA458908	ESTs	TM
33691	2.509287494	Z38630	EST	other
17288	2.5088624644	AA085178	ESTs	SS,
9888	2.5076170902	N35449	ESTs Highly similar to HYPOTHETICAL 30.3 KD PROTEIN IN APE1/LAP4-CWP1 INTERGENIC REGION [Saccharomyces cerevisiae]	other
5932	2.5073880985	X62153	Minichromosome maintenance deficient (S. cerevisiae) 3	other
15885	2.5053862932	X95073	H.sapiens mRNA for translin associated protein X	other
17952	2.5049193223	AA165677	ESTs Weakly similar to F16A11.1 [C.elegans]	other
12197	2.5042458391	AA293206	ESTs	other
6210	2.5042034458	X76942	Homo sapiens golgin-245 mRNA complete cds	other
34047	2.5041917773	AA194166	ESTs Weakly similar to G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG [H.sapiens]	other
16929	2.5034461307	AA058952	ESTs	other
26834	2.5028075682	AA287138	ESTs Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus]	other
5157	2.5017270258	U80034	Human mitochondrial intermediate peptidase precursor (MIPEP) mRNA mitochondrial gene encoding mitochondrial protein complete cds	other
38434	2.5005880672	AA497013	ESTs	?
33269	2.5000262771	W72967	ESTs	other
26991	2.4990009911	AA398284	ESTs	other
7590	2.4948786183	AA173505	ESTs Weakly similar to HYPOTHETICAL 46.1 KD PROTEIN IN PHO2-POL3 INTERGENIC REGION [S.cerevisiae]	other
14960	2.4896232864	U05237	Human fetal Alz-50-reactive clone 1 (FAC1) mRNA complete cds	other

FIG.-8Cj

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE: DESCRIPTOR	ORF STRUCTURAL INFO
13585	2.48666752902	AA455999	ESTs Highly similar to NEUROLYSIN PRECURSOR [Sus scrofa]	other
35901	2.4847673158	AA412151	ESTs	other
38185	2.4826740426	AA487508	Homo sapiens mRNA for KIAA0688 protein complete cds	other
34678	2.4824371274	AA284744	Annexin XI (56kD autoantigen)	other
1424	2.4811113231	J02645	Eukaryotic translation initiation factor 2A	other
16778	2.4800522256	AA047008	ESTs	other
21876	2.4789005203	R43286	EST - RC_R43286	?
17779	2.4695725489	AA149641	ESTs	other
24559	2.4682754649	Z38588	ESTs	other
7781	2.467947166	AA242904	Homo sapiens proline-rich Gla protein 1 (PRGP1) mRNA complete cds	?
7474	2.4677129013	AA126592	ESTs Weakly similar to No definition line found [C.elegans]	other
34290	2.4675279697	AA236866	ESTs	other
5316	2.4673813483	U90905	Human clone 23574 mRNA sequence	TM
10218	2.4645666539	R68884	ESTs Highly similar to HYPOTHETICAL 44.2 KD PROTEIN IN SCO2-MRF1 INTERGENIC REGION	other
18109	2.4634292267	AA188981	[Saccharomyces cerevisiae]	?
6485	2.4613518897	X92098	Homo sapiens retinoblastoma-associated protein HEC mRNA complete cds	?
34954	2.4591845976	AA342959	H.sapiens mRNA for transmembrane protein rnp24	SS, TM
42558	2.4588830205	W74751	EST - RC_AA342959	?
27444	2.4585750563	AA430160	ESTs	other
21284	2.4582503599	R10301	ESTs Weakly similar to F25H9.7 [C.elegans]	other
8920	2.4568596729	AF006265	EST	?
30037	2.4544484116	N27439	Homo sapiens cancer associated surface antigen (RCAS1) mRNA complete cds	other
			ESTs	TM

315 / 454

FIG._8Ck

316 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE: DESCRIPTOR	ORF STRUCTURAL INFO
27602	2.4527990177	AA443702	ESTs Weakly similar to WC2B12.7 [C.elegans]	TM
3390	2.4525517032	S59184	RYK receptor-like tyrosine kinase	TM
25040	2.4523352841	AA010188	ESTs	other
37713	2.4487800271	AA461317	ESTs	other
40477	2.4477660739	N24006	Homo sapiens BAC clone RG300E22 from 7q21-q31.1	other
29382	2.4470532391	H72914	ESTs	other
35521	2.4465885249	AA400831	ESTs	other
20324	2.4464518504	N35406	Phospholipase C beta 4	SS,
18620	2.4460334893	F02506	ESTs	other
21087	2.4406971835	R00186	EST	?
9950	2.4398530157	N71503	ESTs	other
31965	2.4363228422	N93629	ESTs	SS,
15120	2.4345895403	U73524	Human putative ATP/GTP-binding protein (HEAB) mRNA complete cds	TM
28813	2.4339770686	D59257	Human C-1 mRNA complete cds	other
38082	2.4295434916	AA482284	ESTs	other
34723	2.428289395	AA287115	ESTs	other
7960	2.427332589	AA285277	Homo sapiens brain expressed ring finger protein mRNA complete cds	other
18073	2.4231729031	AA180453	EST	other
36755	2.4222443392	AA435698	EST - RC_AA435698	other
18927	2.4187841215	F11087	ESTs	other
3457	2.4186224787	S74728	Antiquitin	TM
38606	2.4177693475	AA598844	ESTs	other
20967	2.41519947	N76086	ESTs	other
24752	2.4141498374	Z40012	Homo sapiens mRNA for KIAA0587 protein complete cds	other
28443	2.4138974256	AA621611	ESTs	?

FIG..8CI

317 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
452	2.4135942278	D38076	RAN binding protein 1	other
11701	2.4134095351	AA253031	Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA complete cds	other
13655	2.412509306	AA458919	ESTs Weakly similar to 26S proteasome subunit p44.5 [H.sapiens]	other
24822	2.4119066031	Z40956	ESTs	other
12672	2.4112720798	AA417067	ESTs	other
4836	2.4106618618	U63717	Human osteoclast stimulating factor mRNA complete cds	other
42200	2.4083828799	T83729	EST - RC_T83729	?
10987	2.4076548868	AA132239	ESTs Highly similar to HYPOTHETICAL 47.4 KD PROTEIN IN SHP1-SEC17 INTERGENIC REGION [Saccharomyces cerevisiae]	other
35672	2.4073821434	AA404995	EST - RC_AA404995	other
6224	2.406310553	X77748	Glutamate receptor metabotropic 3	TM
28395	2.404213441	AA610064	ESTs	other
36390	2.4032664297	AA426291	ESTs Weakly similar to No definition line found [C.elegans]	other
21045	2.4031905697	N93403	ESTs	?
4558	2.4024665999	U49379	Human diacylglycerol kinase epsilon DGK mRNA complete cds	TM
12916	2.3998505067	AA427745	ESTs	other
20850	2.3998090334	N69514	ESTs Weakly similar to oxidoreductase [H.sapiens]	other
29759	2.3986103066	H99972	ESTs	other
36786	2.3971559161	AA435815	Human Clk-associated Rb cyclophilin CARS-Cyp mRNA complete cds	other
31942	2.3947415736	N93185	ESTs	other
7097	2.39382714	AA011452	ESTs	other
39462	2.3936147708	D60063	ESTs	other
14420	2.3919915706	AA600322	ESTs Highly similar to AAC-RICH MRNA CLONE AAC3 PROTEIN [Dictyostelium discoideum]	other

FIG. 8Cm

318 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
34629	2.3916035475	AA282527	EST - RC_AA282527	other
27431	2.3905463084	AA429038	ESTs	TM
6387	2.3904071666	X85372	H.sapiens mRNA for Sm protein F	other
11342	2.3902176276	AA223874	Homo sapiens mRNA for KIAA0704 protein partial cds	other
1497	2.388369765	J04088	Topoisomerase (DNA) II alpha (170kD)	other
9841	2.3841922016	M95724	Centromere autoantigen C	other
11454	2.3820201875	AA233854	ESTs	TM
29950	2.3807499489	N24902	Homo sapiens mRNA for E1B-55kDa-associated protein	TM
8396	2.3807187289	AA426176	ESTs Weakly similar to Similar to S.cerevisiae hypothetical protein L3111 [H.sapiens]	other
32978	2.3805995259	W42788	Human terminal transferase mRNA complete cds	other
27872	2.3784145648	AA459254	ESTs	other
11623	2.3769685069	AA243617	ESTs	other
26582	2.3766957777	AA279768	ESTs	other
22142	2.3761275381	R51382	Homo sapiens mRNA for KIAA0659 protein partial cds	other
13533	2.3759359586	AA454607	ESTs Highly similar to HYPOTHETICAL 40.2 KD PROTEIN K12H4.3 IN CHROMOSOME III [Caenorhabditis elegans]	other
11534	2.3747649776	AA236223	ESTs	other
5976	2.3709397882	X64229	DEK PROTEIN	other
6231	2.3680994679	X78121	Choroideremia	TM
2382	2.3677644584	M16967	Coagulation factor V	other
22887	2.3673034941	T03314	ESTs	TM
24371	2.3663729415	W87415	ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]	other
25286	2.3658134948	AA045261	ESTs	other
9054	2.3647542793	C02472	ESTs Weakly similar to EBV-INDUCED G PROTEIN- COUPLED RECEPTOR 1 PRECURSOR [Homo sapiens]	other

FIG._8Cn

319 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
8163	2.3646144577	AA357394	ESTs	other
12233	2.364077771	AA343513	ESTs Weakly similar to LINE/ig H-chain fusion protein [M.musculus]	SS,
22924	2.3634007127	T08195	ESTs	other
14371	2.361524453	AA599219	ESTs Moderately similar to ALR [H.sapiens]	other
12401	2.3607293644	AA400229	ESTs	other
26169	2.3599633182	AA251089	ESTs Weakly similar to ORF YOR281c [S.cerevisiae]	?
23065	2.3592943521	T23539	ESTs Highly similar to zinc finger protein [M.musculus]	other
20524	2.358218239	N53965	ESTs	other
20837	2.3577032218	N69263	ESTs Highly similar to HEXOKINASE TYPE I [Homo sapiens]	other
18201	2.3573132815	AA195398	Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1 the ADORA2BP adenosine A2b receptor LIKE pseudogene the IRF6	other
7813	2.3566868562	AA248297	ESTs	TM
21195	2.3547018746	R07210	ESTs	other
13377	2.3513919997	AA449720	Homo sapiens clone 24706 mRNA sequence	other
9714	2.3497245732	L44367	ESTs	other
41537	2.3460892052	R55673	ESTs	other
17352	2.34595172	AA100925	ESTs	other
11914	2.3446613991	AA278907	ESTs	?
24890	2.3440589932	Z41634	ESTs	other
28796	2.34344458024	D51272	EST - RC_D51272_s	?
36798	2.342525534	AA435870	ESTs Weakly similar to B0564.1 [C.elegans]	other
22491	2.3409294581	R70012	EST	other
4798	2.3403776443	U61538	Human calcium-binding protein chp mRNA complete cds	other
40847	2.3397210986	N66354	ESTs	other

FIG. 8Co

320 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
15657	2.3392349306	W63627	Small inducible cytokine A5 (RANTES)	TM
24482	2.3374046148	Z38137	ESTs	other
42022	2.3336939603	T53138	Homo sapiens mRNA for hTCF-4	TM
38233	2.3314220199	AA489023	ESTs	other
41221	2.3310635524	R21531	ESTs Weakly similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII [H.sapiens]	other
8053	2.3297250374	AA309880	ESTs	other
363	2.3275393529	D26528	Human mRNA for RNA helicase complete cds	?
26679	2.3241677574	AA281733	ESTs	other
13407	2.3216524472	AA450200	ESTs	TM
17955	2.3180957399	AA166703	ESTs	TM
31858	2.3160841803	N90680	EST	?
24092	2.3151511584	W42845	Homo sapiens protein tyrosine phosphatase PIR1 mRNA complete cds	SS,
16759	2.3118245547	AA046294	ESTs	other
7861	2.311355404	AA252436	Homo sapiens clone 23797 and 23917 mRNA partial cds	other
41176	2.3111568749	R09379	Natural resistance-associated macrophage protein 2	TM
3860	2.3104335895	U13913	Homolog of Drosophila slowpoke (potassium channel - calcium-activated)	TM
40886	2.3077403929	N68149	ESTs Weakly similar to EEIV-INDUCED G PROTEIN- COUPLED RECEPTOR 1 PRECURSOR [Homo sapiens]	other
19428	2.3068982601	H22949	EST	?
36080	2.3048383557	AA417282	EST - RC_AA417282	other
27264	2.3043527378	AA418389	ESTs	other
13600	2.3031968696	AA456286	ESTs	other
13552	2.3026988375	AA454943	ESTs	other
15664	2.3025773291	W67456	ESTs Moderately similar to YY1-associated factor 2 [H.sapiens]	other

FIG..8Cp

321 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
26583	2.3025403178	AA279774	ESTs	?
37434	2.3013886299	AA454149	EST	?
7833	2.2992574443	AA249300	ESTs	other
3674	2.2985613315	U05237	Human fetal A1z-50-reactive clone 1 (FAC1) mRNA complete cds	other
33694	2.2984566375	Z38770	ESTs	other
11178	2.2972286082	AA167436	ESTs	?
16977	2.2912855364	AA064616	ESTs	other
19799	2.290119924	H57330	EST	?
5948	2.2900738182	X63337	EST - X63337	?
42097	2.2881548729	T66318	Isoleucine-tRNA synthetase	?
24247	2.2881065691	W73010	Ribosomal protein L37	other
40879	2.2870463837	N67816	ESTs Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]	other
5875	2.2860441014	X59405	Membrane cofactor protein (CD46 trophoblast-lymphocyte cross-reactive antigen)	?
22325	2.2850330577	R60777	ESTs	other
9621	2.2844572929	J05032	ASPARTYL-TRNA SYNTHETASE	other
9239	2.2823045248	D79100	ESTs	other
41997	2.2818672356	T47788	ESTs	other
31105	2.28091752	N63207	EST	?
39565	2.2794194837	F04320	Replication factor C 37-kD subunit	other
7404	2.2793872556	AA094989	Homo sapiens voltage dependent anion channel protein mRNA complete cds	other
6388	2.2788670475	X85373	H.sapiens mRNA for Sm protein G	other
20263	2.2729348551	N31952	ESTs Moderately similar to HYPOTHETICAL 66.5 KD PROTEIN F02A9.5 IN CHROMOSOME III [Caenorhabditis elegans]	other

FIG.-8Cq

322 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
14529	2.2722894932	AA620307	ESTs	other
21197	2.2718368964	R07320	ESTs	other
28203	2.2692501412	AA490969	ESTs	other
38320	2.2687130032	AA490611	ESTs	other
41625	2.2680307053	R69333	ESTs	other
4674	2.265734645	U54999	Human LGN protein mRNA complete cds	other
28861	2.2637023919	D80037	EST Weakly similar to C50B8.3 [C.elegans]	other
31062	2.2633840539	N62827	ESTs	other
26756	2.2627797292	AA283832	ESTs	other
11567	2.2614480815	AA236747	Homo sapiens mitogen activated protein kinase activated protein kinase gene complete cds	other
25050	2.2605083659	AA011134	ESTs Weakly similar to renin [H.sapiens]	TM
41935	2.2593192037	T29681	Human serine kinase mRNA complete cds	other
26895	2.2582367069	AA292765	H.sapiens mRNA for M-phase phosphoprotein mpp5	other
40585	2.2581993468	N34891	Homo sapiens mRNA for KIAA0595 protein partial cds	other
3343	2.2568482074	M97936	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA	other
42435	2.2532463427	W46994	ESTs	?
5937	2.2489783488	X62534	High-mobility group (nonhistone chromosomal) protein 2	other
21241	2.2477801609	R08617	ESTs	TM
25756	2.2472586561	AA135868	ESTs	TM
34184	2.2459308213	AA227959	Human cysteine protease Mch2 isoform alpha (Mch2) mRNA complete cds	other
8672	2.2450864129	AA477046	ESTs	other
7387	2.2447544716	AA093977	ESTs	other
28822	2.2424116577	D59352	ESTs	TM
18016	2.2410305445	AA173223	ESTs	other

FIG..8Cr

323 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
20843	2.239288723	N69352	Homo sapiens mRNA for ATP-dependent RNA helicase #46 complete cds	other
10054	2.2387950133	R10266	ESTs Highly similar to HYPOTHETICAL GTP-BINDING PROTEIN IN PM140-PAC2 INTERGENIC REGION [Saccharomyces cerevisiae]	other
34094	2.2384154308	AA206088	ESTs	other
41246	2.2380827238	R27296	ESTs	other
22634	2.2346537819	R82837	ESTs	other
19686	2.2319351858	H48502	ESTs	SS,
34568	2.2306030547	AA280609	ESTs Weakly similar to KC2B2.3 gene product [C.elegans]	other
28448	2.2295708871	AA621752	Human 26S proteasome-associated pad1 homolog (POH1) mRNA complete cds	other
20909	2.2284835116	N71704	ESTs	other
651	2.2260753259	D78129	EST - D78129	SS, TM
40409	2.2244318492	H99877	Homo sapiens exportin t mRNA complete cds	other
20340	2.224062527	N38825	ESTs	other
20002	2.2233023294	H93005	EST - RC_H93005	other
37321	2.2209252793	AA451898	ESTs	other
8274	2.2208752623	AA402095	ESTs	other
20221	2.2197714612	N29345	ESTs	other
5792	2.2186801223	X54941	CDC28 protein kinase 1	other
4034	2.21808435	U21858	Human transcription initiation factor TFIID subunit TAFII31 mRNA complete cds	other
36222	2.2149577598	AA421481	ESTs	other
16567	2.2146935655	AA031591	ESTs	other
4721	2.2134595068	U58046	Human mRNA for KIAA0139 gene complete cds	other
28656	2.2125017907	D19708	Human Gu protein mRNA partial cds	TM

FIG._8Cs

324 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
20723	2.2113936194	N66093	ESTs	other
6714	2.2062571749	Y08612	H. sapiens mRNA for Nup88 protein	?
19240	2.205583996	H13265	ESTs	other
36447	2.2050784323	AA428188	ESTs	other
11688	2.202413216	AA252672	Homo sapiens diphthamide biosynthesis protein-2 (DPH2) mRNA complete cds	other
21650	2.2018153311	R37938	Homo sapiens KIAA0440 mRNA partial cds	other
14152	2.2015953698	AA489790	Homo sapiens Ran-GTP binding protein mRNA partial cds	other
42657	2.1975280207	W92771	GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR	other
4642	2.1968027789	U52427	Human RNA polymerase II subunit hSRPB7 mRNA complete cds	?
32779	2.1962611079	W02102	ESTs	TM
38341	2.1951559134	AA490967	ESTs	other
11803	2.1921143838	AA257971	ESTs	other
34835	2.190705129	AA292677	ESTs	TM
39085	2.1895804523	AA620599	ESTs	other
4046	2.1877764122	U22376	MYB PROTO-ONCOGENE PROTEIN	?
11600	2.1876723705	AA242868	ESTs Weakly similar to house-keeping protein [M.musculus]	other
5051	2.1866660566	U76638	Human BRCA1-associated RING domain protein (BARD1) mRNA complete cds	other
33917	2.1864855739	AA167323	ESTs	TM
20674	2.1858972155	N63392	ESTs	TM
41031	2.1768902734	N91246	ESTs	?
25114	2.1759894688	AA020923	EST	?
24711	2.1758363153	Z39645	ESTs	other
4733	2.1721786534	U58658	Human unknown protein mRNA within the p53 intron 1 complete cds	other
4871	2.1712198791	U66033	Human glypican-5 (GPC5) mRNA complete cds	other

FIG. 8Ct

325 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
29733	2.1687028853	H99398	EST	?
23155	2.1678113438	T30550	ESTs	other
34638	2.164515923	AA282987	EST	?
35541	2.1621480372	AA400986	Prothymosin alpha	other
1889	2.1598384252	L20591	Annexin III (lipocortin III)	?
15106	2.1591553963	U68111	PROTEIN PHOSPHATASE INHIBITOR 2	?
40131	2.1583553082	H79779	Homo sapiens histone deacetylase 3 (HDAC3) mRNA complete cds	other
19516	2.158045763	H29207	EST	other
4136	2.1577799237	U28014	ICH-2 PROTEASE PRECURSOR	other
20276	2.1548737104	N32919	ESTs	other
13292	2.1546709291	AA447621	ESTs Highly similar to 40 kD PROTEIN [Borna disease virus]	other
20666	2.154262609	N63165	ESTs	other
6065	2.1526648242	X68560	Sp3 transcription factor	other
18238	2.1516362853	AA205389	ESTs	other
21627	2.1515999154	R37410	EST	?
3438	2.1502571642	S72024	Eukaryotic translation initiation factor 5A	?
34648	2.1498935434	AA283772	ACTIVATOR 1 36 KD SUBUNIT	other
5964	2.1488964343	X63657	Follicular lymphoma variant translocation 1	SS,
13250	2.1466085975	AA446459	ESTs	other
34370	2.1465845856	AA251829	ESTs Weakly similar to HYPOTHETICAL 27.4 KD PROTEIN IN MER2-CPR7 INTERGENIC REGION	other
27996	2.145312871	AA470156	[Saccharomyces cerevisiae]	SS,
4408	2.1398865247	U41745	ESTs Weakly similar to dynein 74K chain cytosolic [R.norvegicus]	other
4187	2.1395632136	U30888	Human PDGF associated protein mRNA complete cds	other
10804	2.1366859886	AA069549	Human tRNA-guanine trans:glycosylase mRNA complete cds ESTs	other

FIG._8Cu

326 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
34552	2.1340290702	AA279985	Human mRNA for KIAA0372 gene complete cds	other
18380	2.1331897016	AA227119	ESTs	other
5223	2.1298428563	U83843	EST - U83843	other
37415	2.1270169134	AA453807	EST	other
14582	2.1260941468	AA621340	ESTs Weakly similar to HYPOTHETICAL 39.6 KD PROTEIN IN MTD1-NUP133 INTERGENIC REGION [Saccharomyces cerevisiae]	other
27756	2.123647107	AA453447	ESTs	other
13787	2.1232866197	AA463745	ESTs Highly similar to PRII-MRNA SPLICING FACTOR RNA HELICASE PRP22 [Saccharomyces cerevisiae]	other
5173	2.1232706565	U81554	Homo sapiens signal recognition particle 72 (SRP72) mRNA complete cds	other
40029	2.1214337319	H68221	Human E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA complete cds	other
19972	2.1193721042	H83639	ESTs	other
23301	2.117519655	T52847	ESTs	other
20504	2.1134521605	N52966	ESTs	other
40145	2.1132200572	H81391	Human mRNA for histamine N-methyltransferase complete cds	other
3461	2.1131164397	S75256	EST - S75256	SS,
41893	2.1124189285	T23611	ESTs	other
39298	2.1092181318	C14805	EST - RC_C14805	other
36021	2.1084566145	AA416876	ESTs Weakly similar to TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521 [H.sapiens]	other
8382	2.1077406838	AA424199	ESTs Weakly similar to C50B8.3 [C.elegans]	other
28288	2.1075593303	AA598447	Homo sapiens exportin t mRNA complete cds	other
5807	2.1071009331	X55740	5' nucleotidase (CD73)	?
19747	2.106109699	H53572	ESTs	other

FIG.-8Cv

327 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
38155	2.1052335506	AA486777	ESTs	TM
924	2.1037724222	HG1112-HT1112	EST - HG1112-HT1112	?
9544	2.1022261514	H72630	ESTs	other
8384	2.1005713227	AA424282	Human 75-kD autoantigen (PM-Sc1) mRNA complete cds	other
25165	2.1005132894	AA027837	Retinitis pigmentosa 3 (X-linked recessive)	SS, TM
24348	2.1000366838	W86469	Tropomyosin alpha chain (skeletal muscle)	?
41401	2.0994968367	R43334	Homo sapiens KIAA0410 mRNA complete cds	other
35340	2.0993762592	AA398900	EST - RC_AA398900	other
10898	2.0990741816	AA112063	ESTs Weakly similar to PRIE-MRNA SPLICING HELICASE BRR2 [S.cerevisiae]	other
381	2.0974305874	D28473	Isoleucine-tRNA synthetase	other
22051	2.0971755	R49047	ESTs Weakly similar to ALU SUBFAMILY J WARNING ENTRY [H.sapiens]	other
3293	2.0965663118	M94893	Testis specific protein Y-linked	TM
11528	2.0954548212	AA236018	ESTs Weakly similar to unknown [S.cerevisiae]	?
11890	2.0952685865	AA278323	Homo sapiens clone 24606 mRNA sequence	TM
13643	2.0952581265	AA458578	Homo sapiens clone 24477 mRNA sequence	other
19927	2.0952547855	H71829	ESTs	other
36511	2.0927695929	AA429632	ESTs	?
2130	2.0925292202	L40407	Homo sapiens thyroid receptor interactor (TRIP9) gene complete cds	?
7193	2.0924678877	AA046768	Homo sapiens clone TUA8 Cri-du-chat region mRNA	TM
5448	2.0921643167	X02751	Neuroblastoma RAS viral (v-ras) oncogene homolog	?
35956	2.0875765163	AA412533	ESTs	other
7525	2.0870133892	AA149259	ESTs	other

FIG. 8Cw

328 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
39592	2.0862891765	F09351	ESTs Weakly similar to weakly similar to S. cervisiae PTM1 precursor [C.elegans]	TM
28029	2.0855738844	AA478479	ESTs	other
18425	2.0855157851	AA232103	ESTs	other
23494	2.0843308862	T70045	ESTs Weakly similar to HYPOTHETICAL 33.2 KD PROTEIN F26A3.7 IN CHROMOSOME I [C.elegans]	other
30882	2.0840312831	N56906	EST	?
32597	2.0839196473	T47333	Human TFIIID subunit TAF1155 (TAFI155) mRNA complete cds	other
33368	2.0838178514	W80814	ESTs	other
10259	2.0829121213	R77527	ESTs	other
21882	2.0825457608	R43365	ESTs	other
20590	2.0820571859	N58146	ESTs	other
12907	2.0807802388	AA427577	ESTs	other
22958	2.0770089467	T10264	ESTs	other
42044	2.0762746251	T58753	ESTs	other
4210	2.0750374179	U31814	Human transcriptional regulator homolog RPD3 mRNA complete cds	other
39	2.074214716	AB003698	Homo sapiens mRNA for Cdc7-related kinase complete cds	other
14350	2.0739236064	AA598831	ESTs	TM
29840	2.0729224128	N21680	ESTs	other
25593	2.0715918096	AA113149	Homo sapiens IPL (IPL) mRNA complete cds	other
26071	2.0708411247	AA236880	Protein phosphatase 2A regulatory subunit B' alpha-1	other
26529	2.0699045563	AA278594	EST	?
12154	2.0692192056	AA291293	ESTs	other
18817	2.0684614007	F10077	ESTs	?
6635	2.0674931973	X99585	H.sapiens mRNA for SMT3B protein	other
6681	2.066065203	Y00971	Phosphoribosyl pyrophosphate synthetase 2	other

FIG. 8Cx

329 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
22077	2.0647745388	R49482	ESTs	other
11752	2.0645929355	AA256042	ESTs	other
41257	2.0634413934	R31680	ESTs	SS,
6904	2.0622381932	Z34897	Histamine receptor H1	TM
16879	2.060262971	AA056538	ESTs	other
38040	2.0595449295	AA481403	ESTs	other
4111	2.0567536207	U26312	Human heterochromatin protein HP1Hs-gamma mRNA complete cds	other
32878	2.0546812272	W37448	ESTs	TM
21743	2.0543668448	R40576	ESTs Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]	?
25968	2.0525018401	AA234935	ESTs	other
24659	2.0506511898	Z39211	Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP) mRNA complete cds	other
38030	2.0505994824	AA481148	ESTs	other
61	2.0484705331	AC002115	Cytochrome c oxidase subunit VIb	?
6306	2.0474040935	X81625	EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1	?
8203	2.0473464771	AA382517	EST - AA382517	other
34357	2.0469305727	AA251430	ESTs Highly similar to RAS-RELATED PROTEIN RAB-10 [Canis familiaris]	other
36972	2.0468599712	AA442767	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein beta polypeptide	?
28156	2.0459278063	AA489057	H.sapiens mRNA for nuclear protein SA-2	other
24434	2.045695222	W92787	ESTs	other
33508	2.0449481783	W88772	Human DNA sequence from cosmid F0811 on chromosome 6. Contains Daxx BING1 Tapasin RGL2 KE2 BING4 BING5 ESTs and CpG islands	other

FIG..8Cy

330 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
37681	2.0449346104	AA460675	H.sapiens mRNA for TRE5	other
27125	2.0448698236	AA405505	Homo sapiens mRNA for putative RNA helicase 3' end	other
3780	2.0445300752	U09851	Zinc finger protein 148 (pHZ-52)	other
9112	2.0443252757	D16611	Coproporphyrinogen oxidase (coproporphyrin harderoporphyria)	TM
8357	2.044244223	AA418921	ESTs Highly similar to RSP5 PROTEIN [Saccharomyces cerevisiae]	other
9133	2.0436113204	D30946	ESTs Highly similar to TRANSLOCON-ASSOCIATED PROTEIN GAMMA SUBUNIT [Rattus norvegicus]	TM
7519	2.0414123824	AA147425	EST - AA147425_s	other
14701	2.0413755305	D59324	ESTs	other
380	2.0411495076	D28423	EST - D28423	?
30571	2.0348528804	N49595	ESTs	other
825	2.0329522889	D87328	Holocarbonylase synthetase (biotin-[propionyl]-Coenzyme A-carboxylase (ATP-hydrolysing)) ligase	TM
27744	2.0318041265	AA452818	ESTs Weakly similar to HYPOTHETICAL PROTEIN HI0034 [Haemophilus influenzae]	other
3997	2.0311208335	U19906	Arginine vasopressin receptor 1 (AVPR1)	?
22717	2.0302732387	R91394	EST - RC_R91394	?
377	2.0289078264	D28364	EST - D28364	other
28581	2.0274006652	C21163	EST	other
11790	2.0269672127	AA256678	ESTs Highly similar to PO1P2 PROTEIN [Saccharomyces cerevisiae]	other
37931	2.0269058272	AA478523	ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	other
24678	2.0209818539	Z39349	ESTs Weakly similar to VACUOLAR ATP SYNTHASE 54 KD SUBUNIT [Saccharomyces cerevisiae]	other

FIG._8Cz

331 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
10940	2.0209035614	AA122217	ESTs Weakly similar to HYFOTHEICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III [C.elegans]	other
13964	2.0207518872	AA479048	ESTs	?
15665	2.019773566	W67631	Homo sapiens clone 24538 mRNA sequence	TM
28379	2.0189373185	AA609710	ESTs	other
13349	2.0172119305	AA449269	ESTs Weakly similar to MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR [Neurospora crassa]	SS,
7322	2.0167797945	AA090692	ESTs Weakly similar to The KIAA0138 gene product is novel. [H.sapiens]	other
29358	2.0165296752	H70641	EST - RC_H70641	?
24230	2.016017562	W72276	ESTs	other
40212	2.0158778189	H88535	Human clone 121711 defective mariner transposon Hsmar2 mRNA sequence	?
729	2.01573779	D83778	Human mRNA for KIAA0194 gene partial cds	other
17951	2.0144787235	AA165526	Homo sapiens bifunctional ATP sulfurylase/adenosine 5'-phosphosulfate kinase mRNA complete cds	other
33943	2.0135799277	AA171739	ESTs	other
5870	2.0118426199	X59244	Zinc finger protein 43 (HTF6)	other
36319	2.0116529739	AA425107	ESTs	other
25654	2.0097423819	AA126951	ESTs Weakly similar to DNA-directed RNA polymerase [D.melanogaster]	other
16344	2.0090457727	AA018907	ESTs	?
8118	2.0090099575	AA328993	ESTs	other
29962	2.0087628098	N25228	ESTs	TM
32236	2.0078250756	R49327	Natural resistance-associated macrophage protein 2	TM
3279	2.0072427596	M94065	DIHYDROOrotate DEHYDROGENASE PRECURSOR	TM
16255	2.0065069683	AA013349	ESTs	other

FIG..8Da

332 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
37972	2.0059209236	AA479215	EST - RC_AA479215	TM
41256	2.005858844	R31577	ESTs	other
34834	2.0050133743	AA292655	ESTs	other
23169	2.0039279023	T33215	ESTs	other
29851	2.0034762995	N22145	ESTs	other
32862	2	W32519	EST	?

FIG._8Db

333 / 454

NEW KEY NUMBER	ACCESSION	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	UNIGENE DESCRIPTOR	
104660	AA007160	23	ESTs	SS
130016	AA055811	14	transmembrane glycoprotein	SS, TM
104954	AA074514	10	ESTs; Moderately similar to (define not available 4753768) [H.sapiens]	Other
105082	AA143763	7	ESTs; Weakly similar to Similarity to S. Pombe BEM1/BUD5 suppressor [C.elegans]	Other
109141	AA176428	7	ESTs	Other
108893	AA135894	6	retinoic acid induced 3	TM
108927	AA143493	5	ESTs; Weakly similar to PLICKSTRIN [H.sapiens]	Other
109027	AA157818	5	Human endogenous retroviral protease mRNA; complete cds	Other
133015	AA047036	4	ESTs	Other
114546	AA056263	4	ESTs; Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]	Other
104974	AA085918	4	H.sapiens HUNK1 mRNA	Other
108695	AA121315	4	ESTs	SS
105049	AA132554	4	ESTs; Moderately similar to myosin heavy chain 12 [H.sapiens]	Other
133834	AA147510	4	Homo sapiens serine protease mRNA; complete cds	Other
109244	AA194237	4	ESTs; Weakly similar to C17H11.6 [C.elegans]	Other
128411	AA007555	3	ESTs; Weakly similar to transformation-related protein [H.sapiens]	SS, TM
114509	AA043551	3	ESTs	Other
104888	AA053660	3	ESTs	Other
114542	AA055768	3	ESTs	SS
132718	AA056731	3	Sjogren syndrome antigen A2 (60kD; ribonucleoprotein autoantigen SS-A/Ro)	Other

FIG._9Aa

334 / 454

NEW KEY NUMBER	ACCESSION	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	UNIGENE DESCRIPTOR	
104953	AA074157	3	ESTs	Other
132784	AA099589	3	GDP dissociation inhibitor 2:	Other
130962	AA102051	3	transmembrane 4 superfamily member 6	SS, TM
134421	AA122386	3	collagen; type V; alpha 2	SS
105035	AA128486	3	ESTs	Other
105039	AA130349	3	ESTs	Other
105062	AA134968	3	ESTs	Other
133617	AA148318	3	Human mRNA for KIAA0069 gene; partial cds	TM
130335	AA156499	3	ESTs; Highly similar to CAMP-DEPENDENT PROTEIN KINASE TYPE II-ALPHA REGULATORY CHAIN [H.sapiens]	Other
105132	AA159501	3	HBV associated factor	Other
109042	AA159525	3	ESTs	Other
109043	AA159605	3	ESTs	Other
132669	AA188378	3	ESTs; Weakly similar to 60S RIBOSOMAL PROTEIN L22 [H.sapiens]	Other
135398	AA194075	3	nuclear receptor coactivator 4	Other
109344	AA213696	3	ESTs	SS
133221	AA235289	3	ESTs; Highly similar to rap2 gene product [H.sapiens]	Other
114496	AA035611	2	ESTs; Weakly similar to IIII ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]	Other
128635	AA043959	2	tropomyosin 4	Other
129912	AA047344	2	ESTs; Weakly similar to WW/rsp5/MWVP domain containing proteins [C.elegans]	Other
104927	AA058855	2	ESTs	SS
132821	AA070724	2	CD44 antigen (homing function and Indian blood group system	Other
108409	AA075578	2	"zm88h3.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:54545 3', mRNA sequence"	Other

FIG..9Ab

335 / 454

NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	Other
133621	2	AA076138	H2A histone family; member Y	Other
108565	2	AA085342	ATPase; Ca++ transporting; cardiac muscle; slow twitch 2	TM
104977	2	AA088228	ESTs	Other
103777	2	AA093131	Homo sapiens PAC clone DJ0167F23 from 7p15	Other
108649	2	AA112540	ESTs	Other
114692	2	AA121995	ESTs; Weakly similar to Similar to potassium channel protein. [C.elegans]	Other
105063	2	AA134985	ESTs	Other
133273	2	AA147725	dendritic cell protein	Other
128515	2	AA149044	ESTs; Highly similar to the KIAA0195 gene is expressed ubiquitously. [H.sapiens]	SS
105182	2	AA191014	ESTs; Weakly similar to Yd-372cp [S.cerevisiae]	Other
109277	2	AA196332	ESTs	Other
132608	2	AA199588	ARP3 (actin-related protein 3; yeast) homolog	Other
109380	2	AA219015	ESTs	Other
130800	2	AA223386	ESTs; Weakly similar to katanin p80 subunit [H.sapiens]	Other
129945	2	AA232104	ESTs; Highly similar to (define not available 4929579) [H.sapiens]	Other
105305	2	AA233609	spindle pole body protein	Other
128924	2	AA234962	ESTs	TM
114895	2	AA236177	Homo sapiens mRNA for KIAA0887 protein; partial cds	Other

FIG..9Ac

336 / 454

NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	
2451	52.6	M21305	Human alpha satellite and satellite 3 junction DNA sequence	?
27090	7.4	AA411502	ESTs; Weakly similar to serine protease [H.sapiens]	?
232	7	D13666	Homo sapiens mRNA for osteoblast specific factor 2 (OSF-2os)	SS
25461	6.8	AA102520	ESTs; Weakly similar to heat shock protein hsp4 homolog [H.sapiens]	TM
27665	6.2	AA453783	ESTs	other
39492	6.2	F13673	ESTs	other
28050	5.6	AA489057	H.sapiens mRNA for nuclear protein SA-2	?
31485	5.6	N71781	ESTs	other
25606	5.4	AA132514	density-regulated protein	other
7000	5	Z74616	collagen; type I; alpha 2	SS
25931	4.7	AA236200	ESTs	other
12118	4.5	AA291528	ESTs	other
32913	4.4	W46810	HMT1 (hnRNP methyltransferase; S. cerevisiae)-like 2	other
26864	4.3	AA393804	H beta 58 homolog	other
22514	4.2	R79392	ESTs	other
25466	4.2	AA112012	lactate dehydrogenase A	other
32276	4.1	R92994	matrix metalloproteinase 12 (macrophage elastase)	TM
32465	4.1	T32108	ESTs	SS
22430	4	R71082	TFAR19 novel apoptosis-related gene	other
30052	4	N32586	ESTs; Weakly similar to Ydr339cp [S.cerevisiae]	other
28354	3.9	C14037	ESTs; Weakly similar to Yel7c-ap [S.cerevisiae]	?
29604	3.9	H98655	Homo sapiens gene for NB31; complete cds	TM
27592	3.8	AA449417	Homo sapiens mRNA for putative glucosyltransferase; partial cds	TM
28691	3.8	D51276	STATHMIN	other
19100	3.7	H10933	ESTs	other

FIG. 10Aa

337 / 454

NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	
5891	3.5	X60486	H4 histone family; member G	?
12288	3.5	AA398243	ESTs; Highly similar to RSP5 PROTEIN [Saccharomyces cerevisiae]	other
23629	3.5	T88700	ESTs	other
25951	3.5	AA236672	ESTs; Weakly similar to DFS7 [H.sapiens]	other
477	3.4	D38583	Human mRNA for calgizzain; complete cds	?
11193	3.4	AA186897	ESTs	TM
27193	3.4	AA421562	Homo sapiens secreted cement gland protein XAG-2 homolog (hAG-2/R)	SS
32899	3.4	W45728	ESTs; Highly similar to HETEROGENEOUS NUCLEAR RIBONUCLEOPR	other
9576	3.3	J03464	collagen; type I; alpha 2	SS
10506	3.3	AA027086	ESTs; Highly similar to HYPOTHETICAL 1.4 KD PROTEIN IN UBPS-SPT	other
22064	3.3	R51309	ESTs	other
39217	3.3	C21242	calponin 2	other
2613	3.2	M29540	CARCINOEMBRYONIC ANTIGEN PRECURSOR	TM
27583	3.2	AA449068	ESTs	TM
40031	3.2	H83442	catechol-O-methyltransferase	other
10131	3.1	R56183	eukaryotic translation initiation factor 3; subunit 6 (48kD)	other
25154	3.1	AA043353	ESTs; Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1	other
25821	3.1	AA164643	ESTs; Weakly similar to Ki- /57 intracellular antigen [H.sapiens]	other
26004	3.1	AA243297	ESTs; Weakly similar to PEANUT PROTEIN [Drosophila melanogaster]	other
27055	3.1	AA406542	ESTs	other

FIG. 10Ab

338 / 454

NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	
10844	3	AA100719	non-specific cross reacting antigen	other
11358	3	AA232104	ESTs	other
17389	3	AA121315	ESTs	other
17415	3	AA122386	"Collagen, type V, alpha 2"	?
23772	3	T92735	ESTs	TM
25331	3	AA070947	tropomyosin 4	other
25358	3	AA076138	histone macroH2A1.2	other
27039	3	AA406145	ESTs	SS, TM
27261	3	AA425544	Homo sapiens clone 23685 mRNA; complete cds	other
28795	3	D80946	SFRS protein kinase 1	other
32192	3	R67275	collagen; type XI; alpha 1	other
3083	2.9	M77349	transforming growth factor; beta-induced; 68kD	SS
5519	2.9	X06700	collagen; type III; alpha 1 (Ehlers-Danlos syndrome type IV; autosomal do	other
5562	2.9	X12876	keratin 18	other
11618	2.9	AA251902	Homo sapiens lysophospholipase (LPL1) mRNA; complete cds	other
17686	2.9	AA147725	Homo sapiens GA17 protein mRNA; complete cds	other
18024	2.9	AA188378	ESTs; Highly similar to 6S RIBOSOMAL PROTEIN L22 [Rattus norvegicus]	other
20941	2.9	N90933	ESTs	other
13612	2.8	AA458899	ESTs; Highly similar to (define not available 412715) [H.sapiens]	TM
17799	2.8	AA157818	Human endogenous retroviral protease mRNA; complete cds	other
25344	2.8	AA075182	Sjogren syndrome antigen A2 (6kD; ribonucleoprotein autoantigen SS-A/R	?
25583	2.8	AA131162	ESTs	other
32170	2.8	R61297	eukaryotic translation initiation factor 3; subunit 6 (48kD)	other
33586	2.8	Z38656	coatomer protein complex; subunit alpha	SS

FIG. 10Ac

339 / 454

NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	
2396	2.7	M18728	non-specific cross reacting antigen	other
3251	2.7	M93036	membrane component; chromosomal 4; surface marker (35kD glycoprotein)	other
8158	2.7	AA372630	Homo sapiens GW112 protein (GW112) mRNA; complete cds	other
9207	2.7	D79052	ESTs; Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 GAMM	other
15051	2.7	U64661	Human poly(A)-binding protein processed pseudogene3	?
15614	2.7	W63627	ESTs; Moderately similar to !!! ALU SUBFAMILY SP WARNING ENTRY !!	TM
25323	2.7	AA070485	Homo sapiens clone 23967 unknown mRNA; partial cds	other
25329	2.7	AA070827	ESTs; Weakly similar to KIAA18 [H.sapiens]	TM
25549	2.7	AA127058	ESTs; Weakly similar to predicted using GeneFinder [C.elegans]	TM
25584	2.7	AA131165	heterogeneous nuclear ribonucleoprotein A2/B1	other
27468	2.7	AA441971	Homo sapiens mRNA for KIAA494 protein; complete cds	TM
32012	2.7	R31180	ESTs	?
38087	2.7	AA488991	Homo sapiens chaperonin containing t-complex polypeptide 1; beta subunit	other
38457	2.7	AA598714	Lon protease-like protein	other
39421	2.7	F03974	H.sapiens mRNA for Sop2p-like protein	other
3758	2.6	U09587	glycyl-tRNA synthetase	other
8952	2.6	C00038	ESTs	TM
12978	2.6	AA431191	ESTs	other
17627	2.6	AA135894	"Homo sapiens putative G protein-coupled receptor (RAIG1), Retinoic acid i	TM
20752	2.6	N68921	ESTs; Weakly similar to necgenin [H.sapiens]	other
22954	2.6	T17185	ESTs	TM
25808	2.6	AA161161	ESTs	other

FIG..10Ad

340 / 454

NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	
27169	2.6	AA418879	proteasome (prosome; macropain) 26S subunit; non-ATPase; 11	other
28096	2.6	AA490962	ESTs; Moderately similar to ubiquitous TPR motif; Y isoform [H.sapiens]	other
28705	2.6	D54289	ESTs	other
33593	2.6	Z39041	ESTs; Weakly similar to DNA-DIRECTED RNA POLYMERASE III LARGE	TM
37363	2.6	AA455521	E2F transcription factor 5; p13-binding	other
39170	2.6	C15324	ESTs	SS, TM
39251	2.6	D20002	"HUMGS972 Human promyelocyte Homo sapiens cDNA clone pm2344 3',	other
2767	2.5	M37583	H2A histone family; member Z	other
5468	2.5	X04347	heterogeneous nuclear ribonucleoprotein A1	other
9243	2.5	D82348	Homo sapiens mRNA for 5-aminoimidazole-4-carboxamide-1- beta-D-ribose	other
14791	2.5	T35725	ESTs; Highly similar to HYPOTHETICAL 44.2 KD PROTEIN IN SCO2-MR	other
14804	2.5	T48195	eukaryotic translation initiation factor 3; subunit 3 (gamma; 4kD)	other
16974	2.5	AA070724	CD44 antigen (homing function and Indian blood group system)	other
20031	2.5	N21085	Homo sapiens androgen receptor associated protein 24 (ARA24) mRNA; c	?
25484	2.5	AA112679	ESTs; Weakly similar to alternatively spliced product using exon 13A [H.sa]	TM
26830	2.5	AA347359	lysosome (renal amyloidosis)	SS
28068	2.5	AA490212	histone macroH2A1.2	other
30071	2.5	N33011	replication protein A3 (14kD)	other

FIG. 10Ae

341 / 454

NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	
32740	2.5	W31600	von Hippel-L
35870	2.5	AA416785	heterogeneo
41908	2.5	T59161	Thymosin; b
6011	2.4	X66401	proteasome
			(large multift
9201	2.4	D63079	ESTs; Weakl
			REDUCTAS
9218	2.4	D79891	ESTs
10085	2.4	R32993	ESTs; Highly
			CYTOPLASI
10253	2.4	R82411	DEK gene
11107	2.4	AA159501	ESTs; Model
11846	2.4	AA262969	ESTs; Weakl
			L8167.12 lik
12767	2.4	AA424346	ESTs; Weakl
			UROIIIS [H.s
13772	2.4	AA464708	ESTs; Weakl
			exon 13A [H.sa
16728	2.4	AA053102	cadherin 17; LI cadherin (liver-intestine)
17774	2.4	AA156243	ESTs; Highly similar to (define not available 412715)
			[H.sapiens]
21386	2.4	R24059	ESTs
25433	2.4	AA099589	GDP dissociation inhibitor 2
25603	2.4	AA132032	Homo sapiens CAGH1a (CAGH1) mRNA; partial cds
25791	2.4	AA159980	ELKL motif kinase
26153	2.4	AA252627	ESTs
26852	2.4	AA365527	ESTs; Weakly similar to TLS-associated protein TASR [H.sapiens]

FIG. 10A

342 / 454

NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE: DESCRIPTOR	
27122	2.4	AA416877	ESTs	other
28365	2.4	C14090	actin; gamma 1	other
28626	2.4	D25560	Homo sapiens DNA from chromosome 19-cosmid R3879 containing USF2;	other
28687	2.4	D51241	Homo sapiens mRNA for putative vacuolar proton ATPase membrane sect	SS, TM
29850	2.4	N24968	vacuolar H(+)-ATPase subunit	other
32892	2.4	W45457	ESTs; Moderately similar to neuronal thread protein AD7c-NTP [H.sapiens]	other
33811	2.4	AA173143	heterogeneous nuclear ribonucleoprotein G	other
40121	2.4	H93492	ESTs; Highly similar to villin [H.sapiens]	other
40141	2.4	H94877	ESTs; Moderately similar to putative G-binding protein [H.sapiens]	other
40167	2.4	H96237	collagen; type XI; alpha 1	other
446	2.3	D38073	minichromosome maintenance deficient (S. cerevisiae) 3	other
3530	2.3	S81914	DIFFERENTIATION-DEPENDENT GENE 2	other
7835	2.3	AA252436	Homo sapiens lysophospholipase (LPL1) mRNA; complete cds	other
10898	2.3	AA121879	proteasome (prosome; macropain) subunit; beta type; 9 (large multifunction	other
10965	2.3	AA134138	ESTs; Highly similar to CYTOSOL AMINOPEPTIDASE [Bos taurus]	other
11015	2.3	AA143763	ESTs; Weakly similar to Similarity to S. Pombe BEM1/BUD5 suppressor [C	other
11895	2.3	AA279420	ESTs; Highly similar to (define not available 433735) [H.sapiens]	TM
13386	2.3	AA451676	ESTs	other
15464	2.3	W28391	proliferation-associated 2G4; 38kD	other
17619	2.3	AA135406	ESTs	other

FIG.- 10Ag

343 / 454

NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	
18225	2.3	AA213696	ESTs	other
20450	2.3	N53927	ESTs; Weakly similar to phenylalkylamine binding protein [H.sapiens]	?
25308	2.3	AA065227	ESTs; Weakly similar to coded for by C. elegans cDNA yk1c1.3 [C.elegans]	other
26590	2.3	AA282151	ESTs; Weakly similar to predicted using Genefinder [C.elegans]	other
27624	2.3	AA452112	Homo sapiens mRNA for putative thioredoxin-like protein	other
27792	2.3	AA460359	ESTs; Weakly similar to DNA-DIRECTED RNA POLYMERASE II 14 KD [P]	?
28231	2.3	AA600153	DEK gene	other
28722	2.3	D59711	ESTs	other
30363	2.3	N47956	eukaryotic translation initiation factor 3; subunit 3 (gamma; 4kD)	other
32928	2.3	W47620	ESTs; Weakly similar to reverse transcriptase related protein [H.sapiens]	other
39585	2.3	H11320	Homo sapiens HRIHFB2.115 mRNA; partial cds	TM
40175	2.3	H96665	peptidylprolyl isomerase I3 (cyclophilin B)	other
40366	2.3	N26691	ESTs; Highly similar to (d:afline not available 467914) [H.sapiens]	other
40733	2.3	N67422	ESTs; Weakly similar to 25 kDa trypsin inhibitor [H.sapiens]	other
4918	2.2	U68105	poly(A)-binding protein-like 1	?
5165	2.2	U81607	GRAVIN	other
12242	2.2	AA372018	ESTs	other
13154	2.2	AA442768	Homo sapiens inner mitochondrial membrane translocase Tim23 (TIM23)	?
14276	2.2	AA598450	ESTs	other
15721	2.2	W95348	ESTs	TM
20588	2.2	N62945	Homo sapiens hMmTRA1b mRNA; complete cds	TM
24021	2.2	W42957	ESTs	other
24250	2.2	W84712	calumenin	other

FIG.. 10Ah

344 / 454

NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	
25245	2.2	AA055768	ESTs	SS
25430	2.2	AA099429	SPLICING FACTOR U2AF 35 KD SUBUNIT	TM
25562	2.2	AA128904	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	other
28745	2.2	D60485	caldesmon 1	other
31997	2.2	R20669	tumor rejection antigen (gp96) 1	other
32491	2.2	T47333	Human TFIIID subunit TAF1155 (TAF1155) mRNA; complete cds	other
32636	2.2	T93807	high-mobility group (non-histone chromosomal) protein 1	other
37703	2.2	AA476237	ESTs; Weakly similar to uroporphyrinogen III synthase; UROIII S [H.sapien]	TM
215	2.1	D13627	Human mRNA for KIAA2 gene; complete cds	TM
2449	2.1	M21259	small nuclear ribonucleoprotein polypeptide E	?
3205	2.1	M88458	ER LUMEN PROTEIN RETAINING RECEPTOR 2	TM
4197	2.1	U31556	E2F transcription factor 5; p13-binding	other
4811	2.1	U62962	eukaryotic translation initiation factor 3; subunit 6 (48kD)	other
5417	2.1	X01060	transferrin receptor (p9; CD71)	TM
6334	2.1	X83228	cadherin 17; LI cadherin (liver-intestine)	SS, TM
6605	2.1	X99133	NEUTROPHIL GELATINASE-ASSOCIATED LIPOCALIN PRECURSOR	?
10471	2.1	AA024482	ESTs; Highly similar to KERATIN; TYPE I CYTOSKELETAL 14 [Homo sa	other
11027	2.1	AA148318	Human mRNA for KIAA68 gene; partial cds	TM
11116	2.1	AA161292	INTERFERON-ALPHA INDUCED 11.5 KD PROTEIN	other
11540	2.1	AA236972	ESTs; Moderately similar to ALU SUBFAMILY J WARNING ENTRY !!!!	other
11937	2.1	AA280865	ESTs; Weakly similar to Similarity to Yeast hypothetical protein YOR3160	other

FIG.-10Ai

345 / 454

NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	
17312	2.1	AA111889	pigment epithelium-derived factor	other
19286	2.1	H18947	ESTs	other
20122	2.1	N26259	ESTs; Weakly similar to uroporphyrinogen III synthase; UROIII [H.sapien]	other
20946	2.1	N91492	Homo sapiens clone 628 unknown mRNA; complete sequence	other
20997	2.1	N98464	ESTs	other
27106	2.1	AA412452	ESTs	other
28036	2.1	AA488433	ESTs; Weakly similar to deduced amino acid sequence is highly homologous	other
28167	2.1	AA521256	ESTs; Highly similar to nuclear pore complex protein NUP17 [R.norvegicus]	other
28336	2.1	AA621604	ESTs	other
28719	2.1	D59570	ESTs	other
28886	2.1	F04674	Homo sapiens mRNA for KIAA746 protein; partial cds	other
32124	2.1	R48608	eukaryotic translation initiation factor 3; subunit 7 (zeta; 66/67kD)	other
33433	2.1	W90444	ESTs; Highly similar to (define not available 4454524) [H.sapiens]	other
33564	2.1	W96151	ESTs; Moderately similar to ganglioside-induced differentiation associated	?
35778	2.1	AA412270	ESTs	other
38588	2.1	AA608751	cathepsin B	other
39301	2.1	D57317	Human transcriptional coactivator PC4 mRNA; complete cds	SS
39945	2.1	H73484	ESTs; Weakly similar to similar to Yeast hypothetical protein L8167.12 like	SS, TM
39977	2.1	H78323	Homo sapiens E2F-related transcription factor (DP-1) mRNA; complete cds	other
40376	2.1	N27198	ESTs	other

FIG. 10A

346 / 454

NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	
41795	2.1	T28799	ESTs; Highly similar to TYROSINE-PROTEIN KINASE RECEPTOR EPH-	TM
1714	2	L09604	proteolipid protein 2 (colonic epithelium-enriched)	TM
2001	2	L33930	"Homo sapiens CD24 signal transducer mRNA, complete cds and 3' region	TM
3278	2	M94556	single-stranded DNA-binding protein	other
4145	2	U28749	high-mobility group (nonhistone chromosomal) protein isoform I-C	TM
8149	2	AA364267	ESTs; Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN C	other
9844	2	N33807	ESTs; Highly similar to NEDD-4 PROTEIN [Homo sapiens]	other
14032	2	AA486092	ESTs; Weakly similar to CH-TOG PROTEIN [H.sapiens]	TM
16395	2	AA025673	ESTs; Moderately similar to (define not available 416878) [H.sapiens]	TM
17327	2	AA112540	ESTs	TM
23083	2	T30881	ubiquitin-conjugating enzyme E2E 1 (homologous to yeast UBC4/5)	other
25625	2	AA133969	ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens]	other
28073	2	AA490494	ESTs	other
28700	2	D53139	ribosomal protein S28	other
29095	2	H27188	collagen-binding protein 2: (collagen 2)	other
32191	2	R67083	calnexin	SS, TM
32897	2	W45664	5' nucleotidase (CD73)	other
10782	1.6	AA074880	ESTs; Weakly similar to HYPOTHETICAL 85. KD PROTEIN IN CPA2-ATP	other
27795	1.6	AA460454	ESTs; Weakly similar to KIAA512 protein [H.sapiens]	other

FIG. 10Ak

347 / 454

NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	
28706	1.6	D54296	Human mRNA for KIAA255 gene; complete cds	TM
36414	1.6	AA430186	ESTs	other
9979	1.5	N91087	ESTs; Weakly similar to F55A12.9 [C.elegans]	other
9987	1.5	N95507	ESTs; Weakly similar to KIAA319 [H.sapiens]	TM
10656	1.5	AA047290	ESTs	other
14977	1.5	U37546	apoptosis inhibitor 1	TM
27065	1.5	AA410294	Human mRNA for KIAA336 gene; complete cds	other
29278	1.5	H72948	biglycan	SS
31917	1.5	N98238	ESTs	other
38272	1.5	AA496533	ESTs	other
41396	1.5	R55342	CD68 antigen	other
41966	1.5	T67710	ESTs	other
8439	1.4	AA436304	Homo sapiens androgen receptor associated protein 24 (ARA24) mRNA; c	?
10311	1.4	AA001936	ESTs	other
10859	1.4	AA112149	ESTs	other
11279	1.4	AA213410	ESTs	SS
13548	1.4	AA456033	ESTs; Highly similar to HYPOTHETICAL 1.4 KD PROTEIN IN UB5-SPT	other
14340	1.4	AA599653	Homo sapiens TCFL5 mRNA for transcription factor-like 5; complete cds	other
32180	1.4	R63727	ESTs	other
35187	1.4	AA398722	ESTs	other
37254	1.4	AA453483	ESTs	TM
1344	1.3	HG4757-	"Oncogene Mll-Af4, Fusion Activated"	other
		HT5207		
5397	1.3	V01516	KERATIN; TYPE II CYTOSKELETAL 6D	SS, TM

FIG. 10A1

348 / 454

NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	
16272	1.3	AA018922	core promoter element binding protein	other
23427	1.3	T70356	ESTs; Highly similar to POLYPROTEIN [Simian sarcoma virus]	other
25718	1.3	AA150741	gene with multiple splice variants near HD locus on 4p16.3	other
33499	1.3	W93403	ESTs	other
36574	1.3	AA434454	ESTs; Weakly similar to orf; hypothetical protein [E.coli]	SS
41548	1.3	R82846	ESTs	other
2386	1.2	M17863	insulin-like growth factor 2 (somatomedin A)	TM
6388	1.2	X86371	lethal giant larvae (Drosophila) homolog 1	other
24427	1.2	Z38208	ESTs	other
27089	1.2	AA411473	adducin 1 (alpha)	other
33177	1.2	W73195	ESTs	other
34852	1.2	AA347691	ESTs	?
35325	1.2	AA400273	ESTs	other
36609	1.2	AA435668	ESTs; Weakly similar to putative p15 [H.sapiens]	other
38477	1.2	AA598939	ESTs	other
40975	1.2	R02547	ESTs	other
41874	1.2	T51150	ESTs	other
8235	1.1	AA401047	Homo sapiens mRNA for neuropsin; complete cds	other
9772	1.1	M81349	SERUM AMYLOID A-4 PROTEIN PRECURSOR	SS
14758	1.1	S83198	BPLP	other
15831	1.1	X90579	H.sapiens DNA for cyp related pseudogene	?
20656	1.1	N66289	ESTs	other
24891	1.1	AA004502	cerebroside (3'-phosphoadenylylsulfate:galactosylceramide 3') sulfotransfer	TM
29045	1.1	H13649	ESTs	other
31584	1.1	N74690	ESTs	TM

FIG. 10Am

349 / 454

NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	
31640	1.1	N78784	Homo sapiens BimEL mRNA; complete cds	other
35293	1.1	AA400013	EST	other
37583	1.1	AA461499	ESTs	other
37852	1.1	AA479896	ESTs	other
38397	1.1	AA521342	ESTs	other
38652	1.1	AA609018	ESTs	other
40397	1.1	N29963	ESTs; Moderately similar to !!!! ALU CLASS C WARNING ENTRY !!!! [H.sa	other
40488	1.1	N40559	ESTs; Highly similar to LEUKOTOXIN SECRETION ATP- BINDING PROT	other
41231	1.1	R41772	EST	other
41333	1.1	R48580	ESTs	other
3255	1	M93143	"Homo sapiens plasminogen-like protein (PLGL) mRNA, complete cds"	other
5742	1	X53065	Accession not listed in Genbank	?
6007	1	X66363	SERINE/THREONINE-PROTEIN KINASE PCTAIRE-1	other
15233	1	W04960	ESTs	other
15262	1	W17304	Homo sapiens mRNA for KIAA97 protein; complete cds	other
15363	1	W26847	ESTs; Highly similar to MITOCHONDRIAL RNA SPLICING PROTEIN MS	other
15606	1	W58725	mitogen-activated protein kinase-activated protein kinase 2	TM
18435	1	AA233898	ESTs	other
21736	1	R41999	ESTs	TM
25306	1	AA065081	"zm13a3.s1 Stratagene pancreas (#93728) Homo sapiens cDNA clone IMA	other
29111	1	H40486	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.s	other

FIG. 10An

350 / 454

NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	
34743	1	AA302772	ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens]	other
34801	1	AA342526	ESTs; Moderately similar to unknown [H.sapiens]	other
35355	1	AA400521	ESTs	other
36940	1	AA446449	ESTs	other
39221	1	C21330	ESTs	other
1322	0.9	HG4535- HT4940	Dematin	other
9982	0.9	N94146	ESTs	other
10084	0.9	R32932	ESTs	other
11701	0.9	AA255546	ESTs	other
12088	0.9	AA287566	Human mRNA for KIAA187 gene; complete cds	other
15267	0.9	W19098	ESTs	other
15901	0.9	Z20905	immunoglobulin superfamily; member 3	SS
21906	0.9	R45512	ESTs	other
22002	0.9	R49459	ESTs	other
23136	0.9	T40827	ESTs	other
28673	0.9	D45719	ESTs	other
29159	0.9	H60824	ESTs	other
32610	0.9	T89122	Human clone 23732 mRNA; partial cds	SS, TM
32674	0.9	W02129	EST	other
35426	0.9	AA401409	ESTs	other
38504	0.9	AA599209	ESTs; Moderately similar to neuronal thread protein AD7c-NTP [H.sapiens]	other
244	0.8	D14446	fibrinogen-like 1	TM
14204	0.8	AA496980	ESTs	other
25250	0.8	AA056210	ESTs	other
9971	0.7	N87590	ESTs	other

FIG.. 10Aa

351 / 454

NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	
20461	0.7	N54429	ESTs	other
41029	0.7	R08615	homogentisate 1;2-diox/genase (homogentisate oxidase)	other
41985	0.6	T71012	fibrinogen; B beta polypeptide	SS, TM

FIG. 10Ap

352 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
134804	12.3	L37036	small inducible cytokine subfamily B (Cys-X-Cys); member 5 (epithelial-derived neutrophil-activating peptide 78)	TM
130617	11.4	M90516	glutamine-fructose-6-phosphate transaminase 1	TM
104209	10.6	AB000221	small inducible cytokine subfamily A (Cys-Cys); member 18; pulmonary and activation-regulated ESTs	SS
109991	10	H09813	ESTs	TM
124315	8.3	H94892	v-rat simian leukemia viral oncogene homolog A (ras related)	Other
132977	8.2	U28686	RNA binding motif protein 3	Other
130407	7.4	N29888	ESTs	Other
116176	6.6	AA463725	ESTs; Weakly similar to KIAA0226 [H.sapiens]	Other
119271	6.5	T16387	ESTs	Other
134711	6.5	X04011	cytochrome b-245; beta polypeptide (chronic granulomatous disease)	TM
134326	6.1	U16306	"Human chondroitin sulfate proteoglycan versican V splice-variant precursor peptide mRNA, complete cds"	Other
125852	5.9	H09290	ESTs; Weakly similar to unknown [H.sapiens]	SS, TM
112169	5.9	R48589	ESTs	TM
132528	5.9	AA283006	chromosome-associated polypeptide C	Other
134367	5.7	X54199	phosphoribosylglycinamide formyltransferase; phosphoribosylglycinamide synthetase; phosphoribosylaminoimidazole synthetase	Other
111929	5.2	R40057	prominin (mouse)-like 1	SS, TM
102165	5	U18321	Death associated protein 3	Other
130441	5	U35835	protein kinase; DNA-activated; catalytic polypeptide	Other
133282	5	U52960	SRB7 (suppressor of RNA polymerase B; yeast) homolog	Other
100783	4.9	HG3748- HT4018	"Basic Transcription Factor, 44 Kda Subunit"	Other

FIG. 11Aa

353 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
122223	4.9	AA436158	ESTs	Other
104660	4.8	AA007160	ESTs	SS
113702	4.8	T97307	ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	Other
101185	4.7	L19872	aryl hydrocarbon receptor	Other
105308	4.7	AA233744	ESTs	Other
107168	4.7	AA621540	ESTs	Other
101201	4.6	L22524	matrix metalloproteinase 7 (matrilysin; uterine)	SS
101809	4.5	M86849	"Homo sapiens connexin 26 (GJB2) mRNA, complete cds"	TM
101478	4.5	M23379	RAS p21 protein activator (GTPase activating protein) 1	Other
104695	4.5	AA012953	ESTs	Other
100365	4.4	D78611	mesoderm specific transcript (mouse) homolog	TM
126819	4.3	AA305536	"EST176522 Colon carcinoma (Caco-2) cell line II Homo sapiens cDNA 5' end, mRNA sequence."	Other
101880	4.3	M97925	defensin; alpha 5; Paneth cell-specific	SS
126838	4.2	AA858097	pigment epithelium-derived factor	Other
101684	4.2	M63256	cerebellar degeneration-related protein (62kD)	Other
117634	4.2	N36421	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	Other
132109	4.1	AA599801	ESTs	Other
115054	4.1	AA252863	ESTs	Other
106553	4	AA454967	ESTs	Other
119717	3.9	W69134	ESTs	Other
131945	3.9	M87339	replication factor C (activator 1) 4 (37kD)	Other
128790	3.9	AA291725	secreted frizzled-related protein 4	SS
120562	3.8	AA280036	ESTs; Weakly similar to W01A6.c [C.elegans]	SS
109517	3.7	D60799	ESTs	Other

FIG. 11Ab

354 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
102618	3.7	U65932	extracellular matrix protein 1	SS
106286	3.7	AA434441	frizzled (Drosophila) homolog 7	Other
133640	3.6	D83004	ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13)	Other
100335	3.6	D63391	platelet-activating factor acetylhydrolase; isoform Ib; gamma subunit (29kD)	Other
104720	3.6	AA018441	ESTs	Other
107348	3.6	U43701	ribosomal protein L23a	Other
134989	3.6	AA236324	ESTs; Weakly similar to !!!! ALU CLASS A WARNING	SS
111345	3.6	N89820	ENTRY !!!! [H.sapiens]	Other
107053	3.6	AA600147	ESTs	Other
107240	3.5	D59368	ESTs	Other
107129	3.5	AA620553	flap structure-specific endonuclease 1	Other
134846	3.5	AA431505	Homo sapiens mRNA for putative Sqv-7-like protein; partial	TM
101897	3.5	S58544	sperm associated antigen	Other
107151	3.5	AA621169	ESTs	Other
106012	3.4	AA411621	ESTs	Other
101950	3.4	S79219	propionyl Coenzyme A carboxylase; alpha polypeptide	Other
116844	3.4	H64938	ESTs	Other
128025	3.4	AA937173	ESTs	TM
106785	3.4	AA478587	leukemia associated gene 1; candidate tumor suppressor frequently deleted in B-cell chronic lymphocytic leukemia (B-CLL)	Other
104518	3.4	R09815	proteasome (prosome; macropain) 26S subunit; ATPase; 5	Other
117667	3.4	N39214	ser-Thr protein kinase related to the myotonic dystrophy protein kinase	Other

FIG. 11Ac

355 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
104954	3.3	AA074514	ESTs; Moderately similar to (define not available 4753768) [H.sapiens]	Other
105372	3.3	AA236481	ESTs	Other
104896	3.3	AA054228	ESTs	Other
113485	3.3	T87863	ESTs	Other
127003	3.3	AA550806	ESTs; Weakly similar to (define not available 3882151) [H.sapiens]	TM
100305	3.3	D50487	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 8 (RNA helicase)	SS
134722	3.2	W47183	ESTs; Weakly similar to !!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!! [H.sapiens]	Other
126801	3.2	AA512902	ESTs	SS, TM
133503	3.2	M33195	Fc fragment of IgE; high affinity I; receptor for; gamma polypeptide	SS, TM
132183	3.2	L19183	Human MAC30 mRNA; 3' end	TM
105298	3.2	AA233459	ESTs	TM
111046	3.2	N55514	ESTs; Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]	TM
135309	3.2	D25984	ESTs	SS
102808	3.2	U90426	nuclear RNA helicase; DEC:D variant of DEAD box family	Other
100552	3.1	HG2167- HT2237	"Protein Kinase Ht31, Camp-Dependent"	Other
127652	3.1	AA804487	ESTs	Other
116127	3.1	AA459703	ESTs; Moderately similar to coded for by C. elegans cDNA CEESD64F [C.elegans]	TM
131904	3.1	AA143019	ESTs; Highly similar to surface 4 integral membrane protein [H.sapiens]	TM
126547	3.1	U47732	transmembrane 4 superfamily member 3	Other
102823	3.1	U90914	carboxypeptidase D	SS

FIG. 11Ad

356 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
132298	3.1	N41849	Homo sapiens cytokine receptor related protein 4 (CYTOR4) mRNA; complete cds	Other
127445	3.1	AA906286	ESTs	Other
134395	3.1	L09717	lysosomal-associated membrane protein 2	SS, TM
105743	3.1	AA293300	ESTs; Weakly similar to semaphorin C [M.musculus]	Other
125827	3.1	AI471525	YY1 transcription factor	Other
101229	3.1	L27943	cytidine deaminase	Other
102306	3	U38317	defensin; alpha 6; Paneth cell-specific	SS
107318	3	T74445	"yc82f8.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:2242 5', mRNA sequence"	Other
120983	3	AA398209	EST	Other
134700	3	AA481414	golgi SNAP receptor complex member 1	TM
131216	3	D31058	ESTs	SS
127565	3	D79516	"HUM272B04B Human aorta polyA+ (TFujiwara) Homo sapiens cDNA clone GEN-272B04 5', mRNA sequence."	Other
106882	2.9	AA489009	ESTs	Other
130874	2.9	T08287	ESTs	Other
101275	2.9	L37936	Ts translation elongation factor; mitochondrial	Other
111179	2.9	N67239	ESTs	Other
126086	2.9	H70975	"yr73g01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:210960 5', mRNA sequence."	Other
105365	2.9	AA236275	ESTs	Other
118789	2.9	N75416	ESTs	Other
115117	2.9	AA256492	H.sapiens PAP mRNA	Other
100484	2.9	HG1103-	"Guanine Nucleotide-Binding Protein Ral, Ras-Oncogene Related"	Other
101300	2.9	HT1103 L40391	Homo sapiens (clone s153) mRNA fragment	Other

FIG. 11Ae

357 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
103075	2.9	X59543	ribonucleotide reductase M1 polypeptide	Other
132164	2.8	U84573	procollagen-lysine; 2-oxo;glutarate 5-dioxygenase (lysine hydroxylase) 2	Other
106716	2.8	AA464962	ESTs	Other
134098	2.8	X06323	Human MRL3 mRNA for ribosomal protein L3 homologue (MRL3	Other
134485	2.8	X82153	cathepsin K (pseudodysplasia)	SS
129634	2.8	AA150726	ESTs	Other
112207	2.8	R49602	ESTs	Other
124904	2.8	R86970	ESTs	Other
125471	2.8	AA477571	UDP-glucose ceramide glucosyltransferase	SS
132180	2.8	AA405569	fibroblast activation protein; alpha	SS
104454	2.8	M84443	galactokinase 2	TM
134282	2.8	T25508	ESTs	Other
101558	2.8	M32011	neutrophil cytosolic factor 2 (65kD; chronic granulomatous disease; autosomal 2)	Other
130529	2.8	AA173238	small inducible cytokine A5 (RANTES)	Other
101804	2.7	M86699	TTK protein kinase	Other
109565	2.7	F01930	ESTs	Other
112427	2.7	R62604	ESTs	Other
115188	2.7	AA261819	ESTs	Other
121831	2.7	AA425374	ESTs	Other
132454	2.7	W78726	ESTs; Highly similar to serine/threonine kinase [H.sapiens]	Other
116399	2.7	AA599729	Homo sapiens homeobox protein A10 (HOXA10) gene; complete cds	Other
100409	2.7	D86957	Human mRNA for KIAA0202 gene; partial cds	Other
130987	2.7	R45698	ESTs	Other
107217	2.7	D51095	ESTs	SS, TM

FIG. 11Af

358 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
125698	2.6	AA748483	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene; partial cds; neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes; complete cds	SS
118722	2.6	N73563	ESTs	SS
104521	2.6	R11604	"y47c1.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:132 5', mRNA sequence"	Other
130800	2.6	AA223386	ESTs; Weakly similar to kaianin p80 subunit [H.sapiens]	Other
134415	2.6	AA329274	protein tyrosine phosphatase type IVA; member 2	TM
116461	2.6	AA621557	ESTs; Moderately similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]	Other
100864	2.6	HG4297- HT4567	Transcriptional Coactivator Pc4	Other
103818	2.6	AA150614	"z143h5.1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:54729 5', mRNA sequence"	Other
105713	2.6	AA291321	ESTs	Other
114969	2.6	AA250775	ESTs	Other
130415	2.6	X07290	Human HF.12 gene mRNA	Other
101791	2.6	M83822	Human beige-like protein (βGL) mRNA; partial cds	Other
128131	2.6	A1283162	claudin 3	SS, TM
131564	2.6	AA491465	ESTs	Other
100279	2.6	D42084	Human mRNA for KIAA0094 gene; partial cds	Other
130149	2.6	J04031	methylenetetrahydrofolate dehydrogenase (NADP+ dependent); methylenetetrahydrofolate cyclohydrolase; formyltetrahydrofolate synthetase	Other
119888	2.6	W81710	ESTs	SS
126638	2.6	AA649257	ESTs	Other
131672	2.6	X12901	Human mRNA for villin	Other

FIG.- 11Ag

359 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
134405	2.6	J04177	collagen; type XI; alpha 1	Other
101188	2.5	L20320	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)	TM
104534	2.5	R22303	ESTs; Weakly similar to putative p150 [H.sapiens]	Other
135179	2.5	U43747	Friedreich ataxia	SS
124308	2.5	H93575	ESTs	SS
125621	2.5	A1051602	acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase)	TM
101342	2.5	L76191	interleukin-1 receptor-associated kinase 1	Other
129351	2.5	AA167268	ESTs	Other
103774	2.5	AA092898	ESTs; Weakly similar to R07G3.8 [C.elegans]	Other
131289	2.5	AA485697	ESTs	SS, TM
132094	2.5	W01996	ESTs; Highly similar to (define not available 4929683) [H.sapiens]	Other
103223	2.5	X74801	chaperonin containing TCP1; subunit 3 (gamma)	Other
105610	2.5	AA279991	ESTs	Other
115719	2.5	AA416997	ESTs	Other
134888	2.5	AA148094	Tat-interacting protein (30kD)	Other
105564	2.5	AA262943	ESTs	Other
129689	2.5	AA130156	ESTs	Other
103391	2.5	X94453	pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase)	Other
104182	2.5	AA479990	ESTs; Weakly similar to glicma amplified on chromosome 1 protein [H.sapiens]	SS, TM
123494	2.5	AA599786	ESTs	Other
122905	2.5	AA470070	ESTs	Other
109175	2.5	AA180496	ESTs	Other

FIG.-11Ah

360 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
129907	2.5	D80170	ESTs	Other
115142	2.4	AA258116	ESTs; Weakly similar to !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! [H.sapiens]	Other
125474	2.4	AA151216	Homo sapiens 14-3-3 protein mRNA; complete cds	SS
125745	2.4	AI283493	ribophorin II	Other
100103	2.4	AF007875	dolichyl-phosphate mannosyltransferase polypeptide 1; catalytic subunit	Other
102687	2.4	U73379	Human cyclin-selective ubiquitin carrier protein mRNA; complete cds	Other
133170	2.4	U21049	epithelial protein up-regulated in carcinoma	SS, TM
109141	2.4	AA176428	ESTs	Other
132811	2.4	U25435	transcriptional repressor	Other
102862	2.4	X01057	interleukin 2 receptor; alpha	SS, TM
104300	2.4	D37933	syntaxin 1B	Other
105091	2.4	AA148859	ESTs; Moderately similar to !!!!! ALU SUBFAMILY J WARNING ENTRY !!!!! [H.sapiens]	Other
110674	2.4	H89315	"yw25e09.s1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:253288 3', mRNA sequence."	TM
122571	2.4	AA452600	EST	Other
123421	2.4	AA598440	ESTs; Moderately similar to neuronal thread protein AD7c-NTP [H.sapiens]	Other
132181	2.4	AA046939	ESTs; Moderately similar to !!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!! [H.sapiens]	Other
129445	2.4	AA306121	ESTs	SS
113923	2.4	W80763	ESTs; Moderately similar to FK506-binding protein 65kD [M.musculus]	Other

FIG. 11Ai

361 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
100598	2.4	HG2463- HT2559	Guanine Nucleotide-Binding Protein G25k	Other
130869	2.4	AA128100	uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase)	Other
132393	2.4	W85888	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	Other
100830	2.4	HG4074- HT4344	Rad2	Other
133765	2.4	D21255	cadherin 11 (OB-cadherin; osteoblast)	SS, TM
100867	2.4	HG4316- HT4586	Transketolase-Like Protein	Other
119859	2.4	W80702	ESTs	Other
135269	2.4	M77698	YY1 transcription factor	Other
115140	2.4	AA258030	ESTs; Weakly similar to (define not available 3874821) [C.elegans]	Other
102162	2.4	U18291	CDC16 (cell division cycle 16; S. cerevisiae; homolog)	Other
100372	2.4	D79997	KIAA0175 gene product	TM
106981	2.4	AA521157	ESTs	Other
130114	2.4	AA234717	ESTs	Other
116129	2.3	AA459956	ESTs	Other
122235	2.3	AA436475	ESTs	Other
107315	2.3	T62771	Homo sapiens nucleoplasmin-3 (NPM3) mRNA; complete cds	SS
125905	2.3	T69868	chaperonin containing TCF1; subunit 2 (beta)	Other
133061	2.3	AB000584	prostate differentiation factor	SS
107531	2.3	Y13936	protein phosphatase 1G (formerly 2C); magnesium-dependent; gamma isoform	Other
125820	2.3	AA730136	teratocarcinoma-derived growth factor 1	Other

FIG. 11A

362 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
131725	2.3	AA456264	ESTs; Highly similar to (cfeine not available 4176448) [H.sapiens]	Other
101228	2.3	L27706	chaperonin containing TCP1; subunit 6A (zeta 1)	Other
132571	2.3	R84594	ESTs; Highly similar to (cfeine not available 4809026) [H.sapiens]	SS, TM
100090	2.3	AC002486	"Human BAC clone RG367O17 from 7p15-p21, complete sequence [Homo sapiens]"	Other
103658	2.3	Z74615	collagen; type I; alpha 1	SS, TM
104897	2.3	AA054641	ESTs	Other
106818	2.3	AA480890	ESTs	Other
113077	2.3	T40442	ESTs	SS
128773	2.3	M28879	granzyme B (granzyme 2; cytotoxic T-lymphocyte-associated serine esterase 1)	SS
129506	2.3	AA258286	Homo sapiens mRNA for KIAA0877 protein; partial cds	TM
133746	2.3	U44378	MAD (mothers against decapentaplegic; Drosophila) homolog 4	Other
134272	2.3	X76040	Lon protease-like protein	Other
106267	2.3	AA431873	Homo sapiens clone 24711 mRNA sequence	Other
133493	2.3	AA284143	Homo sapiens chromosome 1 atrophin-1 related protein (DRPLA) mRNA; complete cds	Other
104278	2.3	C02582	ESTs; Highly similar to (cfeine not available 5114045) [H.sapiens]	Other
127211	2.3	AA480935	"aa28c03.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814564 5'; mRNA sequence."	Other
110721	2.3	H97678	ESTs	Other
114774	2.3	AA150043	ESTs	TM
132968	2.3	N77151	Homo sapiens mRNA for KIAA0799 protein; partial cds	Other
106916	2.3	AA490814	ESTs	Other
113849	2.3	W60439	ESTs; Moderately similar to cbp146 [M.musculus]	Other
131028	2.3	U20240	CCAAT/enhancer binding protein (C/EBP); gamma	Other

FIG. 11A

363 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
130380	2.3	U55853	Homo sapiens 130 kD Gcigi-localized phosphoprotein (GPP130) mRNA; complete cds	SS
125390	2.3	H95094	KIAA0016 gene product	SS, TM
127256	2.3	AA327550	ESTs; Weakly similar to !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! [H.sapiens]	Other
132116	2.3	AA234767	ESTs	SS, TM
117765	2.3	N47797	ESTs	Other
119126	2.3	R45175	ESTs	Other
129482	2.2	AA435849	ESTs; Moderately similar to unknown protein [H.sapiens]	Other
120493	2.2	AA255933	ESTs	SS
108927	2.2	AA143493	ESTs; Weakly similar to PLECKSTRIN [H.sapiens]	Other
122520	2.2	AA449427	ESTs; Moderately similar to pregnancy-specific beta-1 glycoprotein 2 [H.sapiens]	Other
125982	2.2	R98091	RAE1 (RNA export 1; S.pombe) homolog	Other
132325	2.2	N37065	ESTs; Moderately similar to !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! [H.sapiens]	Other
100287	2.2	D43950	Human mRNA for KIAA0098 gene; partial cds	Other
114895	2.2	AA236177	Homo sapiens mRNA for KIAA0887 protein; partial cds	Other
105038	2.2	AA130273	ESTs; Weakly similar to (define not available 4240269) [H.sapiens]	Other
105476	2.2	AA255473	ESTs	SS
106942	2.2	AA496347	ESTs; Highly similar to gene 7442 protein [H.sapiens]	Other
110566	2.2	H59990	ESTs	Other
111068	2.2	N58397	ESTs	Other
127963	2.2	AI299013	"qn13h12.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898183 3' similar to TR:O22813 O22813 PUTATIVE NAD (P)-DEPENDENT CHOLESTEROL DEHYDROGENASE. ;; mRNA sequence."	TM

FIG. 11A

364 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
130985	2.2	AA243700	ESTs	Other
132877	2.2	R40685	Homo sapiens mRNA for KIAA0851 protein; complete cds	TM
135242	2.2	M74093	cyclin E1	TM
129468	2.2	J03040	secreted protein; acidic; cysteine-rich (osteonectin)	SS
132616	2.2	AA386264	ESTs	SS, TM
133780	2.2	M14219	decorin	Other
121853	2.2	AA425887	ESTs	Other
114608	2.2	AA079381	ESTs	Other
129017	2.2	H13108	ESTs	SS
132725	2.2	L41887	splicing factor; arginine/serine-rich 7 (35kD)	Other
125606	2.2	R28463	ESTs	SS
105538	2.2	AA258860	ESTs; Highly similar to (define not available 4583654) [H.sapiens]	Other
133221	2.2	AA235289	ESTs; Highly similar to rap2 gene product [H.sapiens]	Other
106389	2.2	AA446949	ESTs	Other
128949	2.2	AA190993	a disintegrin and metalloproteinase domain 12 (meltrin alpha)	Other
120969	2.2	AA398116	ESTs	Other
102495	2.2	U51240	Human mRNA for KIAA0085 gene; partial cds	TM
101124	2.2	L10343	protease inhibitor 3; skin-derived (SKALP)	SS
102778	2.2	U83463	syndecan binding protein (syntenin)	Other
107307	2.2	T52099	creatine kinase; mitochondrial 2 (sarcomeric)	Other
111605	2.2	R11638	ESTs	Other
101959	2.2	S80343	arginyl-tRNA synthetase	Other
101031	2.2	J05070	matrix metalloproteinase 9 (gelatinase B; 92kD gelatinase; 92kD type IV collagenase)	Other
131701	2.2	AA149008	ESTs; Weakly similar to Hs. sapiens	SS
105344	2.2	AA235303	ENTRY !!! [H.sapiens]	Other
			ESTs	TM

FIG. 11Am

365 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
103166	2.2	X67951	proliferation-associated gene A (natural killer-enhancing factor A)	Other
131463	2.2	X74142	forkhead (Drosophila)-like 1	Other
131412	2.2	U34044	Human selenium donor protein (seID) mRNA; complete cds	Other
134982	2.2	N46086	ESTs	Other
127236	2.1	AI341818	budding uninhibited by benzimidazoles 1 (yeast homolog)	Other
104459	2.1	M91493	EST	Other
124596	2.1	N70088	ESTs	Other
105650	2.1	AA282347	ESTs; Highly similar to (define not available 4454694) [H.sapiens]	Other
134917	2.1	X87241	FAT tumor suppressor (Drosophila) homolog	SS
132478	2.1	H20906	Homo sapiens mRNA for KIAA0746 protein; partial cds	SS, TM
134464	2.1	N79354	ESTs; Weakly similar to Rga [D.melanogaster]	Other
111221	2.1	N68869	ESTs	Other
100892	2.1	HG4557- HT4962	"Small Nuclear Ribonucleoprotein U1, 1snrp"	Other
117170	2.1	H98153	ESTs	Other
124049	2.1	F10523	primase; polypeptide 2A (58kD)	Other
131692	2.1	D50914	Human mRNA for KIAA0124 gene; partial cds	TM
103003	2.1	X52003	trefoil factor 1 (breast cancer; estrogen-inducible sequence expressed in)	SS
134085	2.1	U20979	chromatin assembly factor I (150 kDa)	Other
126216	2.1	N23870	ESTs	Other
102721	2.1	U79241	Human clone 23759 mRNA; partial cds	Other
128040	2.1	AA918528	ESTs	Other
101038	2.1	J05249	replication protein A2 (32kD)	SS
106060	2.1	AA417287	C-terminal binding protein 2	Other
103622	2.1	Z48042	basic transcription factor 3	Other
127884	2.1	AA768630	ESTs	Other

FIG. 11An

366 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
130911	2.1	W72906	HIRA interacting protein 4 (hnaJ-like)	Other
104260	2.1	AF008192	Homo sapiens putative GR6 protein (GR6) mRNA; complete cds	Other
120714	2.1	AA292689	ESTs	Other
101578	2.1	M34423	galactosidase; beta 1	SS
113443	2.1	T86158	ESTs	SS
101516	2.1	M28249	Accession not listed in Genbank	Other
106480	2.1	AA450373	ESTs; Moderately similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]	Other
111365	2.1	N92659	ESTs	Other
121121	2.1	AA399371	ESTs; Weakly similar to (define not available 4688925) [H.sapiens]	Other
124768	2.1	R40177	ESTs	Other
102501	2.1	U51586	Human siah binding protein 1 (SiahBP1) mRNA; partial cds	Other
106432	2.1	AA448850	ESTs	Other
132812	2.1	R48108	ESTs	Other
125681	2.1	AA394176	accessory proteins BAP31/EIAP29	Other
130511	2.1	L32137	cartilage oligomeric matrix protein	TM
128219	2.1	AA978333	ESTs	Other
130962	2.1	AA102051	transmembrane 4 superfamily member 6	Other
101840	2.1	M93056	protease inhibitor 2 (anti-ela stase); monocyte/neutrophil	SS, TM
123928	2.1	AA621363	EST	TM
132073	2.1	N67408	ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]	Other
101671	2.1	M61832	S-adenosylhomocysteine hydrolase	Other
107059	2.1	AA608545	ESTs	Other
132791	2.1	AA446088	ESTs; Weakly similar to YY1-associated factor 2 [H.sapiens]	Other
103131	2.1	X65614	S100 calcium-binding protein P	Other
104791	2.1	AA029046	ESTs	Other

FIG..11Aa

352 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
134804	12.3	L37036	small inducible cytokine subfamily B (Cys-X-Cys); member 5 (epithelial-derived neutrophil-activating peptide 78)	TM
130617	11.4	M90516	glutamine-fructose-6-phosphate transaminase 1	TM
104209	10.6	AB000221	small inducible cytokine subfamily A (Cys-Cys); member 18; pulmonary and activation-regulated ESTs	SS
109991	10	H09813	v-rat simian leukemia viral oncogene homolog A (ras related)	TM
124315	8.3	H94892	RNA binding motif protein 3	Other
132977	8.2	U28686	ESTs	Other
130407	7.4	N29888	ESTs; Weakly similar to KIAA0226 [H.sapiens]	Other
116176	6.6	AA463725	ESTs	Other
119271	6.5	T16387	cytochrome b-245; beta polypeptide (chronic granulomatous disease)	Other
134711	6.5	X04011	"Human chondroitin sulfate proteoglycan versican V splice-variant precursor peptide mRNA, complete cds"	TM
134326	6.1	U16306	ESTs; Weakly similar to unknown [H.sapiens]	Other
125852	5.9	H09290	ESTs	SS, TM
112169	5.9	R48589	chromosome-associated polypeptide C	TM
132528	5.9	AA283006	phosphoribosylglycinamide formyltransferase;	Other
134367	5.7	X54199	phosphoribosylglycinamide synthetase;	Other
			phosphoribosylaminoimidazole synthetase	
111929	5.2	R40057	prominin (mouse)-like 1	SS, TM
102165	5	U18321	Death associated protein 3	Other
130441	5	U35835	protein kinase; DNA-activated; catalytic polypeptide	Other
133282	5	U52960	SRB7 (suppressor of RNA polymerase B; yeast) homolog	Other
100783	4.9	HG3748- HT4018	"Basic Transcription Factor, 44 Kda Subunit"	Other

FIG. 11Aa

353 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
12223	4.9	AA436158	ESTs	Other
104660	4.8	AA007160	ESTs	SS
113702	4.8	T97307	ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	Other
101185	4.7	L19872	aryl hydrocarbon receptor	Other
105308	4.7	AA233744	ESTs	Other
107168	4.7	AA621540	ESTs	Other
101201	4.6	L22524	matrix metalloproteinase 7 (matrilysin; uterine)	SS
101809	4.5	M86849	"Homo sapiens connexin 26 (GJB2) mRNA, complete cds"	TM
101478	4.5	M23379	RAS p21 protein activator (GTPase activating protein) 1	Other
104695	4.5	AA012953	ESTs	Other
100365	4.4	D78611	mesoderm specific transcript (mouse) homolog	TM
126819	4.3	AA305536	"EST176522 Colon carcinoma (Caco-2) cell line II Homo sapiens cDNA 5' end, mRNA sequence."	Other
101880	4.3	M97925	defensin; alpha 5; Paneth cell-specific	SS
126838	4.2	AA858097	pigment epithelium-derived factor	Other
101684	4.2	M63256	cerebellar degeneration-related protein (62kD)	Other
117634	4.2	N36421	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	Other
132109	4.1	AA599801	ESTs	Other
115054	4.1	AA252863	ESTs	Other
106553	4	AA454967	ESTs	Other
119717	3.9	W69134	ESTs	Other
131945	3.9	M87339	replication factor C (activator 1) 4 (37kD)	Other
128790	3.9	AA291725	secreted frizzled-related protein 4	SS
120562	3.8	AA280036	ESTs; Weakly similar to W01A6.c [C.elegans]	SS
109517	3.7	D60799	ESTs	Other

FIG.. 11Ab

354 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
102618	3.7	U65932	extracellular matrix protein 1	SS
106286	3.7	AA434441	frizzled (Drosophila) homolog 7	Other
133640	3.6	D83004	ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13)	Other
100335	3.6	D63391	platelet-activating factor acetylhydrolase; isoform Ib; gamma subunit (29kD)	Other
104720	3.6	AA018441	ESTs	Other
107348	3.6	U43701	ribosomal protein L23a	Other
134989	3.6	AA236324	ESTs; Weakly similar to Hs. sapiens	SS
111345	3.6	N89820	ENTRY III [H. sapiens]	Other
107053	3.6	AA600147	ESTs; Weakly similar to Similar to NADH-cytochrome B5 reductase [C. elegans]	Other
107240	3.5	D59368	ESTs	Other
107129	3.5	AA620553	flap structure-specific endonuclease 1	Other
134846	3.5	AA431505	Homo sapiens mRNA for putative Sqv-7-like protein; partial	TM
101897	3.5	S58544	sperm associated antigen 1	Other
107151	3.5	AA621169	ESTs	Other
106012	3.4	AA411621	ESTs	Other
101950	3.4	S79219	propionyl Coenzyme A carboxylase; alpha polypeptide	Other
116844	3.4	H64938	ESTs	Other
128025	3.4	AA937173	ESTs	TM
106785	3.4	AA478587	leukemia associated gene 1; candidate tumor suppressor frequently deleted in B-cell chronic lymphocytic leukemia (B-CLL)	Other
104518	3.4	R09815	proteasome (prosome; macropain) 26S subunit; ATPase; 5	Other
117667	3.4	N39214	ser-Thr protein kinase related to the myotonic dystrophy protein kinase	Other

FIG. 11Ac

355 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
104954	3.3	AA074514	ESTs; Moderately similar to (define not available 4753768) [H.sapiens]	Other
105372	3.3	AA236481	ESTs	Other
104896	3.3	AA054228	ESTs	Other
113485	3.3	T87863	ESTs	Other
127003	3.3	AA550806	ESTs; Weakly similar to (define not available 3882151) [H.sapiens]	TM
100305	3.3	D50487	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 8 (RNA helicase)	SS
134722	3.2	W47183	ESTs; Weakly similar to !!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!! [H.sapiens]	Other
126801	3.2	AA512902	ESTs	SS, TM
133503	3.2	M33195	Fc fragment of IgE; high affinity I; receptor for; gamma polypeptide	SS, TM
132183	3.2	L19183	Human MAC30 mRNA; 3' end	TM
105298	3.2	AA233459	ESTs	TM
111046	3.2	N55514	ESTs; Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]	TM
135309	3.2	D25984	ESTs	SS
102808	3.2	U90426	nuclear RNA helicase; DECD variant of DEAD box family	Other
100552	3.1	HG2167- HT2237	"Protein Kinase Ht31, Camp-Dependent"	Other
127652	3.1	AA804487	ESTs	Other
116127	3.1	AA459703	ESTs; Moderately similar to coded for by C. elegans cDNA CEESD64F [C.elegans]	TM
131904	3.1	AA143019	ESTs; Highly similar to surface 4 integral membrane protein [H.sapiens]	TM
126547	3.1	U47732	transmembrane 4 superfamily member 3	Other
102823	3.1	U90914	carboxypeptidase D	SS

FIG. 11Ad

356 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
132298	3.1	N41849	Homo sapiens cytokine receptor related protein 4 (CYTOR4) mRNA; complete cds	Other
127445	3.1	AA906286	ESTs	Other
134395	3.1	L09717	lysosomal-associated membrane protein 2	SS, TM
105743	3.1	AA293300	ESTs; Weakly similar to semaphorin C [M.musculus]	Other
125827	3.1	AI471525	YY1 transcription factor	Other
101229	3.1	L27943	cytidine deaminase	Other
102306	3	U33317	defensin; alpha 6; Paneth cell-specific	SS
107318	3	T74445	"yc82f8.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:2242 5', mRNA sequence"	Other
120983	3	AA398209	EST	Other
134700	3	AA481414	golgi SNAP receptor complex member 1	TM
131216	3	D31058	ESTs	SS
127565	3	D79516	"HUM272B04B Human aorta polyA+ (TFujiwara) Homo sapiens cDNA clone GEN-272B04 5', mRNA sequence."	Other
106882	2.9	AA489009	ESTs	Other
130874	2.9	T08287	ESTs	Other
101275	2.9	L37936	Ts translation elongation factor; mitochondrial	Other
111179	2.9	N67239	ESTs	Other
126086	2.9	H70975	"yr73g01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:210960 5', mRNA sequence."	Other
105365	2.9	AA236275	ESTs	Other
118789	2.9	N75416	ESTs	Other
115117	2.9	AA256492	H.sapiens PAP mRNA	Other
100484	2.9	HG1103-	"Guanine Nucleotide-Binding Protein Ral, Ras-Oncogene Related"	Other
101300	2.9	HT1103 L40391	Homo sapiens (clone s1153) mRNA fragment	Other

FIG. 11Ae

357 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
103075	2.9	X59543	ribonucleotide reductase M1 polypeptide	Other
132164	2.8	U84573	procollagen-lysine; 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2	Other
106716	2.8	AA464962	ESTs	Other
134098	2.8	X06323	Human MRL3 mRNA for ribosomal protein L3 homologue (MRL3	Other
134485	2.8	X82153	cathepsin K (pseudodysostosis)	SS
129634	2.8	AA150726	ESTs	Other
112207	2.8	R49602	ESTs	Other
124904	2.8	R86970	ESTs	Other
125471	2.8	AA477571	UDP-glucose ceramide glucosyltransferase	SS
132180	2.8	AA405569	fibroblast activation protein; alpha	SS
104454	2.8	M84443	galactokinase 2	TM
134282	2.8	T25508	ESTs	Other
101558	2.8	M32011	neutrophil cytosolic factor 2 (65kD; chronic granulomatous disease; autosomal 2)	Other
130529	2.8	AA173238	small inducible cytokine A15 (RANTES)	Other
101804	2.7	M86699	TTK protein kinase	Other
109565	2.7	F01930	ESTs	Other
112427	2.7	R62604	ESTs	Other
115188	2.7	AA261819	ESTs	Other
121831	2.7	AA425374	ESTs	Other
132454	2.7	W78726	ESTs; Highly similar to serine/threonine kinase [H.sapiens]	Other
116399	2.7	AA599729	Homo sapiens homeobox protein A10 (HOXA10) gene; complete cds	Other
100409	2.7	D86957	Human mRNA for KIAA0202 gene; partial cds	Other
130987	2.7	R45698	ESTs	Other
107217	2.7	D51095	ESTs	SS, TM

FIG. 11A

358 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
125698	2.6	AA748483	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene; partial cds; neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes; complete cds	SS
118722	2.6	N73563	ESTs	SS
104521	2.6	R11604	"y47c1.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:132 5', mRNA sequence"	Other
130800	2.6	AA223386	ESTs; Weakly similar to katanin p80 subunit [H.sapiens]	Other
134415	2.6	AA329274	protein tyrosine phosphatase type IVA; member 2	TM
116461	2.6	AA621557	ESTs; Moderately similar to !!! ALU SUBFAMILY SQ WARNING ENTRY IIII [H.sapiens]	Other
100864	2.6	HG4297- HT4567	Transcriptional Coactivator Pc4	Other
103818	2.6	AA150614	"z143h5.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:54729 3', mRNA sequence"	Other
105713	2.6	AA291321	ESTs	Other
114969	2.6	AA250775	ESTs	Other
130415	2.6	X07290	Human HF.12 gene mRNA	Other
101791	2.6	M83822	Human beige-like protein (EGL) mRNA; partial cds	Other
128131	2.6	A1283162	claudin 3	SS, TM
131564	2.6	AA491465	ESTs	Other
100279	2.6	D42084	Human mRNA for KIAA0094 gene; partial cds	Other
130149	2.6	J04031	methylenetetrahydrofolate dehydrogenase (NADP+ dependent); methylenetetrahydrofolate cyclohydrolase; formyltetrahydrofolate synthetase	Other
119888	2.6	W81710	ESTs	SS
126638	2.6	AA649257	ESTs	Other
131672	2.6	X12901	Human mRNA for villin	Other

FIG.-11Ag

359 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
134405	2.6	J04177	collagen; type XI; alpha 1	Other
101188	2.5	L20320	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)	TM
104534	2.5	R22303	ESTs; Weakly similar to putative p150 [H.sapiens]	Other
135179	2.5	U43747	Friedreich ataxia	SS
124308	2.5	H93575	ESTs	SS
125621	2.5	AI051602	acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl-Coenzyme A thiolase)	TM
101342	2.5	L76191	interleukin-1 receptor-associated kinase 1	Other
129351	2.5	AA167268	ESTs	Other
103774	2.5	AA092898	ESTs; Weakly similar to R07G3.8 [C.elegans]	Other
131289	2.5	AA485697	ESTs	SS, TM
132094	2.5	W01996	ESTs; Highly similar to (define not available 4929683) [H.sapiens]	Other
103223	2.5	X74801	chaperonin containing TCP1; subunit 3 (gamma)	Other
105610	2.5	AA279991	ESTs	Other
115719	2.5	AA416997	ESTs	Other
134888	2.5	AA148094	Tat-interacting protein (30kDa)	Other
105564	2.5	AA262943	ESTs	Other
129689	2.5	AA130156	ESTs	Other
103391	2.5	X94453	pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase)	Other
104182	2.5	AA479990	ESTs; Weakly similar to glio na amplified on chromosome 1 protein [H.sapiens]	SS, TM
123494	2.5	AA599786	ESTs	Other
122905	2.5	AA470070	ESTs	Other
109175	2.5	AA180496	ESTs	Other

FIG. 11Ah

360 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
129907	2.5	D80170	ESTs	Other
115142	2.4	AA258116	ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	Other
125474	2.4	AA151216	Homo sapiens 14-3-3 protein mRNA; complete cds	SS
125745	2.4	AI283493	ribophorin II	Other
100103	2.4	AF007875	dolichyl-phosphate mannosyltransferase polypeptide 1; catalytic subunit	Other
102687	2.4	U73379	Human cyclin-selective ubiquitin carrier protein mRNA; complete cds	Other
133170	2.4	U21049	epithelial protein up-regulated in carcinoma	SS, TM
109141	2.4	AA176428	ESTs	Other
132811	2.4	U25435	transcriptional repressor	Other
102862	2.4	X01057	interleukin 2 receptor; alpha	SS, TM
104300	2.4	D37933	syntaxin 1B	Other
105091	2.4	AA148859	ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	Other
110674	2.4	H89315	"yw25e09.s1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:253288 3', mRNA sequence."	TM
122571	2.4	AA452600	EST	Other
123421	2.4	AA598440	ESTs; Moderately similar to neuronal thread protein AD7c-NTP [H.sapiens]	Other
132181	2.4	AA046939	ESTs; Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]	Other
129445	2.4	AA306121	ESTs	SS
113923	2.4	W80763	ESTs; Moderately similar to FK506-binding protein 65kD [M.musculus]	Other

FIG. 11Ai

361 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
100598	2.4	HG2463- HT2559	Guanine Nucleotide-Binding Protein G25k	Other
130869	2.4	AA128100	uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase)	Other
132393	2.4	W85888	ESTs; Moderately similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	Other
100830	2.4	HG4074- HT4344	Rad2	Other
133765	2.4	D21255	cadherin 11 (OB-cadherin; osteoblast)	SS, TM
100867	2.4	HG4316- HT4586	Transketolase-Like Protein	Other
119859	2.4	W80702	ESTs	Other
135269	2.4	M77698	YY1 transcription factor	Other
115140	2.4	AA258030	ESTs; Weakly similar to (define not available 3874821) [C.elegans]	Other
102162	2.4	U18291	CDC16 (cell division cycle 16; S. cerevisiae; homolog)	Other
100372	2.4	D79997	KIAA0175 gene product	TM
106981	2.4	AA521157	ESTs	Other
130114	2.4	AA234717	ESTs	Other
116129	2.3	AA459956	ESTs	Other
122235	2.3	AA436475	ESTs	Other
107315	2.3	T62771	Homo sapiens nucleoplasmin-3 (NPM3) mRNA; complete cds	SS
125905	2.3	T69868	chaperonin containing TCP1; subunit 2 (beta)	Other
133061	2.3	AB000584	prostate differentiation factor	SS
107531	2.3	Y13936	protein phosphatase 1G (formerly 2C); magnesium-dependent; gamma isoform	Other
125820	2.3	AA730136	teratocarcinoma-derived growth factor 1	Other

FIG.. 11Aj

362 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
131725	2.3	AA456264	ESTs; Highly similar to (define not available 4176448) [H.sapiens]	Other
101228	2.3	L27706	chaperonin containing TC1P1; subunit 6A (zeta 1)	Other
132571	2.3	R84594	ESTs; Highly similar to (define not available 4809026) [H.sapiens]	SS, TM
100090	2.3	AC002486	"Human BAC clone RG367O17 from 7p15-p21, complete sequence [Homo sapiens]"	Other
103658	2.3	Z74615	collagen; type I; alpha 1	SS, TM
104897	2.3	AA054641	ESTs	Other
106818	2.3	AA480890	ESTs	Other
113077	2.3	T40442	ESTs	SS
128773	2.3	M28879	granzyme B (granzyme 2; cytotoxic T-lymphocyte-associated serine esterase 1)	SS
129506	2.3	AA258286	Homo sapiens mRNA for KIAA0877 protein; partial cds	TM
133746	2.3	U44378	MAD (mothers against decapentaplegic; Drosophila) homolog 4	Other
134272	2.3	X76040	Lon protease-like protein	Other
106267	2.3	AA431873	Homo sapiens clone 24711 mRNA sequence	Other
133493	2.3	AA284143	Homo sapiens chromosome 1 atrophin-1 related protein (DRPLA) mRNA; complete cds	Other
104278	2.3	C02582	ESTs; Highly similar to (define not available 5114045) [H.sapiens]	Other
127211	2.3	AA480935	"aa28c03.r1 NCICGAP_GCB1 Homo sapiens cDNA clone IMAGE:814564 5', mRNA sequence."	Other
110721	2.3	H97678	ESTs	Other
114774	2.3	AA150043	ESTs	TM
132968	2.3	N77151	Homo sapiens mRNA for KIAA0799 protein; partial cds	Other
106916	2.3	AA490814	ESTs	Other
113849	2.3	W60439	ESTs; Moderately similar to cbp146 [M.musculus]	Other
131028	2.3	U20240	CCAAT/enhancer binding protein (C/EBP); gamma	Other

FIG. 11Ak

363 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
130380	2.3	U55853	Homo sapiens 130 kD Golgi-localized phosphoprotein (GPP130) mRNA; complete cds	SS
125390	2.3	H95094	KIAA0016 gene product	SS, TM
127256	2.3	AA327550	ESTs; Weakly similar to !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! [H.sapiens]	Other
132116	2.3	AA234767	ESTs	SS, TM
117765	2.3	N47797	ESTs	Other
119126	2.3	R45175	ESTs	Other
129482	2.2	AA435849	ESTs; Moderately similar to unknown protein [H.sapiens]	Other
120493	2.2	AA255933	ESTs	SS
108927	2.2	AA143493	ESTs; Weakly similar to PLECKSTRIN [H.sapiens]	Other
122520	2.2	AA449427	ESTs; Moderately similar to pregnancy-specific beta-1 glycoprotein 2 [H.sapiens]	Other
125982	2.2	R98091	RAE1 (RNA export 1; S.pcmbe) homolog	Other
132325	2.2	N37065	ESTs; Moderately similar to !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! [H.sapiens]	Other
100287	2.2	D43950	Human mRNA for KIAA0038 gene; partial cds	Other
114895	2.2	AA236177	Homo sapiens mRNA for KIAA0887 protein; partial cds	Other
105038	2.2	AA130273	ESTs; Weakly similar to (define not available 4240269) [H.sapiens]	Other
105476	2.2	AA255473	ESTs	SS
106942	2.2	AA496347	ESTs; Highly similar to gene 7442 protein [H.sapiens]	Other
110566	2.2	H59990	ESTs	Other
111068	2.2	N58397	ESTs	Other
127963	2.2	A1299013	"qn13h12.x1 NCI_CGAP_lu5 Homo sapiens cDNA clone IMAGE:1898183 3' similar to TR:O22813 O22813 PUTATIVE NAD (P)-DEPENDENT CHOLESTEROL DEHYDROGENASE. ; mRNA sequence."	TM

FIG. 11A

364 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
130985	2.2	AA243700	ESTs	Other
132877	2.2	R40685	Homo sapiens mRNA for KIAA0851 protein; complete cds	TM
135242	2.2	M74093	cyclin E1	TM
129468	2.2	J03040	secreted protein; acidic; cysteine-rich (osteonectin)	SS
132616	2.2	AA386264	ESTs	SS, TM
133780	2.2	M14219	decorin	Other
121853	2.2	AA425887	ESTs	Other
114608	2.2	AA079381	ESTs	Other
129017	2.2	H13108	ESTs	SS
132725	2.2	L41887	splicing factor; arginine/serine-rich 7 (35kD)	Other
125606	2.2	R28463	ESTs	SS
105538	2.2	AA258860	ESTs; Highly similar to (define not available 4583654) [H.sapiens]	Other
133221	2.2	AA235289	ESTs; Highly similar to rap2 gene product [H.sapiens]	Other
106389	2.2	AA446949	ESTs	Other
128949	2.2	AA190993	a disintegrin and metalloproteinase domain 12 (meltrin alpha)	Other
120969	2.2	AA398116	ESTs	Other
102495	2.2	U51240	Human mRNA for KIAA0085 gene; partial cds	TM
101124	2.2	L10343	protease inhibitor 3; skin-derived (SKALP)	SS
102778	2.2	U83463	syndecan binding protein (syntenin)	Other
107307	2.2	T52099	creatine kinase; mitochondrial 2 (sarcomeric)	Other
111605	2.2	R11638	ESTs	Other
101959	2.2	S80343	arginyl-tRNA synthetase	Other
101031	2.2	J05070	matrix metalloproteinase 9 (gelatinase B; 92kD gelatinase; 92kD type IV collagenase)	SS
131701	2.2	AA149008	ESTs; Weakly similar to IIII ALU SUBFAMILY SQ WARNING ENTRY IIII [H.sapiens]	Other
105344	2.2	AA235303	ESTs	TM

FIG. 11Am

365 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
103166	2.2	X67951	proliferation-associated gene A (natural killer-enhancing factor A)	Other
131463	2.2	X74142	forkhead (Drosophila)-like 1	Other
131412	2.2	U34044	Human selenium donor protein (seld) mRNA; complete cds	Other
134982	2.2	N46086	ESTs	Other
127236	2.1	A1341818	budding uninhibited by benzimidazoles 1 (yeast homolog)	Other
104459	2.1	M91493	EST	Other
124596	2.1	N70088	ESTs	Other
105650	2.1	AA282347	ESTs; Highly similar to (define not available 4454694) [H.sapiens]	Other
134917	2.1	X87241	FAT tumor suppressor (Drosophila) homolog	SS
132478	2.1	H20906	Homo sapiens mRNA for KIAA0746 protein; partial cds	SS, TM
134464	2.1	N79354	ESTs; Weakly similar to Hga [D.melanogaster]	Other
111221	2.1	N68869	ESTs	Other
100892	2.1	HG4557- HT4962	"Small Nuclear Ribonucleoprotein U1, 1snrp"	Other
117170	2.1	H98153	ESTs	Other
124049	2.1	F10523	primase; polypeptide 2A (58kD)	Other
131692	2.1	D50914	Human mRNA for KIAA0124 gene; partial cds	TM
103003	2.1	X52003	trefoil factor 1 (breast cancer; estrogen-inducible sequence expressed in)	SS
134085	2.1	U20979	chromatin assembly factor I (150 kDa)	Other
126216	2.1	N23870	ESTs	Other
102721	2.1	U79241	Human clone 23759 mRNA; partial cds	Other
128040	2.1	AA918528	ESTs	Other
101038	2.1	J05249	replication protein A2 (32kD)	SS
106060	2.1	AA417287	C-terminal binding protein 2	Other
103622	2.1	Z48042	basic transcription factor 3	Other
127884	2.1	AA768630	ESTs	Other

FIG.. 11An

366 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
130911	2.1	W72906	HIRA interacting protein 4 (dhaJ-like)	Other
104260	2.1	AF008192	Homo sapiens putative GR6 protein (GR6) mRNA; complete cds	Other
120714	2.1	AA292689	ESTs	Other
101578	2.1	M34423	galactosidase; beta 1	SS
113443	2.1	T86158	ESTs	SS
101516	2.1	M28249	Accession not listed in Genbank	Other
106480	2.1	AA450373	ESTs; Moderately similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]	Other
111365	2.1	N92659	ESTs	Other
121121	2.1	AA399371	ESTs; Weakly similar to (define not available 4688925) [H.sapiens]	Other
124768	2.1	R40177	ESTs	Other
102501	2.1	U51586	Human siah binding protein 1 (SiahBP1) mRNA; partial cds	Other
106432	2.1	AA448850	ESTs	Other
132812	2.1	R48108	ESTs	Other
125681	2.1	AA394176	accessory proteins BAP31/BAP29	TM
130511	2.1	L32137	cartilage oligomeric matrix protein	Other
128219	2.1	AA978333	ESTs	Other
130962	2.1	AA102051	transmembrane 4 superfamily member 6	SS, TM
101840	2.1	M93056	protease inhibitor 2 (anti-elastase); monocyte/neutrophil	TM
123928	2.1	AA621363	EST	Other
132073	2.1	N67408	ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]	Other
101671	2.1	M61832	S-adenosylhomocysteine hydrolase	Other
107059	2.1	AA608545	ESTs	Other
132791	2.1	AA446088	ESTs; Weakly similar to YY1-associated factor 2 [H.sapiens]	Other
103131	2.1	X65614	S100 calcium-binding protein P	Other
104791	2.1	AA029046	ESTs	Other

FIG.. 11Aa

367 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
135181	2.1	AA621349	ESTs; Weakly similar to similar to Yeast hypothetical protein L8167.12 like [C.elegans]	Other
104334	2.1	D82614	ESTs	Other
132103	2.1	AA025086	ESTs	Other
126743	2.1	AA179253	poly(A)-binding protein-like 1	Other
100439	2.1	D87453	Human mRNA for KIAA0264 gene; partial cds	Other
114860	2.1	AA235112	ESTs; Moderately similar to similar to murine RNA-binding protein [H.sapiens]	Other
116732	2.1	F13779	ESTs; Weakly similar to !!!!! ALU SUBFAMILY J WARNING ENTRY !!!!! [H.sapiens]	Other
131045	2.1	H30863	ESTs; Weakly similar to The KIAA0132 gene product is related to Drosophila melanogaster ring canel protein. [H.sapiens]	Other
133209	2.1	AA114183	ESTs; Moderately similar to glutamate pyruvate transaminase [H.sapiens]	Other
101758	2.1	M77836	Human pyrroline 5-carboxylate reductase mRNA; complete cds	Other
102214	2.1	U23752	SRY (sex-determining region Y)-box 11	Other
130100	2.1	AA425593	ESTs	Other
109799	2.1	F10770	Homo sapiens clone 669 unknown mRNA; complete sequence	Other
130860	2.1	U66061	T-cell receptor; beta cluster	SS, TM
106685	2.1	AA461551	ESTs; Highly similar to 73 kDa subunit of cleavage and polyadenylation specificity factor [H.sapiens]	TM
125724	2.1	AA083407	stimulated trans-acting factor (50 kDa)	Other
134258	2.1	L28010	heterogeneous nuclear ribonucleoprotein F	Other
129642	2.1	R50008	7-dehydrocholesterol reductase	TM
125336	2.1	T86823	ESTs	Other
125303	2	Z39821	ESTs	Other

FIG. 11Ap

368 / 454

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
100749	2	HG3521- HT3715	Ras-Related Protein Rap1b	Other
126185	2	AI393989	ESTs	TM
126880	2	AI151406	ESTs	SS, TM
105263	2	AA227926	ESTs	Other
123288	2	AA495836	EST	Other
105807	2	AA393803	ESTs	Other
105040	2	AA131047	KIAA0698 gene product	TM
131977	2	F09788	procollagen-proline; 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase); alpha polypeptide II	SS
117992	2	N52000	ESTs	SS, TM
134037	2	X53586	Human mRNA for integrin alpha 6	SS
132744	2	X54326	glutamyl-prolyl-tRNA synthetase	Other
101581	2	M34996	"Human MHC cell surface glycoprotein (HLA-DQA) mRNA, 3'end"	SS, TM
103576	2	Z26317	desmoglein 2	SS
131235	2	AA223284	ESTs; Moderately similar to (define not available 4680395) [H.sapiens]	Other
127910	2	AA781881	ESTs; Weakly similar to sperm fertilization protein sp56 precursor [M.musculus]	SS
101552	2	M31642	hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	Other
106318	2	AA436570	Homo sapiens mRNA for pre-mRNA cleavage factor I subunit	Other
101192	2	L20859	Human leukemia virus receptor 1 (GLVR1) mRNA; complete cds	TM
104592	2	R81003	Homo sapiens serine protease mRNA; complete cds	SS
129095	2	L12350	thrombospondin 2	SS
105705	2	AA290767	ESTs	Other
128461	2	M63262	arachidonate 5-lipoxygenase-activating protein	SS, TM

FIG. 11Aq

369 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGEN: DESCRIPTOR	ORF STRUCTURAL INFO
16074	>10	AA001507	ESTs	other
25047	>10	AA011031	ESTs	other
25082	>10	AA017257	ESTs	other
16490	>10	AA026418	ESTs	other
25179	>10	AA031268	H.sapiens mR	other
25215	>10	AA035540	APC/LOPRO	other
25282	>10	AA044825	ESTs	other
16810	>10	AA053636	ESTs	other
16835	>10	AA054438	ESTs	SS,
10747	>10	AA055841	ESTs	other
10748	>10	AA055892	ESTs	other
16993	>10	AA065300	Human mRNA	other
17051	>10	AA070801	ESTs	TM
10840	>10	AA084104	ESTs	other
7296	>10	AA085661	ESTs	other
7325	>10	AA090842	ESTs Weakly	other
17419	>10	AA113349	EST	?
17541	>10	AA127459	ESTs	other
17559	>10	AA128407	ESTs	other
25669	>10	AA128978	ESTs	?
17600	>10	AA130596	ESTs	other
10992	>10	AA132523	ESTs	other
17654	>10	AA133250	Human sapiens	other
17734	>10	AA137246	ESTs	TM
25801	>10	AA148530	EST - RC_AA	other
25806	>10	AA149007	EST	TM
11121	>10	AA156359	Human TAR D	?

FIG. 12Aa

370 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
11160	>10	AA164289	ES's	other
25925	>10	AA164494	ES's Weakly	other
25934	>10	AA165355	Human clone	?
17987	>10	AA169379	ES's	other
18008	>10	AA171895	Homo sapiens	TM
33953	>10	AA173290	Human HOXA	other
33980	>10	AA180223	CAMP-DEPEN	other
34013	>10	AA190888	EST - RC_AA	other
34014	>10	AA191348	ES's	other
34015	>10	AA191353	ES's	TM
34070	>10	AA196549	ES's	other
18260	>10	AA206801	ES's	?
34105	>10	AA207123	ES's	SS,
34107	>10	AA209469	ES's	other
18330	>10	AA216722	Human mRNA	TM
18362	>10	AA223912	Ribonuclease	other
18392	>10	AA227751	ES's	SS,
34188	>10	AA228030	ES's	TM
34197	>10	AA232315	Homo sapiens	other
25948	>10	AA234365	Homo sapiens	SS,
25951	>10	AA234556	EST	TM
11561	>10	AA236533	Evi-1	?
26059	>10	AA236685	ES's	other
26100	>10	AA242835	Human mRNA	other
11603	>10	AA243052	ES's Highly	other
7785	>10	AA243375	EST - AA2433	other
34372	>10	AA251973	ES's	?

FIG. 12Ab

371 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
26240	>10	AA252282	Human mRNA	TM
34382	>10	AA252512	ESTs	other
34391	>10	AA252703	EST - RC_AA	other
26274	>10	AA253011	ESTs	?
34400	>10	AA253400	ESTs	other
26291	>10	AA253422	ESTs	?
26355	>10	AA256379	ESTs	other
11813	>10	AA258158	ESTs	other
34518	>10	AA278721	ESTs	?
26545	>10	AA278979	ESTs	other
26574	>10	AA279504	ESTs	other
34554	>10	AA280016	DNA polymera	other
34561	>10	AA280298	ESTs	TM
26628	>10	AA280641	ESTs Highly	TM
11969	>10	AA280670	ESTs	SS,
34575	>10	AA280738	ESTs	TM
26677	>10	AA281636	ESTs	?
26700	>10	AA282197	EST	?
34672	>10	AA284372	ESTs	other
34692	>10	AA285079	ESTs	other
12143	>10	AA290991	ESTs	other
8092	>10	AA316272	ESTs	other
34904	>10	AA321746	ESTs	TM
8111	>10	AA323787	EST	other
8125	>10	AA330771	ESTs	other
26916	>10	AA331393	Human protein	TM
26926	>10	AA342402	ESTs	other
			ESTs	other

FIG.-- 12Ac

372 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
26935	>10	AA347193	ESTs Weakly	TM
35038	>10	AA350541	ESTs Modera	TM
35049	>10	AA350857	ESTs	other
35106	>10	AA371561	EST Weakly s	?
35197	>10	AA398120	ESTs	other
35277	>10	AA398536	ESTs	other
35309	>10	AA398660	EST	other
35322	>10	AA398710	H. sapiens RN	other
27037	>10	AA400198	ESTs	TM
35495	>10	AA400527	ESTs	TM
27046	>10	AA400670	Homo sapiens	?
35500	>10	AA400715	ESTs	other
12480	>10	AA403116	Homo sapiens	other
35693	>10	AA405485	ESTs Weakly	other
35697	>10	AA405512	ESTs	other
35766	>10	AA406169	Homo sapiens	other
35769	>10	AA406206	ESTs	other
35798	>10	AA410231	ESTs	other
35801	>10	AA410291	ESTs	other
35803	>10	AA410295	ESTs	other
35822	>10	AA411144	ESTs	other
35874	>10	AA412024	EST	TM
35958	>10	AA412550	ESTs	?
36052	>10	AA417027	EST	other
36258	>10	AA423962	ESTs Weakly	TM
36288	>10	AA424502	ESTs	other
36307	>10	AA424803	EST	?

FIG.-12Ad

373 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
36371	>10	AA426017	ESTs	TM
36395	>10	AA426353	ESTs	other
36405	>10	AA426406	Homo sapiens	other
36506	>10	AA429610	ESTs	other
36571	>10	AA430726	EST - RC_AA	SS,
36695	>10	AA433910	ESTs	other
36739	>10	AA435610	EST - RC_AA	?
36753	>10	AA435686	ESTs	other
36845	>10	AA436198	ESTs	?
13136	>10	AA436560	ESTs	SS, TM
13143	>10	AA436619	ESTs	SS,
36958	>10	AA442060	ESTs	other
36962	>10	AA442082	ESTs	?
36981	>10	AA442845	EST	?
13237	>10	AA443971	ESTs Weakly	?
13242	>10	AA445994	ESTs	other
37057	>10	AA446131	ESTs	other
37068	>10	AA446312	ESTs Weakly	other
37074	>10	AA446344	ESTs	SS,
37084	>10	AA446486	Homo sapiens	?
37135	>10	AA447540	EST	?
37159	>10	AA447714	EST - RC_AA	other
37168	>10	AA447772	ESTs	?
37246	>10	AA449311	Homo sapiens	other -
37310	>10	AA451707	ESTs	other
37453	>10	AA454610	ESTs	?
37456	>10	AA454632	ESTs	TM

FIG._12Ae

374 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
27787	>10	AA454660	ESTs	?
37492	>10	AA455248	EST - RC_AA	other
37546	>10	AA456641	ESTs	TM
37601	>10	AA458864	ESTs	other
37611	>10	AA458996	Human signal	SS, TM
37615	>10	AA459101	Human serine	other
37653	>10	AA460017	ESTs	other
37677	>10	AA460530	Homo sapiens	other
37777	>10	AA464860	Homo sapiens	other
8648	>10	AA465016	Homo sapiens	?
37816	>10	AA469954	EST	?
37829	>10	AA470084	ESTs	other
28015	>10	AA477421	ESTs	other
37978	>10	AA479294	EST - RC_AA	other
37979	>10	AA479295	ESTs Highly	other
37983	>10	AA479348	H.sapiens mR	other
14054	>10	AA485223	ESTs	TM
38121	>10	AA485724	EST - RC_AA	other
28122	>10	AA485928	ESTs Weakly	other
38167	>10	AA487207	EST - RC_AA	other
38172	>10	AA487424	EST - RC_AA	other
38179	>10	AA487492	Homo sapiens	other
38182	>10	AA487501	ESTs	other
38194	>10	AA487969	ESTs	other
28141	>10	AA488432	ESTs	?
38211	>10	AA488687	ESTs	other
38235	>10	AA489030	ESTs	other

FIG.. 12Af

375 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
38280	>10	AA489791	EST - RC_AA	other
38316	>10	AA490500	Homo sapiens	other
38330	>10	AA490882	ESTs	other
38456	>10	AA504343	ESTs	SS,
38460	>10	AA504462	ESTs	other
38553	>10	AA521471	ESTs	other
38580	>10	AA598545	ESTs	?
38590	>10	AA598648	Human mRNA	other
38601	>10	AA598738	ESTs	?
28323	>10	AA599639	ESTs	other
38828	>10	AA609177	ESTs	TM
38838	>10	AA609215	EST - RC_AA	?
38867	>10	AA609318	Human cbl-b m	TM
38871	>10	AA609333	EST	?
38970	>10	AA609749	ESTs	other
38984	>10	AA609839	ESTs Modera	?
39045	>10	AA610077	ESTs	other
39062	>10	AA620333	EST	?
39080	>10	AA620552	EST - RC_AA	?
39110	>10	AA620709	ESTs Weakly	other
39176	>10	AA621091	ESTs	other
39218	>10	AA621330	ESTs	other
39221	>10	AA621346	Homo sapiens	other
39232	>10	AA621409	ESTs	other-
21	>10	AB000905	H.sapiens hist	?
8963	>10	AFFX-HUMTF	AFFX-HUMTF	?
33890	>10	AFFX-HUMTF	AFFX-HUMTF	?

FIG.- 12Ag

376 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
39302	>10	C14944	ESTs	other
39329	>10	C20797	EST	?
28644	>10	D12163	ESTs	other
218	>10	D13540	PROTEIN-TYR	other
236	>10	D13645	Human mRNA	other
9127	>10	D30037	PHOSPHATID	other
459	>10	D38293	Human mRNA	TM
39405	>10	D50975	ESTs	other
39433	>10	D52037	Human thymid	other
39436	>10	D52692	Human Ca2+	TM
14708	>10	D59388	EST	?
39488	>10	D60831	ESTs	other
39504	>10	D80632	ESTs	other
765	>10	D86096	Prostaglandin	?
787	>10	D86969	Human mRNA	other
789	>10	D86971	Human mRNA	other
39529	>10	F02202	ESTs	?
39535	>10	F02450	ESTs Modera	TM
18676	>10	F04022	ESTs	other
18718	>10	F04915	ESTs	other
18762	>10	F09458	ESTs	other
18782	>10	F09739	ESTs	other
29080	>10	F13655	ESTs Modera	other
19001	>10	H02890	ESTs	other
19164	>10	H10395	EST	?
39725	>10	H11323	ESTs	other
19203	>10	H11593	ESTs	other

FIG. 12Ah

377 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
19328	>10	H17808	ESTs	other
19387	>10	H20128	ESTs	?
39787	>10	H20131	ESTs	SS,
19389	>10	H20165	EST	?
39832	>10	H26279	EST - RC_H2	other
19591	>10	H40688	ESTs	other
29229	>10	H48459	Human mRNA	other
19727	>10	H52702	ESTs	other
19787	>10	H56679	ESTs	?
39995	>10	H62474	EST	other
29331	>10	H68116	ESTs	SS,TM
29344	>10	H68839	EST	TM
40064	>10	H72283	Human mRNA	?
40083	>10	H73466	MITOCHOND	other
19949	>10	H78263	ESTs	other
40204	>10	H88296	EST - RC_H8	TM
29523	>10	H88353	ESTs Weakly	other
29551	>10	H90134	ESTs	?
29645	>10	H95840	ESTs	?
20057	>10	H98079	ESTs	?
976	>10	HG2036-HT20	EST - HG2036	other
1158	>10	HG3344-HT35	EST - HG3344	?
1210	>10	HG37-HT37	EST - HG37-H	?
1346	>10	HG4716-HT51	EST - HG4716	?
1349	>10	HG4747-HT51	EST - HG4747	?
1445	>10	J03027	MHC class I p	?
1570	>10	K01383	EST - K01383	?

FIG.- 12Ai

378 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
1684	>10	L07541	Replication fa	other
1852	>10	L17328	Human FEZ2	TM
1856	>10	L18920	MELANOMA-A	?
1863	>10	L19161	TRANSLATIO	other
2070	>10	L37378	Homo sapiens	SS, TM
2123	>10	L40396	Homo sapiens	other
2144	>10	L41349	Phospholipase	SS,
9723	>10	L44542	ESTs	other
2188	>10	L47276	EST - L47276	other
2343	>10	M15353	Eukaryotic tra	other
2627	>10	M29610	Glycophorin E	TM
2857	>10	M58597	Fucosyltransfe	TM
3021	>10	M68941	Protein tyrosin	other
3163	>10	M84424	Cathepsin E	?
3196	>10	M86917	Oxysterol bind	other
20088	>10	N20054	ESTs Weakly	other
29795	>10	N20641	ESTs Highly	other
40427	>10	N21147	ESTs	other
40444	>10	N22140	ESTs Highly	other
29893	>10	N23003	ESTs	TM
40498	>10	N26086	Homo sapiens	SS,
40559	>10	N33024	ESTs	SS,
30190	>10	N33264	EST	?
30207	>10	N33920	H. sapiens mR	other
20304	>10	N34686	Homo sapiens	?
20307	>10	N34830	ESTs	other
30265	>10	N35115	ESTs	other
40594	>10	N35388	ESTs	other

FIG. 12Aj

379 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE: DESCRIPTOR	ORF STRUCTURAL INFO
40604	>10	N38893	Homo sapiens	other
40631	>10	N45124	EST's	other
40660	>10	N49104	NUCLEAR FA	other
30610	>10	N50138	EST	?
30617	>10	N50646	EST's	other
30631	>10	N50807	EST	?
30790	>10	N52935	EST	?
20564	>10	N55443	EST's	TM
40760	>10	N57927	EST's Weakly	other
30938	>10	N58561	Cathepsin B	other
20614	>10	N59230	EST's	SS,
20657	>10	N62889	EST's	other
31136	>10	N63512	EST's Weakly	TM
40827	>10	N64051	Homo sapiens	other
31310	>10	N66831	EST	?
40876	>10	N67607	Human Rho-a	other
20791	>10	N68057	Homo sapiens	?
40905	>10	N68738	EST's	other
40911	>10	N69114	H.sapiens mR	other
40913	>10	N69218	EST's	other
31484	>10	N69466	EST's	other
31619	>10	N73449	EST's	other
41005	>10	N79516	EST's	TM
31818	>10	N89774	Homo sapiens	other
31872	>10	N91109	EST	other
41040	>10	N91948	EST's	other
31944	>10	N93193	EST's	other

FIG. 12Ak

380 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
41065	>10	N93618	ESTs	other
32034	>10	N98926	ESTs Modera	other
41107	>10	R01634	ESTs	other
41163	>10	R08176	ESTs	other
21238	>10	R08564	Plasminogen-	other
21240	>10	R08613	ESTs	other
21412	>10	R20670	ESTs	other
21519	>10	R27975	EST - RC_R2	other
41381	>10	R42278	H.sapiens mR	?
32189	>10	R43183	ESTs	TM
32195	>10	R43471	ESTs Weakly	other
21902	>10	R43822	EST	?
21946	>10	R44707	ESTs	TM
22072	>10	R49406	ESTs	?
32240	>10	R50976	Ribonuclease	other
32258	>10	R55623	ESTs	other
22258	>10	R56432	ESTs	other
22282	>10	R59197	ESTs	other
32277	>10	R61493	Human mRNA	other
22372	>10	R62831	EST	?
22400	>10	R64109	ESTs	other
41593	>10	R64129	ESTs	other
10233	>10	R71427	ESTs Highly	other
41654	>10	R76437	THROMBOXA	TM
22557	>10	R76722	ESTs	other
22576	>10	R79111	ESTs	other
22593	>10	R79777	EST	?

FIG._ 12AI

381 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
41678	>10	R80675	EST	?
41719	>10	R89260	EST - RC_R8	other
22793	>10	R96208	ESTs	other
41752	>10	R97063	ESTs	other
3375	>10	S50223	HKR-T1	other
3406	>10	S66896	SQUAMOUS	other
3522	>10	S80267	Spleen tyrosin	other
41793	>10	T03887	ESTs	?
23198	>10	T40530	ESTs Weakly	other
23360	>10	T58531	ESTs	other
32635	>10	T61116	ESTs	other
42177	>10	T79786	ESTs	?
23623	>10	T84047	ESTs	?
23662	>10	T86674	ESTs	other
42242	>10	T89579	Homo sapiens	other
23759	>10	T90313	ESTs	other
23832	>10	T92018	ESTs	other
32740	>10	T92950	ESTs	other
42290	>10	T95105	ESTs	?
3598	>10	U01157	Glucagon-like	SS, TM
3659	>10	U04313	Protease inhib	other
3799	>10	U10690	Human MAGE	?
3870	>10	U14518	Centromere p	other
3913	>10	U16261	Human MDA-	SS,
4029	>10	U21090	Human DNA p	other
4157	>10	U28811	Human cystei	other
4178	>10	U30246	Human bumet	TM

FIG. 12Am

382 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
15006	>10	U30246	Human bumet	TM
4193	>10	U31116	Human beta-s	TM
4306	>10	U36798	Homo sapiens	TM
4362	>10	U39817	Bloom syndro	other
4386	>10	U40622	DNA repair pr	other
4388	>10	U40714	Human tyrosy	other
4455	>10	U43944	MALATE OXID	other
4477	>10	U45880	Human IAP-lik	other
4680	>10	U55766	Human Rev in	TM
4702	>10	U57341	EST - U57341	other
4713	>10	U57721	Human L-kynu	other
4787	>10	U61145	Human enhan	other
4862	>10	U65437	Human homeo	?
4945	>10	U69108	Homo sapiens	other
4975	>10	U71088	Human MEK5	other
4994	>10	U72514	Human C2f m	other
5002	>10	U72761	Human karyop	other
5021	>10	U73524	Human putativ	TM
5149	>10	U79716	Human reelin	SS,
5214	>10	U83303	H.sapiens mR	?
5243	>10	U85946	Human brain s	other
32789	>10	W02779	ESTs Modera	other
42354	>10	W19346	ESTs	other
42390	>10	W40150	Homo sapiens	other
33006	>10	W46286	ESTs Weakly	TM
33020	>10	W46891	ESTs Weakly	other
33109	>10	W59961	Human mRNA	other

FIG. 12An

383 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
24197	>10	W67277	ESTs	other
24215	>10	W69425	ESTs	other
33301	>10	W73883	ESTs	other
33343	>10	W79834	ESTs Weakly	other
33377	>10	W81219	ESTs Weakly	other
42602	>10	W86423	ESTs	TM
33556	>10	W90705	Murine leukem	other
33616	>10	W93726	Protease inhib	other
33666	>10	W95876	ESTs	TM
5510	>10	X05360	Cell division c	?
5558	>10	X07876	Wingless-type	SS,
5603	>10	X14253	Teratocarcino	TM
5619	>10	X14850	HISTONE H2A	SS,
5623	>10	X14975	T-CELL SURF	?
5692	>10	X17644	G1 to S phase	other
5789	>10	X54925	Matrix metallo	other
5799	>10	X55330	Aspartylglucos	SS,
5802	>10	X55544	CYCLIC-AMP	?
5857	>10	X58377	Human mRNA	other
5960	>10	X63575	ATPase Ca++	TM
5963	>10	X63629	Cadherin 3 (P	SS, TM
5986	>10	X64810	Proprotein con	?
6041	>10	X67155	MITOTIC KIN	other
6095	>10	X69962	Fragile X men	other
6106	>10	X70683	SRY (sex dete	TM
6155	>10	X74331	DNA primase	other
6167	>10	X74987	Ribonuclease	other

FIG.- 12Aa

384 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
6188	>10	X76029	NEUROMEDI	TM
6315	>10	X81889	H.sapiens mR	other
6382	>10	X85133	H.sapiens RB	other
6384	>10	X85137	Human kinesin	other
6438	>10	X89398	UFIACIL-DNA	?
6449	>10	X89986	H.sapiens mR	TM
6478	>10	X91648	H.sapiens mR	SS, TM
6479	>10	X91653	EST - X91653	?
6494	>10	X92689	H.sapiens mR	TM
6713	>10	Y08564	EST - Y08564	?
6790	>10	Y12394	Homo sapiens	other
24915	>10	YEL003w/	EST - YEL003	?
42773	>10	YEL019c/MMS	EST - YEL019	?
24545	>10	Z38462	ESTs	other
33713	>10	Z39427	ESTs	other
33791	>10	Z40883	ESTs	other
42766	>10	Z99394	ESTs Modera	other
21558	>10	R33112	Human AF-6 m	other
26718	>10	AA282576	ESTs	?
40113	9.9955090946	H78003	ESTs	?
10801	9.9879448276	AA069285	ESTs Weakly	other
37491	9.9513600842	AA455239	ESTs Highly	other
23900	9.9272347693	T95789	ESTs	other
254	9.9198395324	D14657	Human mRNA	other
6885	9.8970927914	Z29331	Ubiquitin-conj	other
29693	9.8850766398	H97819	ESTs	SS,
26482	9.8765189024	AA262491	ESTs	other

FIG. 12Ap

385 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
23123	9.8699502035	T25306	EST	?
26525	9.8160399123	AA278392	ESTs	other
13110	9.7643356605	AA435840	Homo sapiens	other
34863	9.7087597628	AA299784	EST	other
39432	9.7034550083	D51691	Phosphoribos	?
31312	9.6513325388	N66845	ESTs Weakly	?
21112	9.6358446349	R01179	ESTs	?
31572	9.6254820695	N71294	ESTs	other
17903	9.6221229759	AA160259	EST	?
20747	9.6094813734	N66842	ESTs	other
4676	9.589223908	U55206	Homo sapiens	TM
34363	9.5627081023	AA251587	Homo sapiens	other
39094	9.540768988	AA620636	ESTs	other
3888	9.5372000133	U15128	Human beta-1	?
39386	9.506250529	D12184	ESTs	TM
7674	9.4458059039	AA203742	ESTs	other
4192	9.4329744134	U31099	Human DP pr	TM
4507	9.422674945	U47050	Human putativ	TM
35606	9.412026255	AA402227	ESTs Modera	other
4970	9.3649551013	U70862	Human nuclea	?
19829	9.3432151573	H58813	EST	?
14837	9.2878584141	T40145	ESTs	TM
17336	9.2822148675	AA099585	ESTs	other
40541	9.2532836505	N30160	ESTs	other
29496	9.2487643833	H85434	EST	?
29943	9.1797074262	N24786	ESTs Modera	TM
17997	9.1629681314	AA169633	EST	other

FIG. 12Aq

386 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
21320	9.1243463318	R11673	ES's	other
13883	9.1178796537	AA476917	ES's Weakly	other
30539	9.0886887776	N49072	ES's	other
32778	9.0877919549	W02063	ES'	?
26380	9.0809559378	AA257012	ES'	?
15888	9.0595893607	X95632	Hurnan Abl int	other
40812	9.0012874244	N63419	ES's	other
903	8.9640387908	D90070	ATL-derived P	other
22674	8.9515777733	R87160	ES's	TM
40807	8.9510132281	N62995	TRANSCRIPT	other
15244	8.9195644974	W00904	ES's	TM
32296	8.8658776567	R67075	Zinc finger pro	other
18269	8.8575656769	AA209467	ES's	other
19662	8.8507626284	H47391	ES's	other
41607	8.833925517	R67868	CLF:AVAGE S	other
2548	8.8299864699	M25897	Platelet factor	TM
7736	8.8279341243	AA232121	Hurnan tyrosy	other
34490	8.7844537272	AA262354	ES's	other
38658	8.7669313482	AA599477	ES's	other
7528	8.765157554	AA149543	ES's	other
39939	8.7555031142	H53454	ES' - RC_H5	other
25111	8.7232692309	AA020787	ES's	other
21655	8.716167279	R38239	ES'	?
39663	8.665982852	H04756	ES's Highly	other
1042	8.652112324	HG2510-HT26	ES' - HG2510	?
32330	8.636115426	R77776	ES's	other
25382	8.6239456487	AA059007	ES's	other

FIG.- 12Ar

387 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
27074	8.5900813076	AA401475	ESTs Weakly	SS,
3955	8.5298909183	U18259	MHC class II t	other
4959	8.52646827	U70322	Human transp	other
2315	8.5259185808	M14123	EST - M14123	?
37253	8.4896914632	AA449357	ESTs	other
39624	8.471316877	F10836	ESTs	?
23213	8.4569920887	T40891	ESTs	?
2798	8.455596435	M54995	Connective tis	TM
41154	8.4413390141	R07499	ESTs	?
32479	8.4093689549	T16282	WEE1-LIKE P	other
41251	8.3587565415	R28279	Human clone	other
19081	8.3583603183	H06701	ESTs Weakly	other
21098	8.3105927559	R00545	ESTs	other
14723	8.3061679053	D59894	ESTs	other
37154	8.2994822341	AA447666	Human CENP	other
8068	8.2835586361	AA313387	ESTs Highly	other
7485	8.281679348	AA129547	ESTs	other
16501	8.2517969834	AA026969	ESTs	other
34527	8.2419163754	AA279091	ESTs	other
6700	8.1948675662	Y07867	H.sapiens mR	other
2852	8.1928816537	M58460	Human 75-kD	other
11188	8.1862492468	AA172372	ESTs	TM
42293	8.183311064	T95333	ESTs Weakly	TM
5443	8.1763317544	X02530	Interferon (gam	SS,
40937	8.1534810594	N70607	ESTs	TM
23371	8.1499496068	T59505	EST - RC_T59	?
26272	8.1339974519	AA252981	ESTs Weakly	other

FIG. 12As

388 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
17306	8.1332403762	AA086201	ESTs	other
18497	8.1192326373	AA233795	ESTs	other
235	8.0944363901	D13644	Human mRNA	other
24525	8.0860187097	Z38347	ESTs	TM
7826	8.0750029554	AA248884	EST - AA2488	TM
32142	8.0739258775	R38715	Homo sapiens	other
39067	8.0557768803	AA620405	ESTs	other
6235	8.0448957236	X78416	Casein alpha	TM
29517	8.0017588725	H88261	ESTs	other
28570	7.9852455973	C21104	Homo sapiens	other
39344	7.9162087762	C21034	ESTs Modera	other
18951	7.9002189759	H00580	ESTs	other
18953	7.8709160227	H00615	ESTs	other
18376	7.8564099916	AA226925	ESTs	other
19830	7.847878447	H58911	ESTs	other
36023	7.840835828	AA416881	ESTs	other
13347	7.8344414518	AA449238	ESTs	other
36614	7.8284591351	AA431466	ESTs	other
2192	7.8254072032	L48211	Homo Sapien	?
33016	7.8006574068	W46577	H.sapiens mR	other
17215	7.7941954038	AA083044	ESTs	other
34894	7.7659738105	AA311881	EST	?
40614	7.695001222	N39257	ESTs	other
36295	7.6834749899	AA424534	ESTs	other
19564	7.6744302788	H38833	ESTs	TM
16914	7.6686405336	AA058665	ESTs	SS,
35967	7.6378079107	AA412694	Human splicin	other

FIG. 12At

389 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
21672	7.6364823402	R38635	ESTs	other
19918	7.6303275831	H69787	ESTs	?
10511	7.6297744492	AA024482	ESTs Highly	other
17721	7.6057911016	AA136590	ESTs	?
42302	7.6031859697	T96130	EST	SS,
26134	7.6000619383	AA243763	ESTs	other
18766	7.5621799008	F09497	ESTs	other
34492	7.501590494	AA262439	ATL-derived P	other
270	7.4512152125	D14822	EST - D14822	other
35975	7.4177746986	AA412738	ESTs	other
29842	7.4095809671	N21688	ESTs	?
35389	7.3913043319	AA399555	ESTs	other
19979	7.3868157166	H88477	ESTs	other
5793	7.3865864025	X54942	CDC28 protei	other
19978	7.380969715	H87770	EST - RC_H8	other
1280	7.3691089318	HG4126-HT43	EST - HG4126	?
31571	7.3676263454	N71250	ESTs	other
23765	7.3541191734	T90443	ESTs Weakly	?
35123	7.3397933455	AA380927	EST	?
38252	7.3341119467	AA489247	ESTs	other
38216	7.3282021037	AA488861	ESTs	other
29418	7.2489407005	H77915	EST - RC_H7	?
4834	7.1980951054	U63541	Human mRNA	other
42504	7.1913036522	W69803	ESTs	other
6111	7.158000198	X71125	H. sapiens mR	TM
41773	7.154479618	T03024	ESTs Weakly	other
9951	7.1363626365	N71513	ESTs	other

FIG.-12Au

390 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
28109	7.0941968224	AA485212	ESTs	other
988	7.0783044659	HG2160-HT22	EST - HG2160	?
29848	7.0610668511	N22107	ESTs	other
30628	7.0607950168	N50744	ESTs	other
22567	7.0225726353	R77771	ESTs	TM
9347	7.006323071	H03686	ESTs	TM
11696	7.0026773299	AA252894	ESTs	other
40584	7.0010096333	N34870	EST	?
193	6.9767029188	D10923	PFI0BABLE G	TM
18305	6.9740536051	AA214048	Ccollagen type	other
6078	6.9699682397	X69141	FARNESYL-D	other
26741	6.902658703	AA283198	ESTs	other
35069	6.8992865685	AA358397	EST	?
23504	6.8977135983	T71042	ESTs	other
299	6.8824513029	D16815	Homo sapiens	other
40583	6.8689903023	N34855	ESTs	other
31428	6.8623762224	N68594	ESTs	other
6169	6.8606959727	X75091	SET PROTEIN	other
39524	6.8567355171	F01905	MALATE OXID	other
34578	6.8430689439	AA280837	ESTs	other
38678	6.837527995	AA599920	Small inducibl	other
23936	6.8251471804	T96930	ESTs	other
9326	6.8181321394	D89377	Mish (Drosoph	other
19188	6.8067351968	H11255	ESTs Highly	TM
18185	6.7882148811	AA194983	Homo sapiens	other
27028	6.757529124	AA399630	ESTs Weakly	other
41289	6.7519531681	R37265	EST	other

FIG.- 12Av

391 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
34511	6.7364448798	AA278298	EST - RC_AA	other
1566	6.7056207716	J05614	EST - J05614	?
25675	6.6692299748	AA129757	ESTs Highly	other
5814	6.6584342828	X56088	CYTOCHROM	SS,
13861	6.6236291607	AA470145	ESTs	other
29794	6.6026313352	N20598	ESTs	other
39333	6.5902382643	C20910	Cyclin B1	other
3770	6.5835303599	U09609	Nuclear factor	other
31831	6.5829933764	N89894	ESTs	?
33063	6.5808125026	W53000	Homo sapiens	other
20326	6.5640084836	N35583	ESTs Weakly	?
34384	6.5535703492	AA252537	ESTs	other
25599	6.5490481991	AA114091	Human (clone	other
39749	6.5369363254	H14988	ESTs	other
42596	6.5200567072	W85900	ESTs	?
39606	6.5119482185	F10243	ESTs Weakly	?
14617	6.5105504748	C14983	ESTs	other
27831	6.45670814	AA456044	ESTs	?
34896	6.4496517783	AA312551	EST	?
27360	6.4434305006	AA425356	ESTs	other
20126	6.4326610424	N22015	ESTs	TM
6663	6.4324809977	Y00291	RETINOIC AC	TM
30692	6.4196636207	N51563	ESTs	other
36472	6.4189542265	AA428633	EST	?
9578	6.3961788753	H87652	Homo sapiens	other
39670	6.3818496159	H05626	ESTs	other
22697	6.3652792447	R89218	ESTs	other

FIG. 12Aw

392 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
37308	6.3647804993	AA451694	EST	TM
16101	6.3517262802	AA002147	EST	?
20629	6.3486854401	N59798	ESTs	other
36100	6.3364146287	AA417740	ESTs	?
15488	6.3252590241	W28097	Homo sapiens	other
36667	6.3131273544	AA432136	ESTs	other
30766	6.3115037924	N52627	EST - RC_N5	?
32882	6.2745311453	W37683	ESTs	TM
18072	6.2675797205	AA180448	EST	?
18231	6.2652604863	AA199747	Human mRNA	other
38282	6.2514165678	AA489814	EST	?
28125	6.250317021	AA486073	ESTs	other
37464	6.2484456382	AA454747	ESTs	?
36618	6.1946328223	AA431478	ESTs	other
5082	6.1931116815	U78524	Human Gu bin	other
1441	6.1777287039	J02963	Integrin alpha	other
42105	6.14875944	T67710	ESTs	?
6061	6.1394863141	X68314	Glutathione pe	SS,
32570	6.1156028796	T30222	ESTs Weakly	TM
32504	6.1019612076	T17063	EST	?
23335	6.0977927504	T56804	EST	?
10867	6.0970991075	AA088458	ESTs Weakly	other
30883	6.0911993489	N56923	EST	?
14528	6.0859008453	AA620295	ESTs	TM
29454	6.0685955036	H81308	EST	?
6798	6.0539173278	Y13153	Homo sapiens	TM
21248	6.0525426545	R08871	- ESTs	?

FIG.- 12Ax

393 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
21940	6.0499964138	R44538	ESTs	?
29066	6.0455247653	F10927	Homo sapiens	other
18774	6.0446826953	F09609	ESTs	?
36722	6.0172343991	AA435512	ESTs	SS,
18062	6.0034342969	AA179845	ESTs Modera	other
22989	5.9992817406	T16305	ESTs	other
41745	5.9905623898	R95895	ESTs	?
8787	5.9894877658	AA504307	X-LINKED HE	other
20550	5.984861795	N55013	ESTs	other
26470	5.9417764101	AA262179	ESTs	other
16574	5.9356497569	AA031926	EST	other
693	5.9169537385	D80007	Human mRNA	other
4093	5.914830973	U25182	Human antiox	TM
1192	5.9086264407	HG3546-HT37	EST - HG3546	?
22956	5.8954735623	T10248	ESTs	other
36723	5.891606409	AA435524	EST	?
2114	5.8844986595	L40384	EST - L40384	other
26872	5.868238789	AA291137	ESTs	other
6602	5.8663883018	X98266	EST - X98266	other
42701	5.8594493433	Z38612	ESTs	other
28573	5.84591116	C21118	ESTs	other
18290	5.8189427595	AA211901	ESTs	other
732	5.8043917941	D83781	Human mRNA	other
5330	5.8014145611	U91327	EST - U91327	?
33503	5.7990715189	W88720	EST	?
2553	5.7797505864	M26167	Human platele	?
34705	5.7658806254	AA286907	ESTs Weakly	other

FIG..12Ay

394 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
42665	5.7594091043	W93659	ESTs	other
38180	5.7539310793	AA487495	EST - RC_AA	other
4244	5.7476738809	U33286	Human chrom	other
32822	5.7418957453	W16834	ESTs	TM
3977	5.7245885557	U18991	Retinal pigme	?
24673	5.7202366155	Z39301	ESTs	TM
6928	5.7120261128	Z46629	SRV (sex-dete	other
38726	5.7030796258	AA608733	ESTs	?
39290	5.6892372058	C14573	Human mRNA	other
11405	5.6818873796	AA232231	ESTs	other
22538	5.6792006591	R73567	Human sapiens	TM
40747	5.6605393208	N56872	Human sapiens	TM
31596	5.6554024604	N72094	ESTs	other
6329	5.6415652518	X82279	EST - X82279	?
31578	5.6273323661	N71361	ESTs	other
33207	5.6271818482	W70051	H.sapiens mR	other
2545	5.6105860146	M25753	Cyc in B1	other
22580	5.5988402647	R79156	ESTs	other
33592	5.5935314518	W93127	ESTs	other
28843	5.5734698755	D60252	ESTs	other
6160	5.5689050619	X74794	CDC21 HOMO	other
37987	5.561345667	AA479666	ESTs	other
42515	5.5217868611	W72116	Human sapiens	other
4732	5.5130668527	U58522	Human huntin	other
3299	5.5099850678	M95623	Hydroxymethy	?
28320	5.473406981	AA599574	ESTs	?
746	5.471260899	D84454	Human mRNA	TM

FIG. 12Az

395 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
39373	5.4635804954	C21517	ESTs	other
3117	5.4398413537	M81182	Peroxisomal m	other
21257	5.4343612441	R09196	ESTs Modera	other
31487	5.4318648859	N69507	ESTs	other
28954	5.4137130511	F03153	ESTs	other
38928	5.389782721	AA609595	ESTs	other
29903	5.3722320622	N23366	EST	?
30925	5.3437432315	N58295	ESTs Weakly	?
19091	5.3344615669	H07864	ESTs	TM
28209	5.3138951918	AA491250	ESTs	other
9470	5.3118897984	H46617	EST - H46617	other
9435	5.3070056656	H30201	EST - H30201	?
28552	5.2954432572	C20914	ESTs	other
27411	5.2940164267	AA428137	ESTs	other
30615	5.2924125264	N50556	ESTs	other
28313	5.2657977167	AA599309	ESTs	TM
39321	5.2649035384	C20632	ESTs	?
29934	5.2531047395	N24194	ESTs	other
1094	5.2496703122	HG2846-HT29	EST - HG2846	?
39578	5.2481126384	F08925	ESTs	TM
11232	5.2466798424	AA186804	ESTs Weakly	other
2466	5.2426349328	M21539	Human small	other
26843	5.2387758661	AA287450	ESTs	?
40331	5.2353385567	H97562	ESTs Weakly	other
8035	5.205798365	AA305116	EST - AA3051	other
29793	5.1955425722	N20593	ESTs Weakly	other
34109	5.1481590107	AA210722	EST	?

FIG.- 12Ba

396 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
26408	5.1432577257	AA258177	ESTs Weakly	other
19263	5.1427029807	H15054	ESTs	TM
24596	5.1416089352	Z38810	ESTs	other
28589	5.1365059753	C21245	H.sapiens mR	other
5684	5.1121931412	X17098	Pregnancy-sp	other
30710	5.1079347344	N51761	EST	?
35765	5.0973514948	AA406167	EST	?
26360	5.0863127861	AA256460	ESTs	?
2351	5.0849612092	M15796	Proliferating c	?
30262	5.0836877534	N35065	Homo sapiens	other
41792	5.0737512465	T03886	ESTs	?
36710	5.0703839864	AA434411	ESTs	other
39090	5.0546885407	AA620628	ESTs	TM
42185	5.0539926381	T79951	ESTs	?
18745	5.0460321557	F09134	ESTs	other
35746	5.0396841996	AA406063	ESTs	other
35356	5.0354809581	AA399053	EST	?
36769	5.0312706878	AA435750	EST	?
36900	5.0279911548	AA436866	H.sapiens mR	other
27595	5.0244757301	AA443328	ESTs	TM
16290	5.0056611904	AA016145	ESTs	?
27117	5.0016146599	AA405098	ESTs Weakly	other
4304	4.9951954397	U36764	Eukaryotic tra	other
33458	4.9907402071	W86835	Homo sapiens	other
26693	4.9800090679	AA282120	EST	?
12669	4.9758138651	AA417030	Homo sapiens	other
29701	4.9708526387	H97970	EST	?

FIG. 12Bb

397 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
20480	4.9557253636	N52168	ESTs	TM
8720	4.9439110602	AA481218	EST - AA4812	other
34828	4.9431269475	AA292436	Homo sapiens	SS, TM
14985	4.941621032	U15128	Human beta-1	?
16115	4.9377553522	AA004420	ESTs	?
42506	4.9348587118	W70074	EST	other
34761	4.9316837445	AA287833	ESTs	other
11870	4.9281056201	AA262587	ESTs	TM
23211	4.9258391854	T40889	ESTs	other
40611	4.9160502275	N39138	Homo sapiens	other
42611	4.9128605354	W87006	Homo sapiens	other
39652	4.9045174605	H03099	ESTs	other
17581	4.889674751	AA129395	EST	?
37239	4.8704375389	AA449121	ESTs	?
18712	4.8703618781	F04677	ESTs	other
30709	4.8611171953	N51752	ESTs Weakly	other
34179	4.8503613948	AA227903	ESTs Highly	other
21433	4.825670988	R22183	EST	?
39731	4.8186142741	H11760	ESTs	other
31295	4.8116614607	N66653	ESTs	other
24647	4.804163055	Z39108	EST	?
31292	4.8008871817	N66615	ESTs	other
1285	4.7997542393	HG4157-HT44	EST - HG4157	?
1106	4.7932425858	HG2981-HT31	EST - HG2981	?
18212	4.7912262565	AA196506	ESTs	other
34367	4.782207045	AA251758	Homo sapiens	other
34802	4.7797760205	AA291468	ESTs	TM

FIG.. 12Bc

398 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
34762	4.7775301546	AA287834	ESTs	other
11595	4.7696612848	AA242819	ESTs	other
8295	4.7639839111	AA405082	ESTs	?
17622	4.758635576	AA131584	ESTs: Weakly	other
35781	4.7572463523	AA406335	ESTs	other
34754	4.7483874972	AA287642	Human mRNA	other
23237	4.7444854356	T47291	EST	?
37667	4.7280445357	AA460318	ESTs: Highly	other
11568	4.7257189975	AA236786	ESTs	other
38622	4.7190695733	AA598967	ESTs	?
5137	4.7057359474	U79296	Dihydrodiploam	other
25038	4.7002244728	AA010065	CDC28 protei	other
19288	4.7000147312	H16567	ESTs	other
32503	4.6979488292	T17045	Collagen type	other
3278	4.6953739298	M94055	SOLILUM CHA	TM
9696	4.6942061018	L38961	Integral transm	TM
35400	4.6901390898	AA399591	Horrio sapiens	other
35246	4.6862691303	AA398367	EST Weakly s	?
36387	4.6822499271	AA426270	ESTs	other
21509	4.6730072542	R27314	ESTs	other
31381	4.6729672124	N67889	ESTs	other
26723	4.6727894925	AA282781	ESTs: Highly	other
36326	4.6703621086	AA425151	Human GAP S	other
17409	4.6688418667	AA113136	EST - RC_AA	other
4908	4.6552339935	U67156	Human mitoge	other
30594	4.6496238328	N49967	ESTs	other
38286	4.64639735	AA489847	ESTs: Weakly	?

FIG. 12Bd

399 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
13073	4.6426509459	AA433950	ESTs	other
40435	4.6240181066	N21614	Homo sapiens	other
14474	4.6228694379	AA609427	ESTs Modera	other
38213	4.615309907	AA488847	ESTs Weakly	?
5312	4.606644198	U90716	Human cell su	SS, TM
24225	4.6041550359	W70326	ESTs	?
35588	4.5868982366	AA401750	EST	?
29739	4.5863199051	H99626	EST	?
7203	4.5792992577	AA053096	EST - AA0530	other
2157	4.5772055869	L41939	Homo sapiens	SS, TM
32086	4.5661024279	R11510	ESTs	?
8085	4.5648114738	AA314779	ESTs Weakly	SS,
224	4.5622018989	D13633	Human mRNA	other
34006	4.5609980241	AA188761	DNA polymera	other
33656	4.5557384389	W95477	ESTs	other
34065	4.5537335124	AA195517	ESTs Weakly	TM
6028	4.5357922097	X66503	Acetylosuccin	other
4166	4.5032930671	U29463	Cytochrome B	?
40262	4.5024727522	H93562	ESTs	TM
22687	4.5018672549	R88209	ESTs	TM
41069	4.4977510482	N93969	H.sapiens mR	SS,
8264	4.4793100575	AA401334	ESTs	other
27588	4.472017297	AA443187	ESTs	other
35882	4.4717597552	AA412047	ESTs	?
34479	4.465519191	AA262080	Human bumet	TM
15921	4.4548516436	Y12065	Homo sapiens	?
11279	4.4380038671	AA195399	ESTs	other

FIG. 12Be

400 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
39222	4.4367650786	AA621348	ESTs Highly	other
34428	4.4364736766	AA256526	ESTs	other
8771	4.432067373	AA491188	ESTs	other
22193	4.4189610024	R53891	Homo sapiens	other
7898	4.4066170674	AA263032	ESTs	other
19902	4.3886145805	H66736	ESTs	other
9276	4.3868095209	D82374	ESTs	other
10716	4.3794529068	AA053319	ESTs	TM
13193	4.3751913512	AA442763	ESTs Highly	other
5690	4.3723059417	X17620	NUCLEOSIDE	other
35102	4.37147138	AA371509	EST - RC_AA	TM
17983	4.3612985467	AA169226	ESTs	other
24962	4.3497206925	AFFX-HUMTF	AFFX-HUMTF	?
31680	4.3416539669	N74438	ESTs	other
27168	4.330306894	AA410258	ESTs	?
28731	4.3231846659	D20981	EST	other
28348	4.3212284906	AA608752	ESTs	?
16335	4.3019961487	AA018587	ESTs Weakly	other
33036	4.2915644973	W48580	ESTs Weakly	other
30180	4.2897721925	N33144	ESTs	SS,
35591	4.2895541242	AA401758	ESTs Weakly	?
25340	4.2721717135	AA054554	EST	other
28106	4.2659103748	AA485084	ESTs	other
38690	4.2649184307	AA600121	ESTs	other
20203	4.2626499431	N26855	ESTs Modera	SS,
10251	4.2608760694	R76185	ESTs Weakly	SS,
12684	4.2604192389	AA417558	ESTs	

FIG.-12Bf

401 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
31636	4.2509469427	N73680	Natural resista	TM
20769	4.2479765348	N67277	ESTs	other
1572	4.2353281083	K01884	EST - K01884	?
10923	4.2292322072	AA116036	ESTs	other
34380	4.2283792392	AA252414	ESTs	other
10132	4.2222816115	R35733	EST - R35733	other
16629	4.2161752119	AA036811	ESTs	other
25146	4.1969683794	AA026356	ESTs	?
28730	4.1965943098	D20959	ESTs Modera	other
10200	4.1874912391	R64521	ESTs	other
38695	4.1545794663	AA600176	ESTs	other
31365	4.150549979	N67550	ESTs	other
42379	4.1496120668	W37999	ESTs	other
28050	4.1428703354	AA479139	Acid phosphat	other
2620	4.1386565707	M29474	Human recom	?
8927	4.1340593744	AF008442	Homo sapiens	other
13379	4.1269549188	AA449741	ESTs Weakly	other
5134	4.1218251808	U79293	Human clone	other
2626	4.1213948	M29581	Zinc finger pro	other
38005	4.1160483666	AA479969	ESTs	?
36575	4.1127196584	AA431085	EST	?
18296	4.1121837207	AA213620	ESTs Weakly	TM
29531	4.1111459313	H88953	EST - RC_H8	?
143	4.1095880506	AFFX-HUMTF	AFFX-HUMTF	other
10970	4.0967613396	AA129390	ESTs	SS,
25836	4.0952825397	AA152305	Interferon (gam	?
19735	4.0937927853	H53038	EST	

FIG.-12Bg

402 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
40711	4.0909709431	N53564	ES's	other
4149	4.0901471427	U28386	RA3 (recomb	TM
5767	4.0862784557	X53793	MULTIFUNCT	other
5503	4.0861035825	X05232	Stromelysin	SS,
20310	4.0641711656	N34893	ES's Highly	other
456	4.0599824566	D38145	Prostaglandin	SS,
7814	4.0559685576	AA248406	ES's	other
40230	4.0447282719	H90161	ES's	SS,
33651	4.039204804	W95409	ES's	other
16777	4.0231657929	AA046968	EST	?
19110	4.0094905222	H08778	ES's	other
34442	4.0077010365	AA258093	HKR-T1	other
5099	4.004992433	U79247	Human clone	TM
8209	3.9990473163	AA384220	ES's	other
24408	3.9976586074	W90146	ES's	other
26596	3.9974919787	AA279943	ES's	other
16485	3.9811264008	AA026269	Spleen focus	other
32969	3.9804901745	W42451	ES's	TM
27006	3.9799768093	AA398695	ES's Weakly	other
29809	3.9526765967	N21043	EST	?
9596	3.9440163451	H91564	ES's	TM
29024	3.9377933938	F09315	Homo sapiens	other
21694	3.9356365584	R39317	Homo sapiens	other
13207	3.929998104	AA443321	ES's	other
37865	3.9143752629	AA476623	ES's Highly	other
36201	3.9129828172	AA421164	ES's	?
8961	3.8981160269	AFFX-HUMTF	AFFX-HUMTF	?

FIG.. 12Bh

403 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
17444	3.8927133917	AA115933	ES'Is	other
25869	3.8919834527	AA157267	ES'Is Highly	TM
24862	3.89042252	Z41415	ES'Is Highly	other
26685	3.889363206	AA281950	ES'Is	?
42300	3.8850230366	T95850	ES'Is	?
6495	3.8830844863	X92715	Zinc finger pro	other
38604	3.8828045942	AA598803	ES'Is	TM
36358	3.8826713718	AA425756	ES'Is	other
30560	3.873276445	N49284	MYB PROTO-	other
14413	3.8724466158	AA600150	ES'Is	other
23823	3.8574824967	T91805	Homo sapiens	other
38158	3.853096838	AA487021	ES'Is	?
2572	3.8519747554	M27281	Vascular endo	other
40100	3.8464168967	H75933	Laminin recep	other
40258	3.8462992993	H93340	ES'Is	TM
20944	3.8461621525	N74443	ES'Is	other
20411	3.8459400966	N48963	Homo sapiens	other
10345	3.8457714481	AA001663	ES'Is	other
31261	3.8451974374	N66248	ES'Is	other
8513	3.8378410994	AA446990	ES'Is	other
13877	3.8363409835	AA476604	ES'Is	other
40748	3.8253562321	N56879	ES'Is	?
14509	3.8152852193	AA609943	ES'Is	other
10281	3.8065567331	R80333	ES'Is	other
25284	3.8044158642	AA045074	ES'Is Weakly	other
6730	3.7900025129	Y09305	H.sapiens mR	other
16033	3.7884592402	AFFX-HUMIS	AFFX-HUMIS	?

FIG. 12Bi

404 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
39242	3.7827164808	AA621523	ESTs	other
27354	3.7794760435	AA425221	ESTs	?
4552	3.777263605	U49188	Human placen	SS, TM
18385	3.7756199108	AA227219	Homo sapiens	other
16754	3.7677416053	AA046067	EST - RC_AA	other
12752	3.7671137403	AA421250	ESTs	other
42463	3.7601033106	W60180	ESTs	other
10614	3.7581669016	AA037357	ESTs	?
867	3.7459337969	D87716	Human mRNA	other
7608	3.7336047135	AA180967	ESTs	other
31795	3.732738742	N80703	ESTs	other
35377	3.7273784603	AA399453	EST - RC_AA	?
22828	3.7243928524	R98192	ESTs	other
25240	3.7243198336	AA039713	ESTs	other
11008	3.7197361366	AA134289	ESTs Weakly	?
4341	3.7162349944	U38545	Human ARF-a	other
28833	3.7147818393	D59787	EST - RC_D5	?
3750	3.7121007154	U09279	Collagen type	SS, TM
17483	3.6943413512	AA122147	ESTs	TM
16854	3.6915208471	AA055552	ESTs Weakly	other
3709	3.6891656771	U07550	Heat shock 10	?
1608	3.6652978422	L00205	KERATIN TYP	TM
24577	3.6617721053	Z38727	Homo sapiens	other
31032	3.6570916386	N62508	ESTs	other
4951	3.6536195433	U69546	Human RNA b	other
37660	3.6523275307	AA460225	ESTs	other
20418	3.6495357091	N49209	ESTs	other

FIG. 12Bj

405 / 454

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
27995	3.6485167436	AA470155	Homo sapiens	?
7971	3.6434397185	AA287423	ES's	other
27606	3.64303453	AA443793	ES's	other
24677	3.6427250633	Z39338	ES's Highly	other
11070	3.6406198277	AA148521	ES's Weakly	TM
9328	3.6356048599	D89618	Homo sapiens	other
36826	3.634689802	AA435996	ES's	other
17678	3.6300045795	AA134275	Human HIV1 t	other
36209	3.6274694477	AA421266	ES's Weakly	other
34120	3.6258090412	AA211615	ES'	?
38152	3.6246442011	AA486737	H.sapiens mR	TM
38463	3.6184693268	AA504491	ES's Weakly	TM
20064	3.6183699978	H98653	ES's	TM
31256	3.5992620732	N66152	ES'	?
9713	3.5985228843	L44338	Homo sapiens	other
28622	3.5768056147	D11837	ES's	?
38057	3.5736105703	AA481549	ES' - RC_AA	other
28763	3.5688723791	D45568	ES'	?
16996	3.5680705709	AA069038	ES' - RC_AA	TM
28628	3.5604144617	D11888	ES's Modera	?
25804	3.5442954572	AA148885	ES's	?
2492	3.5423964239	M22898	Tumor protein	?
14904	3.5411970737	T83389	ES's Highly	other
25265	3.5347588502	AA043765	H.sapiens RY	other
13606	3.5327912417	AA456437	ES's Weakly	other
42307	3.5318436465	T96595	ES' - RC_T96	TM
1544	3.526202414	J05068	TRANS COBA	SS,

FIG.. 12Bk

406 / 454

CODE	PRIMEKEY	D OF TUMOR OVE	EXEMPLAR ACCESSION	COMPLETE TITLE
CZA8	111929	3.7	R40057	prominin (mouse)-like 1
BCX2	128790	4.0	AA291725	secreted frizzled-related protein 4
CBC2	101809	5.7	M86849	Homo sapiens connexin 26 (GJB2) mRNA, complete cds
CBC1	100365	4.8	D78611	mesoderm specific; transcript (mouse) homolog
CBC3	102618	2.5	U65932	extracellular matrix protein 1
	134804	6.3	L37036	small inducible cytokine subfamily B (Cys-X-Cys); member 5 (epithelial-derived neutrophil-activating peptide 78)
	104209	2.1	AB000221	small inducible cytokine subfamily A (Cys-Cys); member 18; pulmonary and activation-regulated
CJA8	115697	8.1	AA411502	ESTs; Weakly similar to airway trypsin-like protease [H.sapiens]
	124315	5.4	H94892	v-ral simian leukemia viral oncogene homolog A (ras related)
	109415	4.3	AA227219	Homo sapiens CAGF9 mRNA; partial cds
	103613	5.1	Z46629	SRY (sex-determining region Y)-box 9 (campomelic dysplasia; autosomal sex-reversal)
	109166	6.2	AA179845	RAB6 interacting; kinesin-like (rabkinesin6)
CJA9	116176	5.7	AA463725	ESTs; Weakly similar to KIAA0226 [H.sapiens]
CGA7	115522	8.1	AA331393	ESTs
	125852	5.7	H09290	ESTs; Weakly similar to unknown [H.sapiens]
BCN5	112244	3.1	R51309	ESTs
CQA1	132592	5.6	AA129390	ESTs
BCN7	117280	5.4	N22107	ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]
	102663	4.8	U70322	karyopherin (importin) beta 2
CQA2	104660	6.0	AA007160	ESTs
	113702	2.4	T97307	ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
	100154	6.0	D14657	KIAA0101 gene product

FIG. 13Aa

407 / 454

CODE	PRIMEKEY	D OF TUMOR OVE	EXEMPLAR ACCESSION	COMPLETE TITLE
102260		3.7	U28386	Human nuclear localization sequence receptor hSRP1 alpha mRNA, complete cds
101809		5.7	M86849	Homo sapiens connexin 26 (GJB2) mRNA, complete cds
133272		3.2	AA465016	ESTs; Highly similar to serine protease homolog
100365		4.8	D78611	mesoderm specific: transcript (mouse) homolog
126819		4.7	AA305536	EST176522 Colon carcinoma (Caco-2) cell line II Homo sapiens cDNA 5' end, mRNA sequence.
132543		4.6	AA417152	ESTs; Highly similar to protein regulating cytokinesis 1 [H.sapiens]
103023		5.5	X53793	multifunctional polypeptide similar to SAICAR synthetase and AIR carboxylase
132109		3.1	AA599801	ESTs
104037		3.5	AA372630	differentially expressed in hematopoietic lineages
104978		3.5	AA088458	ESTs; Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]
108695		3.0	AA121315	ESTs
107248		3.8	D59894	ESTs
132902		3.4	AA490969	ESTs
120104		4.0	W95477	ESTs
128790		4.0	AA291725	secreted frizzled-related protein 4
101923		3.8	S75256	HNL=neutrophil lipocalin [human, ovarian cancer cell line OC6, mRNA Partial, 534 nt]
119943		3.4	W86835	copine III
130648		3.9	AA075427	ESTs
132358		3.5	X60486	H4 histone family; member G
106286		3.2	AA434441	frizzled (Drosophila) homolog 7
117557		2.3	N33920	diubiquitin

FIG.. 13Ab

CODE	PRIMEKEY	D OF TUMOR OVE	EXEMPLAR ACCESSION	COMPLETE TITLE
129691		3.3	X06700	collagen; type III; alpha 1 (Ehlers-Danlos syndrome type IV; autosomal dominant)
114767		4.5	AA148885	minichromosome maintenance deficient (S. cerevisiae) 4
100335		3.8	D63391	platelet-activating factor acetylhydrolase; isoform Ib; gamma subunit (29kD)
134989		3.5	AA236324	ESTs; Weakly similar to !!!! ALU CLASS A WARNING ENTRY !!!! [H.sapiens]
110009		3.4	H10933	ESTs
124059		4.0	F13673	ESTs
104755		2.2	AA024482	ESTs; Weakly similar to epidermal type I keratin [H.sapiens]
107151		3.4	AA621169	ESTs
132669		2.9	AA188378	ESTs; Weakly similar to 60S RIBOSOMAL PROTEIN L22 [H.sapiens]
104394		5.5	H46617	yp19h1.r1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:187921 5', mRNA sequence
117667		2.5	N39214	ser-Thr protein kinase related to the myotonic dystrophy protein kinase
104954		3.3	AA074514	ESTs; Moderately similar to (define not available 4753768) [H.sapiens]
132994		3.7	AA505133	ESTs
102681		3.7	U72761	karyopherin (importin) beta 3
103989		2.2	AA314779	ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
132183		2.5	L19183	Human MAC30 mRNA; 3' end
118695		3.0	N71781	ESTs
100552		3.4	HG2167- HT22	Protein Kinase H131, Camp-Dependent
120471		2.5	AA251829	ESTs; Moderately similar to (define not available 4680697) [H.sapiens]
126547		4.2	U47732	transmembrane 4 superfamily member 3
106057		3.3	AA417067	ESTs

FIG. 13Ac

409 / 454

CODE	PRIMEKEY	D OF TUMOR OVE	EXEMPLAR ACCESSION	COMPLETE TITLE
125103		4.0	T95333	ESTs; Weakly similar to Strabismus [D.melanogaster]
135243		3.4	AA215333	ESTs
121457		2.5	AA411448	ESTs; Moderately similar to alternatively spliced product using exon 13A [H.sapiens]
131216		2.7	D31058	ESTs
112971		2.4	T17185	ESTs
111179		2.1	N67239	ESTs
123533		2.3	AA608751	ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]
105175		2.4	AA186804	ESTs; Weakly similar to unknown [S.cerevisiae]
105156		2.7	AA172372	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]
111223		2.5	N68921	ESTs; Weakly similar to neogenin [H.sapiens]
132180		2.7	AA405569	fibroblast activation protein; alpha
106400		2.1	AA447621	ESTs
129260		3.1	AA093834	ESTs; Highly similar to (define not available 4679014) [H.sapiens]
115291		3.9	AA279943	ESTs
128628		2.1	C14037	ESTs; Weakly similar to Yel007c-ap [S.cerevisiae]
116399		2.7	AA599729	Homo sapiens homeobox protein A10 (HOXA10) gene; complete cds
130987		3.5	R45698	ESTs
105082		2.6	AA143763	ESTs; Weakly similar to Similarity to S. Pombe BEM1/BUD5 suppressor [C.elegans]
103453		3.2	X99585	H.sapiens mRNA for SMT3B protein
115947		2.6	AA443793	ESTs
105012		2.8	AA116036	ESTs; Highly similar to (define not available 4589929) [H.sapiens]
105507		3.2	AA256678	ESTs; Moderately similar to (define not available 4106061) [H.sapiens]
130800		2.6	AA223386	ESTs; Weakly similar to katanin p80 subunit [H.sapiens]

FIG. 13Ad

CODE	PRIMEKEY	D OF TUMOR OVE	EXEMPLAR ACCESSION	COMPLETE TITLE
	116461	3.4	AA621557	ESTs; Moderately similar to !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! [H.sapiens]
	129945	2.5	AA232104	ESTs; Highly similar to (define not available 4929579) [H.sapiens]
	100864	2.1	HG4297- HT45	Transcriptional Ccactivator Pc4
	128131	2.3	AI283162	claudin 3
	131564	2.8	AA491465	ESTs
	100279	3.1	D42084	Human mRNA for KIAA0094 gene; partial cds
	134405	1.8	J04177	collagen; type XI; alpha 1
	130287	2.6	AA1113149	tumor suppressing subtransferable candidate 3
	108828	2.1	AA131584	ESTs; Weakly similar to coded for by C. elegans cDNA cm16f6 [C.elegans]
	131289	2.2	AA485697	ESTs
	109141	4.2	AA176428	ESTs
	119307	2.5	T32108	ESTs
	134319	2.1	AA129547	ESTs; Moderately similar to !!!!! ALU SUBFAMILY J WARNING ENTRY !!!!! [H.sapiens]
	133458	5.0	M18728	non-specific cross: reacting antigen
	116732	2.3	F13779	ESTs; Weakly similar to !!!!! ALU SUBFAMILY J WARNING ENTRY !!!!! [H.sapiens]
CGA8	115239	3.0	AA278650	ESTs

410 / 454

FIG. 13Ae

411 / 454

CODE	PRIMEKEY	D OF TUMOR OVE	EXEMPLAR ACCESSION	COMPLETE TITLE
CZA8	111929	3.7	R40057	prominin (mouse)-like 1
BCX2	128790	4.0	AA291725	secreted frizzled-related protein 4
CBC2	101809	5.7	M86849	Homo sapiens connexin 26 (GJB2) mRNA, complete cds
CBC1	100365	4.8	D78611	mesoderm specific transcript (mouse) homolog
CBC3	102618	2.5	U65932	extracellular matrix protein 1
CJA8	115697	8.1	AA411502	ESTs; Weakly similar to airway trypsin-like protease [H.sapiens]
CJA9	116176	5.7	AA463725	ESTs; Weakly similar to KIAA0226 [H.sapiens]
CGA7	115522	8.1	AA331393	ESTs
BCN5	112244	3.1	R51309	ESTs (now Sulfatase by in-house sequencing)
CQA1	132592	5.6	AA129390	ESTs
BCN7	117280	5.4	N22107	ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]
CQA2	104660	6.0	AA007160	ESTs

FIG. 14

FIG. 15

413 / 454

ATGACCATGATTACGCCAAGCTTGGCAGGAGGAGACAGCCACTTGGCCAGTCAACCAAAACAAGGAGGAGGTCGAAGAC
 TGTCCGTGTGGACCCCTGACTCAGCAGAGATCATTCAGAGATAAAATAAATAATCCCACTGAATTCAGAAATCATGAAA
 AGCAGGAAAGCCAGGATCTCAGAGCTACTGCAAAAGTTCTTCTCCACCAACGAGCACCAGAGCTGAGAAATGCTGTT
 TCCTCAGGTAACAGAGATTCAAAAGGTACCTTCAGAAAGGAAAGAAATCTCTCTACACAGATGAGTCATCCAAACCTGGAAA
 AAATAAAAGAACTGCAATCACTCCAAACTTTAAGAAAGCTTCATGAAGCTCATTTTAAGGAAATGGAGTCCATTGATC
 AATAATTGAGAGAAATAAGAAACATTTTGAAGAACACACAATTCATGAATGAATGAAGCAGCAGCCCATCAATAAGGGA
 GGGTCAGGACTCCAGTACCTCCAAGAGGAAGACTCTCTGTGGCTTCTACTCCCATCAGCCAACGACGCTCGCAAGGCCG
 GTCTTGTGGCCCTGCAAGTCAGAGTACCTTGGGTCTGAAGGGGTCACTCAAGCGCTCTGTCTATCTCTGCAGCTAAACGG
 GTGTCAAGTTTTCAGTGTCTACTAAAGATAATGAGCATAAGCGTTCACTGACCAAGACTCCAGCCAGAAAGTCTGCACAT
 GTGACCGGTCTGGGGCACCCCAAAAGGCGAGGCTGTGTGGGACACACAAATTAAGACCATCACGGGGAATCTGTC
 TGCTGTATTATACCCCATTCAGTTGACAACTGAGGCAACGAGACTCCAGTCTCCATAAAGAAACCAAGTGTGTGATCTTA
 AAGCAAGTTTGTCTGTCCTCCCTCAACTATGAACCAACAAAGGAAAGCTAAACCATGGGGGCAATCTAAGAAATAAT
 TATCTAAATCAACATGTCAACAGAAATTAATCTTCAAGAAACTTACAAACAAACCCCATCTCCAGACAAAGGAGCA
 ACGGAAAGAAACGCGAGCAAGAACGAAAGGAGAAAGCAAGGTTTGGGAATGCGAAGGGGCTCATTTTGGCTGAAG
 ATTA

FIG.- 16

MTMITPSLARGRQPLGHVTKTRRRCKTVRVDPSQQNHSEIKISNPTEF,NHEKQESQDLRATAKVPSPPDEHQEAENAV
 SSGNRDSKVPSEGGKSLYTDESSKPGKNKRTAITTPNFKKLHFAHFKEMI\$IDQYIERKKKHFEHNSMNEIKQQPINKG
 GVRTFPVPRGL\$VASTPI\$QRRSQGRSCGPASQSTLGLKGLKRSASISAKTGVRFSAATKDNEHKRSLTKTPARKSAH
 VTVSGGTQKGEAVLGT\$HKLKTI\$TGNSAAVITP\$FKLTTEATQTPVSNKKP\$FDLKASLSRPLNYEP\$HKGLKLPWGQSKENN
 YLNQHVNRINFYKTKYKQPHLQTKEEQ\$RQ\$RERKEK\$KAKVL\$GMRRGL\$LAED

FIG.- 17

FIG. 18

Acetyl-KQPHL QTKEE QPKKC-Amide

FIG. 19

human_CAA2
mouse_CAA2

-----KKHFEHNMMNELKQP::NKGGRVTPVPPRGLSVASTPISQRRRS
ARFKKMESIDEYIMRKKHLKESSINELKLDIK--GIWTPVPPRGLSVPCTEPARQQCE
::**.*:*:* * : *****..** ** : *

human_CAA2
mouse_CAA2

QGRSCGPASQSTGLKSLKRSAISAAKTGVRI' SAATKDNEHKRSLTKTPARKSAHVTVS
QG-----H--S-ATKMVRI' SAATKDNEHKCSLTKTPARKSPHVTAP
** *:* . : ***** *

human_CAA2
mouse_CAA2

GGTQKGEAVLGTHKLKTITGNSAAVITPFKLTTEATQTTPSVNKKPVFDLKASLSRPLNYE
GSASKGOAVFRTPKSKATERTSIAVITPFKLMIEATQTTPSSSKKPVFDDLKASLSRPLNYK

human_CAA2
mouse_CAA2

PHKGKLPWGQSKENNYLNQHVNRIIFYKTTYKQPHLOTKEEQRKKREQRKEKKAFLVG
PHKGKLPWGQAKENNSLNERVSRVTFRHTYKQPHLOTRERWKRQEQRKEKKEKLLE
*****:::*****:
*****:::*****:
*****:::*****:

human_CAA2
mouse_CAA2

ARRNLGVTKAQ
MRRGLILAED-

FIG. 20

415 / 454

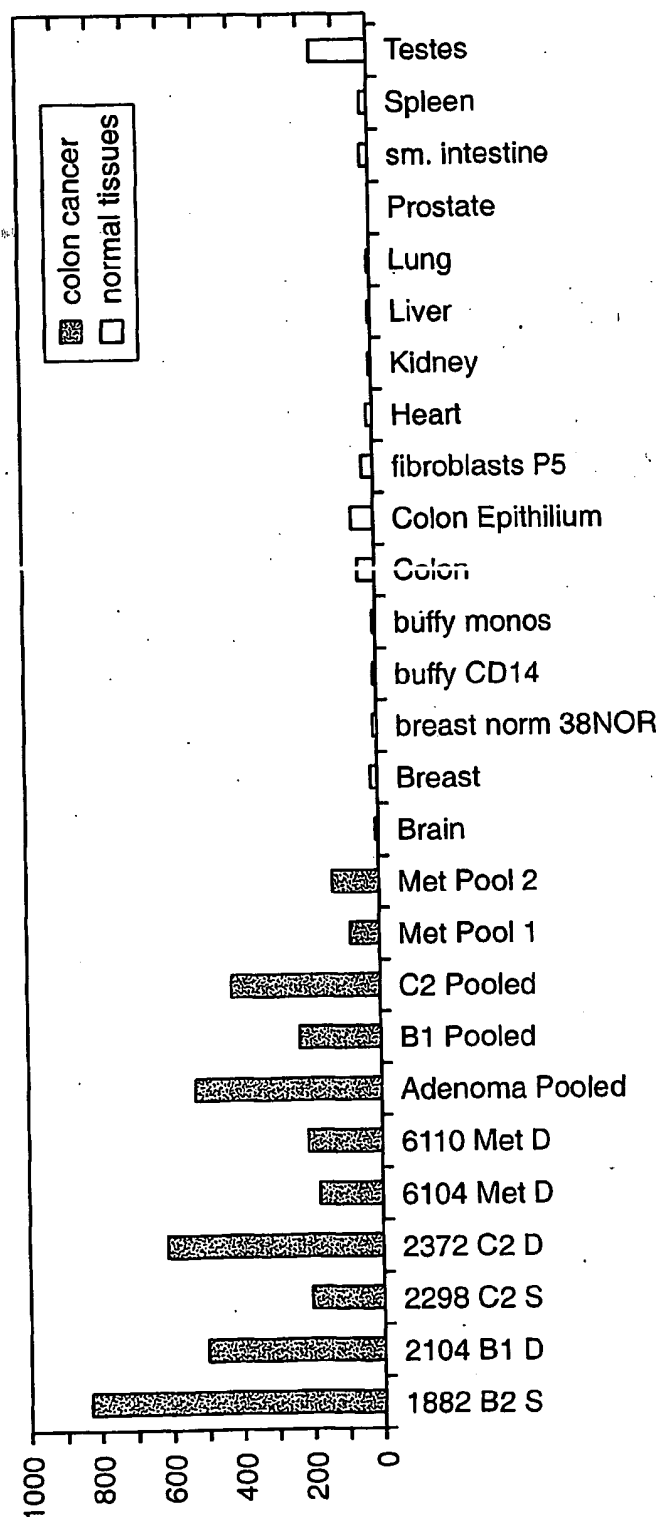


FIG. 21

416 / 454

GGTGGCCCTCTGTGGCCCTCAGGCTAGCGGGCGGCCCGCAGGGCGGGGGGAGAAAGACTCTCTCACCTGGTCTTGCGGCTG
TGGCCACCGCCGGCCAGGGGTGTGGAGGGCGTGTCTCCGGAGACGTCCGC'CGGGCTCTGCAGTTCCGCCGGGGGTCTGGGC
AGCTATGAGCCCGGGCCACGGGCGCCCTCTCCGGCGCCCGGGACTG'CCGGGGTCCGGGAGACGCCGTGAGCCCGCTG
CGCTGGCCGACGACAGGGTGGAACTGCCCGACGGCTGTGCCCTCGGT'CCCGAGGATGCTGCGCCCGCGAGCCCGGGAC
GGCGCGGGGTCCCGCATGAGGGCCCGCGSGCGCGGGACGGGCTGG'ACAGACCTTTGGGGCCACCCCGAGCCAGAG
CCGTTTCCAGGTGGACCTGGTTTCCGAGAACGCCGGGGCGGGCCCGTGT'CCGGCGGGCGGGCGGGCGGGCAGCGGGCGG
CGGCTGGTGTCTGGGGCGGGGCCAAGCAGACCCCGCGGACGGGGAAGC'AGCGGGCGAGAGCGGAGCCAGCTAAAGGCAGC
GAGGAAGCCAAAGGCCGCTTCCCGCGTGAAC'TTCGTGGACCCAGCTGCC'TCTCGTGGCTGAAGACAGCC'TGTGATGC
TGCCGGGGTGGAGTCCGACGGGGCCCAACGTGAGCTTCCAGAACGGCGGG'ACACGGTGTCTGAGCGAGGGCAGCAGCC'TGC
ACTCCGGCGGGCGGGCAGTGGCAGCCACGACTACTATTATGA'FACCCACACCAACACCTACTACCTGCGCACC
TTCGGCCACAACACCATGGACGCTGTGCCAGGATCGATCACTACCGGC'ACAGCGCGCAGCTGGCGGAGAAAGTCT
CCGGCCTAGCCTGGCGGAGCTCCACGACGAGCTGGAAGAAAGGAACCTTT'FAGGATGGCTTTGCAATGGGGAAGAAAGTA
CTCAACACAGAGATGCTGTGGGTGATGCTTTTCA'TTAGATTGT'ATGGATTGTGGGTCAAGCTGGAATAGGTCT
GTACGTTGTATGTTAAACATTTGGGGTGTGATGCTTTTCA'TTAGATTGT'ATGGATTGTGGGTCAAGCTGGAATAGGTCT
ATCAGTCCCTTGTAATAATGATGGCCACTGTTGTGACAACTATCACAGGA'TGTCTACTTCAGCAATAGCAACTAATGGAT
TTGTAAGAGGAGGAGCATATTATTTAATATCTAGAACTTAGGCC'AGAATTTGGTGGTGCATTTGGTCTAATCTTC
GCC'TTGGCCAACGCTGTTGCACTGTGTAATGTAATGTTGGTGGATTGCA'AAACCGTGGTGGAGTTGCTTAAGGAACATTC
CATACTTATGATAGATGAATCAATGATATCCGAATTA'TTGGAGCCATTAAGTCTGTAATCTTTTAGGTATCTCAGTAG
CTGGAATGGAGTGGGAAGCAAAAGCTCAGATTGTTCTTTTGGTGTATCCCTACTTCTTGCTATTGGTGAATTCGTCTATAGGA
ACATTTATCCCACTGGAGAGCAAGAACCAAAAGGGTTTTTGGTTATAAATCTGAATAATTTAATGAGAACTTTGGGCC
CGATTTTCGAGAGGAAGAGACTTTCTTTTCTGTATTTGCCATCTTTTTTCTGCTGCAACTGGTATTCCTGGCTGGAGCAA
ATATCTCAGGTGATCTTGCAGATCCCTCAGTCAGCCATACCCAAAGGAACACTCC'TAGCCA'TTTTAATTAATCACTATGGTT
TACGTAGGAATTCAGTATCTGTAGGTTCTTGTGTTGTTGTCGAGATGCCCATGGAACGTTAATGACACTATCGTAACAGA
GCTAACAAACTGTACTTCTGCAGCCTGCAAAATAAAC'TTTGATTTTCA'CTTTGTGAAGCAGTCCCTTGTTCCTATGGCC
TAATGAACAACTTCCAGGTAATGAGTATGGTGTGAGGATTTACACCACCTAATTTCTGCAAGGTATATTTTTCAGCCACTCTT
TCTTCAGCATTAGCATCCCTAGTGAAGTGTCCCAAAATATTTTCAGGCTCTATGTAAGGACAACATCTACCCAGCTTTCCA
GATGTTTGTAAAGGTTATGGGAAAAAATAATGAACCTCTCGTGGCTACATCTTAACATTTCTAATGCACTTGGATTCAT
TCTTAATTGCTGAACCTGAATGTTATTGTCACCAATATATCTCAAACTTCTTCTTGGCATCATATGCATTGATCAATTTTCA

FIG.-22A

417 / 454

GTATTCCATGCATCATTGCAAAATCTCCAGGATGGCGTCCTGCAATTCAAATACACAACATGTGGATATCATTCTTTGG
AGCAATTCTTTGTTGCATAGTAATGTTTCGTCATTAACCTGGTGGCTGCATNGCTAAACATATATGATAGTCTCTTGGGCTGT
ATATTATGTTACCTACAAAAAACAGATGTGAATTGGGGATCCTCTACACAAGCCCTGACTTACCTGAATGCACGTGCAG
CATTCAATTCTGCTTTCTGGAGTGAAGACACCGTGAAAAACCTTTAGGCCACAGTGTCTTGTATGACAGGTGCTCCAAA
CTCAGCTCCAGCTTTACTTCTTCTGTTTCATGATTTCACAAAAAATGTTGTGTTGATGATCTGTGGCCATGTACATATGG
GTCTCTGAAGACAAGCCATGAAGAGATGTCCATCGATCAAGCCAAAATATCAGCGATGGCTTTATTAAGAAACAAAATGAAG
GCATTTATGCTCCAGTACATGCAGATGACTTGGAGAGAAAGGTGCACAGTAATTTGATGCAAGGCTGTGGTCTTGGTCTGTAT
GAAGCCAAACACACTTGTCTTGGATTAAAGAAAGATGTTGGTGCAGCAGATATGAGGGAATGTGGATATATCTCATCTTCAA
TATTTCAATGATGCTTTTGACATACAATATGGAGTAGTGGTTATTCGCCCTAAGAGAGGCTCTGGATATATCTCATCTTCAA
GGACAAGAAAGTAATTTGTCAATCACAAAGAAATCTCTCTGGCACCACAGGAATGTGGTAGTAAGTGTGGAATATAGTAAAAA
GTCCGATTTAGATACTTCCAAACCACTCAGTGAAAAAACCAATTAACACACAAGTTGAGGAAGAGGATGGCAAGACTGCAA
CTCAACCACTGTTGAAAAAAGAAATCCAAAGGCCCTATTGTGCCCTTAAATGTAGCTGACCAAAAAGCTTCTTTGAAGCTAGT
ACACAGTTTCAGAAAAAACAAAGGAAGAAATCTATTGATGCTGTGGTGGCTTTTGTGATGATGGAGGTTTGACCTTATTGAT
ACCTTACCTTCTGACGACCAAGAAAAAATGGAAAGACTGTGAAGATCAGAGTATTCATTGGTGGAAAGATAAAACAGAAATAG
ACCATGACCCGGAGAGCGATGGCTACTTTTGTCTTAGCAAGTTCCGGATAGACCTTTTCTGATATCATGGTCTTAGGAGATATC
AATACCAAAACCAAGAAAGAAATATTATAGCTTTTGAGGAAATCATTTGAGCCATACAGACTTCATGAAGATGATAAAGA
GCAAGATATTGCAGATAAAATGAAAGAGATGAACCATGGCGAATAACAGATAATGAGCTTGAACCTTTATAAGACCAAGA
CATACCGGCAGATCAGGTTAAATGAGTTAATAAGGAACATTCAGCACAGCTTAATAATTATTTGTCTATGAGTCTCCAGTT
GCACGAAAAAGGTGCTGTGTCTAGTCTCTCTACATGGCATGGTTAGAAAGCTCTATCTTAAGGACCTACCACCAATCCTCCT
AGTTCTGGGGAATCATCAGAGTGTCTTACCTTCTATTCTATAAATGTTCTATACAGTGGACAGCCCTCCAGAAATGGTACT
TCAGTGCCTAGTGTAGTAACCTGAAATCTTCAATGACACATTAACATCACAAATGGCGAATGGTGACTTTTCTTTTACCGAT
TTCATTAATTTGAAAGCACACAGGAAAGCTTGTCTCCATTGATAACGTGTAAGGAGACTTCGGGTTTGTAGTCAATTTCCATAT
CTCAATCTTAATGGTGATTTCTTCTGTGTTGAACCTGAAGTTTGTGAGAGTAGTTTCTCTTTGCTACTTGAATAGCAATAAA
AGCGTGTTAACTTTTGG

FIG._22B

418 / 454

ATGAGCCGGCGCCACAGGCGCCCTCCCTCCGGCGCCCGGGACTGGCCGGGGTCTGGGGAGACGCCGTCTAGCCCGCTGCGCT
GGCCGACGCCAGGTGGAACCTGCCCGGACGGCTGTGCCCTCGGTGCCGAGGATGCTGCGCCCGCGAGCCCGGACGGCG
GCGGGTCCCGATGAGGGCCCCCGCGCGCGCGGGACGGGCTGGGACAGACCTTTGGGGCCCCACCCCGAGCCAGAGCCGT
TTCCAGGTGGAACCTGGTTCCGAGAACGCGCGCGCGGGCCCGCTGTGCGGCGCGGGCGGGCGGGCAGCGCGCGGGCGG
TGGTCTGGGGCGGGCCAAAGCAGACCCCGCGGACGGGGAGCCAGCGCGGAGAGCGAGCCAGCTAAAGGCAGCGGAGG
AAGCCAAAGGGCCGCTTCCGCGGTGAACCTTCGTGGACCCAGCTGCCCTCCCTCGGTGAGACAGCCCTGTCTCAGATGCTGCC
GGGGTCGGAGTCGACGGGCCCAACGCTGAGCTTCCAGAACGGCGGGGACACGGTCTGAGCGAGGGCAGCAGCCCTGCACTC
CGCGCGCGGGCGGCGAGTGGGACCAACGAGCACTACTATATATGATACCCACCAACACCTACTACCTGCGCACCTTCG
GCCAACACCATGGACGCTGTGCCCGAGGATCGATCACTACCGGCACACAGCCGCGCAGCTGGCGGAGAGCTGCTCCGG
CCTAGCCTGGCGGAGCTCCACGACGAGCTGGAAGAAAGGAACCTTTTGAGGATGGCTTTGCAATGGGGAAGAAAGTACTCC
AACCAGAGATGCTGTGGGTGATGCTTTTTCATTTAGATTGTCTATGTTGGCTGGATCAAGGGTGTATTAGTAC
GTTGTATGTTAAACATTTGGGGTGTGATGCTTTTTCATTTAGATTGTCTATGTTGGTGGTCAAGCTGGAATAGGTCTATCA
GTCCCTTGTAATAATGATGGCCACTGTTGTGACAACTATCACAGGATTGTCTACTTCAGCAATAGCAACTAATGGATTGT
AAGAGGAGGAGGACATATTAATTAATATCTAGAAGCTTAGGGCCAGAAATTTGGTGGTGCATTTGCTTAAGGAACAATCCCAT
TTGCCAACGCTGTTGCAGTTGCTATGATGTGGTTGGATTTCAGAAACCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGG
CTTATGATAGATGAATCAATGATATCCGAATTAATGGAGCCATTACAGCTCGTGGATTCTTTAGGTATCTCAGTAGCTGG
AATGGAGTGGGAAGCAAAAGCTCAGATTGTTCTTTTGGTGATCCTACTTTTGGTAAATATCTGAAATATTAATGAGAACTTTGGGCCCCGAT
TTATCCCACTGGAGAGCAATTTCTTTTCTGTAATTTGCCATCTTTTTCCTGTTGCAACTGGTATTTCTGGCTGGAGCAAAATAT
TTTCGAGAGGAAGAGACTTTCTTTTCTGTAATTTGCCATCTTTTTCCTGTTGCAACTGGTATTTAATTACTACATTGGTTTACG
CTCAGGTGATCTTGCAGATCCCTCAGTCAGCCATACCCAAAGGAACACTCTTAGCCATTTAATTACTACATTGGTTTACG
TAGGATTTGCAGTATCTGTAGGTTCTTGTGTTGTTGAGATGCCACTGGAAACGTTAATGACACTATCGTAACAGAGCTA
ACRAACTGTACTTCTGCAGCCCTGCAAAATTAACCTTTGATTTTTCATCTTTTGAAAGCAGTCCCTTGTTCCTATGGCCCTAAT
GAACAACTTCCAGGTAATGAGTATGGTGTGAGGATTTACACCACTAATTTCTGCGAGGTATATTTTCAGCCACTCTTCTT
CAGCATTAGCATCCCTAGTGTGCTCCCAAAATATTTTCAGGCTCTATGTAAGGACAACACTATCCCAGCTTTCCAGATG
TTTGTCTAAAGGTTATGGGAAAAAATAATGAACCTCTTCTGTTGGGTACATCTTAAACATCTTAAATTGCACCTGGATTCTCTT
AATTGCTGAACCTGAATGTTATTTGCACCAATTTATCTCAAACTTCTTCTTCTTTCATCATATGCATTTGATCAATTTTTCAGTAT
TCCATGCATCACTTGCAAAAATCTCCAGGATGGCGTCCCTGCATTCAAAATAATACAACTGTGGATATCACTTCTTGGAGCA

FIG.-23A

419 / 454

ATTCCTTTGTCATAGTAATGTTTCGTTCATTAACTGGTGGGCTGCATTGCTACATATGTGATAGTCTTGGGCTGTATAT
TTATGTTACCTACAAAAAACCCAGATGTGAATTTGGGATCCTCTACACAAGCCTGACTTACCTGAATGCATGCGAGCATT
CAATTCGCTCTTCTGGAGTGAAGACCCACGTGAAAAAATTTAGGCCACAGTGTCTTTGTTATGACAGGTGCTCCAAACTCA
CGTCCAGCTTTACTTTCATCTTGTTCATGATTTTCACAAAAATGTTGGTTTATGATCTGTGGCCATGTACATATGGGTCC
TCGAAGACAAGCCATGAAAGAGATGTCATCGATCAAGCCAAATATCAGCTATGGCTTATTAAGAACAAAAATGAAGGCAT
TTTATGCTCCAGTACATGCAGATGACTTGAGAGAAGGTGCACAGTATTTGATGCAAGCTGTGGTCTTGGTCCGTATGAAG
CCAAACACACTTGTCTTGGATTTAAGAAAGATTGGTTGCCACCAAGGATGTGATAGTAAGTCTGGATATATCTCATCTTCAAGGAC
TCATGATGCTTTTGACATACATAATATGGAGTAGTGTATTCGCCCTAAAGAGGTCTGGATATATCTCATCTTCAAGGAC
AAGAAGAAATTATTGTCTATCACAAGAGAAATCTCTGGCACCACCAAGGATGTGATAGTAAGTCTGGATATATCTCATCTTCAAGGAC
GATTTAGATACCTTCCAAACCACTCAGTGAAAAACCAATTACACACAAAAAGTIGAGGAAGAGGATGGCAAGACTGCAACTCA
ACCACTGTTGAAAAAAGAAATCCAAAGGCCCTATTTGTCCTTTAAATGTAGCTGACCCAAAGCTTCTTGAAGCTAGTACAC
AGTTTCAGAAAAAACCAAGGAAGAAATACTATTGATGTCCTGGTGGCTTTTATGATGGAGGTTTGACCTTATTGATACCT
TACCTTCTGACGACCAAGAAAAAATGGAAGACTGTAAGATCAGAGTATTCATTGGTGAAGAGATAAACAAGATAGACCA
TGACCGGAGAGCGATGGCTACTTTGCTTAGCAAGTCCGGATAGACTTTTCTGATATCATGTTCTTAGGAGATATCAATA
CCAAACCAAGAAAGAAAAATATATAGCTTTTGAGGAATCATTTGAGCCAACACAGACTTCAAGATGATAAAGAGCAA
GATATTGCAGATAAAATGAAGAGATGAACCATGGCGAATAACAGATAAAGAGCTTGAACTTTATTAAGACCAAGACATA
CCGGCAGATCAGGTTAAATGAGTTATTAAGGAACATTCAAGCACAGCTAATATTTATGTCATGAGTCTCCAGTTGCAC
GAAAAGGTGCTGTCTAGTGTCTCTACATGGCATGGTTAGAACTCTATCTAAGGACCTACCACCAATCCTCCTAGTT
CGTGGGAATCATCAGATGTCTTACCTTCTATTCATTA

FIG. 23B

MEPRPTAPSSGAPGLAGVGETPSAAALAAARVELPGTAVPSVPEDAAPASRDGGGVDEGPAAAGDGLGRPLGPTPSQSR
 FQVDLVSENAGRAAAAAAGAGAGAKQTPADGEASESEPAK3SEAKGRFRVNFVDPAASSSAEDSLSDAA
 GVGVDGPNVSFQNGGDTVLSEGSILHSGGGGSGHHQHYDDTHNTYYLRTFGHNTMDAVPRIDHYRHTAAQLGEKLLR
 PSLAELHDELEKEPFEDGFANGEESTPTRDAVVITYTAESKGVKFGWIKGVLVRCMLNIWGVMLFIRLSWIVGQAGIGLS
 VLVIMTAIVVTITGLSTSAIATNGFVRGGGAYYLISRLSGPEFGAIGLIFAFANAVAVAMYVVGFAETVVELLKEHSI
 LMIDEINDIRIIGALTIVVILLIGISVAGMEWEAKQIVLLVILLALIGDFVIGTFIPLESKKPKGFFGKSEIFNENFGPD
 FREETFSSVFAIFFPAATGILAGANISGDLPDQSAIPKGTLLAILLITLVYVGLAVSVGCVVRDATGNVNDTIVTEL
 TNCTSAACKLNFDSSCESPPCSYGLMNNFQVMSMVSGFTPLISAGIFSA TLSSALASLVSA PKIFQALCKDNIYPAFQM
 FAKGYGKNNELRGYILTFILALGFILIAELNVLAIIISNFFLASALINFSVFHASLAKSPGWRPAPFKYNNWISLLGA
 ILCCIVMFVINWAAALLTYVIVLGLYIYVYKPKDVNWGSSTQALTYLNA LQHSIRLSGVEDHVKNFRPQCCLVMTGAPNS
 RPALLHLVHDFTKNVGLMICGHVHMGPRRQAMKEMSIDQAKYQRWLIKWFKAFAYPVHADDLREGAQYLMQAAGLGRMK
 PNTLVLGFKKDWLQADMRDVMYINLFHDAFDIQYGVVIRLKEGLDISELQGEELLSSQEKSPGCTKDVVVSVEYSKKS
 DLDTSKPLSEKPI THKVEEDGKTATQPLIKKESKGP IVPLNVADQKLLEASTQFQKKQKNTIDVWWLFDGGLTLLIP
 YLLTTKKKWKDKIRVIGGKINRIDHRRAMATLLSKFRIDFSDIMVLGIDINTKPKKENIIAFEEIIIEPYRLHEDDKEQ
 DIADRMKEDEPWRTDNELELYKTKTYRQIRLNELKEHSSSTANIIVMSIPVARKGAVSSALYMWLEALSKDLPPILLV
 RGNHQSVLTFYS

FIG..24

Peptide Names	Solubility	
CAA9p1	1mg / 1ml H2O	H-CDPAAASSSAEDSLSD-NH2
CAA9p2	1mg / 1ml H2O	Ac-KKSDLDTSKPLSEKC-NH2
CAA9p3	1mg / 1ml H2O	Ac-PLLKESKGPVIVPLC-NH2
CAA9p4	min.amt.DMSO / H2O	Ac-EHSILMIDEIC-NH2
CAA9p4MAPS	1mg / ml buffer pH7.5	Ac-EHSILMIDEIC-on 8-Branch Maps
CAA9p5	1mg / 1ml H2O	Ac-DFREEETC-NH2
CAA9p5MAPS	1mg / 1ml H2O	Ac-DFREEETC-on 8-Branch Maps

FIG..25

421 / 454

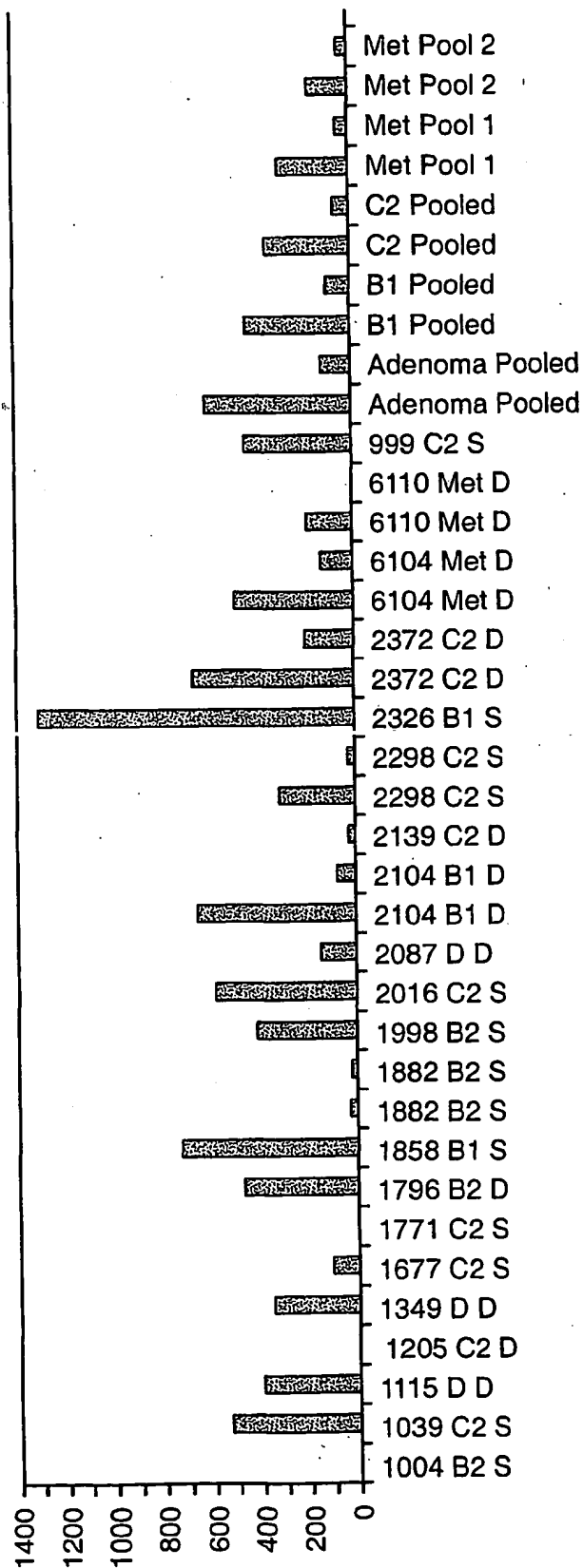


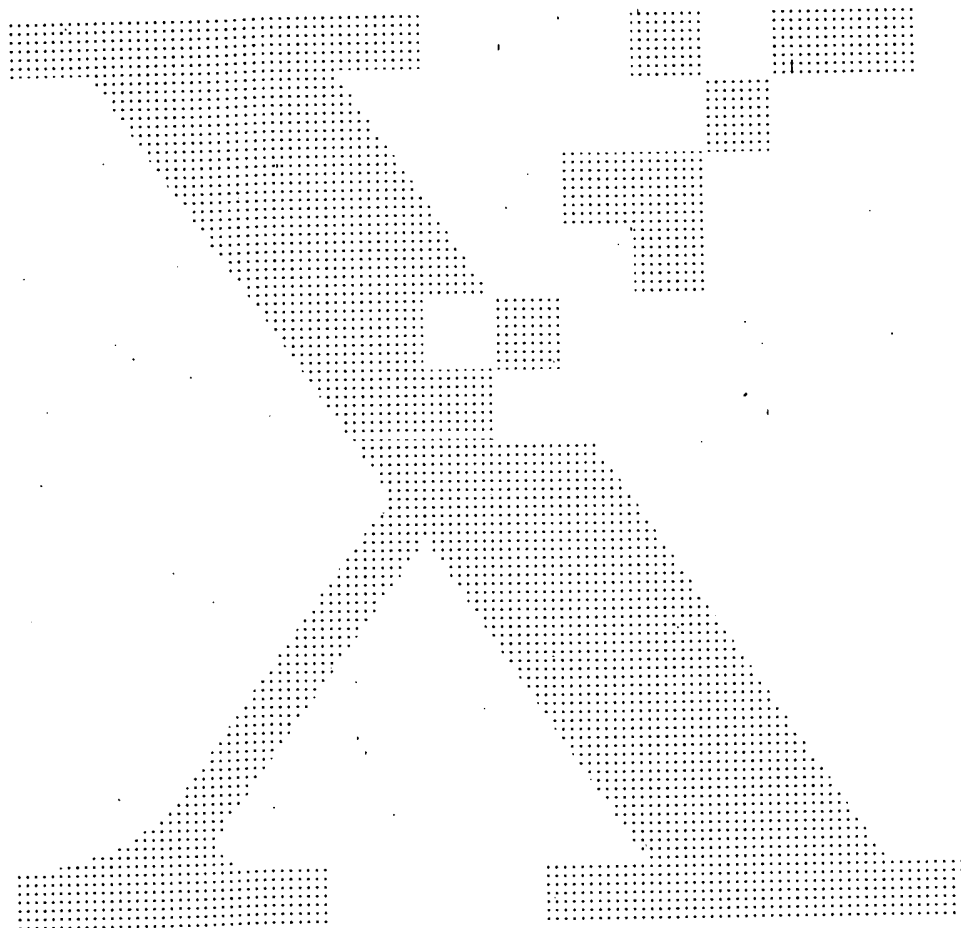
FIG..26A

FIG..26A FIG..26B

FIG..26

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422 / 454

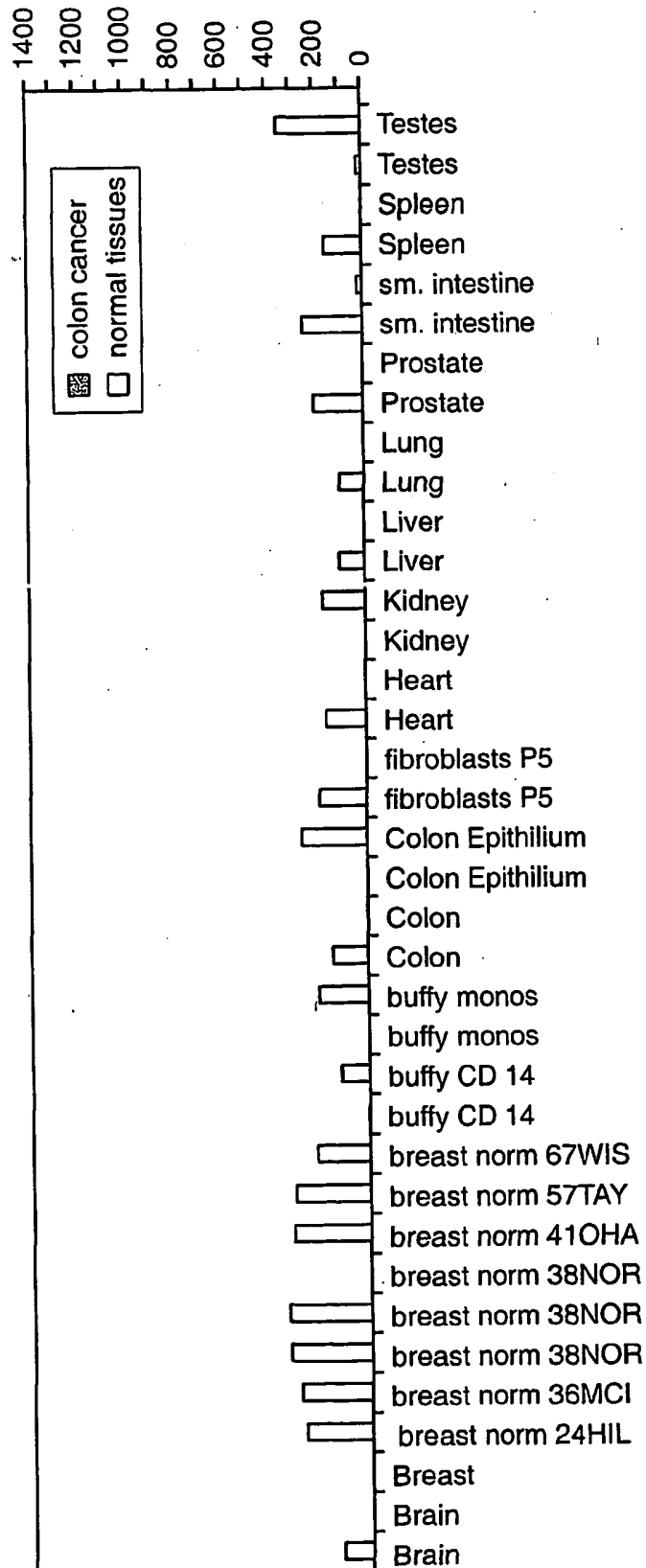


FIG. 26B

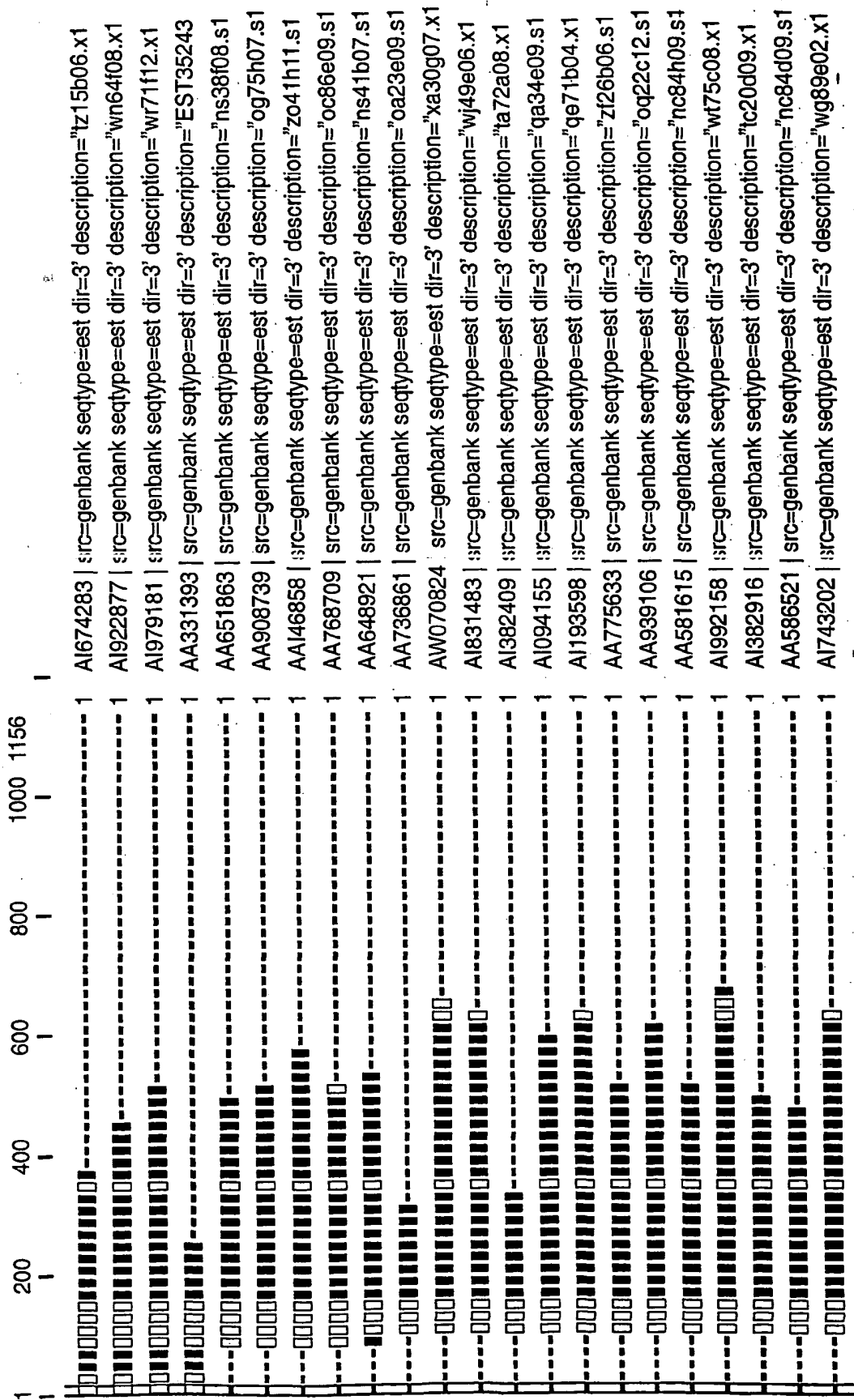
423 / 454

GGCACGAGGAGAACTTAAAGAAATTCAGATATGTGAAGTTGATTTCCATCGAAACCTCGTCA
TCCTCTGATGACAGTTGTGACAGCTTTGCTTCTGATAATTTTGCAAACACGAGGCTGCAGTC
AGTTCCGGGAAGGCTGTAGGACCCGCAGCCAGTGCAGGCACCTCTGGACCTCTCAGGGTGGCGA
TGAAGTTTCCAGCGCGGAGTACCAGGGGAGCAACCAACAAAAAGCAGAGTCCCGCCAGCCC
TCAGAGAATTTCTGTGACTGATTCCAACCTCCGATTTCAGAAGATGAAAGTGGAATGAATTTTTT
GGAGAAAAGGGCTTTAAATATAAAGCAAAACAAAGCAATGCTTGCAAAACTCATGTCTGAAT
TAGAAAGCTTCCCTGGCTCGTTCCGTGGAAGACATCCCCTCCCAGGCTCCGACTCACAATCA
AGGAGACCGCGAAGGCGTACATTCCCGGGTGTGTGCTTCCAGGAGAAACCCTGAACGGAGAGC
TCGTCTCTTACCAGGTCAAGGTCCCGGATCCTCGGGTCCCTTGACGCTCTACCCATGGAGG
AGGAGGAGGAAGAGGATAAGTACATGTTGGTGAGAAAGAGGAAGACCGTGGATGGCTACATG
AATGAAGATGACCTGCCCAGAACCCGTGCTNCAGATCATCCGTGACCTTCCGCATATAAT
TCGCCCAGTGGAAGAAATACAGAAGGAGAGGAGTTGGAGAACGCTCTGCAGCAATTTCTCGAAG
AGAAGATTATAACCGTTCACTGGGYTCTACTTGTTCATCAATGCCGTCAGAAGACTATTGATA
CCAAAACAACTGCAGAAACCCAGACTGCTGGGGCGTTCGAGGCCAGTTCTGTGGCCCCCTGC
CTTCGAAACCGTTATGGTGAAGAGGTCAGGGATGCTCTGCTGGATCCGAACTGGCATTGCC
GCCTTGTGCGAGGAATCTGCAACTGCAGTTTCTGCCGGCAGCGAGATGGACGGTGTGCGACTG
GGGTCTTGTGTATTTAGCCAAATATCATGGCTTTGGGAATGTGCATGCCTACTTGAAAAGC
CTGAAACAGGAATTTGAAATGCAAGCATAATATCTGGAAAAATTTGCTGCCTGCCTTCTACTT
CTCAAATCTTTCTTGTAAAAGTTTCCAATTTTCTCACTGAAACCTGAGTTAAAAATCTTGA
TGATCAGCCTGTTTCATAAGAACTCCAATCAAGTTAMTCTTAGCAGACATGTGTTTCTGGA
GCATCAGAGAAGGTATATTGCTAGTTACACTTTGCCCTCCTGCAGTTTCTTCTCTGCTCCCA
CCCCCATCTCATAGCATTCCCCCTCTATTTTCCATTGCTCCCTCTCCCAACCCGCTTAAGT
TTCTGAAATTTCTTTTAAAWTTACAGTTTAAAGGAAAAGCCATATTTTATTTACCTGGGT
GTTGGAAATAGCCCCCTCCATAAAACCCTAAGCACTTGGAAACACAATAATAGTATTAACCTA
ACTAGATCCTATTGAATTTTCAGAGAAGAGCCTTCTAACTTGTTTACACAAAAACGAGTATGA
TTTAGCATTCTACTAGTTGAAATTTTAAATAGAATCAAGGCACAAAAGTCTTAAACCATG
TGGAATAATAGGTAATTATKGCARATTGAKGGTCYCYCAATCCCAYGWATKGSCTTATGK
TACMARKKGKTGTTCMCAGTTTRAGACYTAATTTTCYCTAATTTCTTCYGCCGAAGGKWAAGK
GGKCGCTCCRGCTTACMCAGTCATAATTCMAAGGKTGGKGGSCAATGTAAYMCTTAATTA
ATAATKRWGAAGAGCYATCTGGAGATTAWGAGTAAGCTGATTTGAATTTTCAGTATAAAC
TTTAGTATAATTGTAGTTTGCAAAGKTATTTTCAGTTACATGTAAGGKATTGCMATAAAT
TCTTGGAACAATTTTGKATGGAACTTGATATTAATACTAGTCTGTGGKTCTTTGCAGTTTC
TTGTAAATTTATAAACAGGCACAAGGTTCAAGTTTAGATTTTAAGCACTTTTATAACAATG
ATAAGTGCCTTTTGGAGATGTAACCTTTTAGCAGTTTGTTAACCTGACATCTCTGCCAGTCT
AGTTTCTGGGCAGGTTTCTGTGTGAGTATTCCCCCTCCTCTTGCATTAATCAAGGTATTT
GGTAGAGGTGGAATCTAAGTGTTTGTATGTCCAATTTACTTGCATATGTAAACCATTGCTGT
GCCATTCAATGTTTGTATGATAATTTGGACCTTGAATCGATAAGTGTAATAACAGCTTTTGAT
CTGTAATGCTTTTATACAAAAGTTTATTTTAAATAAAATGTTTGTCTTAAAAA
AAAAAATTGCGCCGCAAGCTTATTTCCWTTAGTGAGKSWTAATTTTAGCTTGGCACTGG
CCGTCGTTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCA
GCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCA
ACAGTTGCGCAGCCTGAATGGCGAATGGGACGCGCCCTGTAGCGGCGCATTAAGCGCGCGG
GTGTGGTGGTTACGCSAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTC
GCTTCTTCTCCTTCTCGCMCGTTCCCGGCTTTCYCCCKCAAGCTNTAAATCGGGG

FIG. 27

FIG. 28A-1

One position equals 20 bases. ■ if more than 2 bases disagree with consensus sequences.
 □ if more than 10 positions are unknown.
 - if more than 10 positions are gap characters.



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425 / 454

1	N95719 src=genbank seqtype=est dir=3' description="zb53e04.s1
1	AA284818 src=genbank seqtype=est dir=3' description="z124e09.s1
1	AI346620 src=genbank seqtype=est dir=3' description="qp46f05.x1
1	R.C.AA465473 src=genbank seqtype=est dir=5' description="aa22g08.r1
1	T24898 src=genbank seqtype=est dir=?' description="EST473
1	R.C.AA406456 src=genbank seqtype=est dir=5' description="zv10a04.r1
1	R.C.AA096093 src=genbank seqtype=est dir=5' description="18199.seq.F
1	R.C.AA379531 src=genbank seqtype=est dir=5' description="EST92378
1	R.C.N53714 src=genbank seqtype=est dir=5' description="yz06b06.r1
1	H60046 src=genbank seqtype=est dir=3' description="yr19d02.s1
1	R.C.AA377822 src=genbank seqtype=est dir=5' description="EST90803
1	N51950 src=genbank seqtype=est dir=3' description="yz06g06.s1
1	AA372701 src=genbank seqtype=est dir=5' description="EST84625
1	AI473650 src=genbank seqtype=est dir=3' description="tm02e10.x1
1	AI225213 src=genbank seqtype=est dir=3' description="qx06g04.x1
1	AA406348 src=genbank seqtype=est dir=3' description="zv10a04.s1
1	AI351496 src=genbank seqtype=est dir=3' description="qr05f11.x1
1	AA749314 src=genbank seqtype=est dir=3' description="ny12A11.s1
1	cons for 1
2	AI378205 src=genbank seqtype=est dir=3' description="tc65a07.x1

FIG. 28A-1

FIG. 28A-2

FIG. 28A-2

NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2288627 3', mRNA s" srcf=gbcu7/29773
 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2450247 3', mRNA " srcf=gbest:6/51593
 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2493167 3', mRNA s" srcf=gbest37/46306
 Embryo, 8 week 1 Homo sapiens cDNA 3' end, mRNA sequence." srcf=gbest13/573
 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1185927 3', mRNA " srcf=gbes:17/53268
 NCI_CGAP_Ov8 Homo sapiens cDNA clone IMAGE:1454173 3', mRNA s" srcf=gbest21/613
 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IM" srcf=gbest10/2075:
 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1356616 3', mRNA " srcf=gbest19/36742
 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1186165 3', mRNA " srcf=gbest17/50927
 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1305832 3', mRNA " srcf=gbest18/70299
 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568348 3', mRNA " srcf=gbest:8/61005
 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406178 3', mRNA " srcf=gbest35/22416
 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:20" srcf=gbest26/68899
 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1688680 3', mR" srcf=gbest:23/18508
 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:17443" srcf=gbest2:1/35326
 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:3780" srcf=gbest13/43614
 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1587094 3', mRNA s" srcf=gbes:21/28363
 NCI_CGAP_GC1 Homo sapiens cDNA clone IMAGE:797537 3', mRNA se" srcf=gbes:16/43395
 Soares_thymus_NHFTh Homo sapiens cDNA clone IMAGE:2513294 3", srcf=gbest37/59215
 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2064401 3', mR" srcf=gbest26/69406
 NCI_CGAP_GC1 Homo sapiens cDNA clone IMAGE:797489 3', mRNA se" srcf=gbes:16/48294
 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:237" srcf=gb:u8/18434

Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:30732" srcf=gbest6/55806
Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:714088" srcf=gbest12/8311
NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926081 3', mRNA s" srcf=gbest26/33599
NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814046 5', mRNA s" srcf=gbest15/9675
Human colorectal cancer Homo sapiens cDNA clone 17B12, mRNA seque" srcf=gbest1/46394
Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:753198 5', mRNA" srcf=gbes:14/23757
Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5', " srcf=gbest9/36451
Skin tumor I Homo sapiens cDNA 5' end, mRNA sequence. " srcf=gbest13/48697
Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMA" srcf=gbest6/14372
Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE" srcf=gbest4/55137
Synovial sarcoma Homo sapiens cDNA 5' end, mRNA sequence." srcf=gbest13/46983
Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMA" srcf=gbest6/12908
Colon adenocarcinoma IV Homo sapiens cDNA 5' end, mRNA sequence" srcf=gbest13/141867
NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:2155434 3', mRNA " srcf=gbes28/8505
NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2000598 3', mRNA" srcf=gbe:i24/66924
Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:753198 3', mRNA" srcf=gbest14/23649
Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:19" srcf=gbest26/38475
NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1271516 3', mRNA " srcf=gbe:i19/17507

Soares NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2069460 3', mR" src=gbes:26/64695

FIG. 28B-2

FIG.-28B

FIG. 28B-1

FIG.-28B-2

428 / 454

METSSSSDDSDS CDSFASDNFA NTRLQSVREG CTRRSQCRHS GPLRVAMKFP
ARSTRGATNK KAESRQPSSEN SVTDSNSDSE DESGNTLEK RALNIKQNK
MLAKIMSELE SFPGSFRGRH PLPGSDSQSR RPRRTIPGV ASRRNPERRA
RPLTRRSRI LGSLDALPME EEEEEKMYL VRKRKT'DGY MNEDDLPRTR
RYRSSVTLPH IIRPVEEIQK ERSWRTSAAL LEEKII'VHW ALLVINAVRR
LILPKQTAET QTAGAFEASS VAPAFETVMV KRSGLA'WIR TGI AVLVEES
ATAVSAGSEM DGVRLGSLCI

FIG._29

MAQLQTRFYTDNKKYAVDDVPFSIPAASEIADLSNI INKLLKDKNEFHKHVEFDF
LIKQQLRMPLDKHEMENISSEEVVEIEYVEKYTAPO:QCMFHDDWISSIKGA
EEWILTGSYDKTSRIWSLEGSIMTIVGHTDVVKDVAVWKDLSCLLSASMDQ
TILLWENNVERNKVKAHCCRGHAGSVDSIAVDGSGTKF'CSGSWDRMLKIWSTVP
TDEEDEMEESTNRPRKKQKTEQLGTRTPIVTLSGHMEAVSSVLWSDAEEICSA
WDHTIRVWDVESGSLKSTLTGNKVFNCISYSPCKRIASJSTDRHIRLWDPRTKD
GSLVLSLTSHTGWVTSVKWSPTHEQLISGSLDNIVKLWDRSCKAPLYDLAAH
EDKVLSDVDTGTGLLLSGGADNKLYSYRSPSTTSHVGA.

FIG._33

MSNECANPVSPPRPSESVGIPILIALLSIASI'VWVLEKRVIEDK'Y'PCGQPLHFI PRKQICDGE LDCPL
GEDEEHCVKSFPEGPAAVRLSKDRSTLQVLD SATGNWFSACFDNFTALAE TACRQMGYSKPTFRAVEI
GPDQDLDVVEITENSQELRMNRSSGPGCLSGSLVSLHCLACGKSLKTRRVVGEEASVDSWPWQVSIQYDKQ
HVC GGSILDPHWVLTAAHCFRKHTDVFNKVRAGSKLGSFP SLAVAKIIIEFNPMYPKDNIDIALMKLQF
PLTFSGTVRPICLPFFDEELTPATPLWII GWGFTKQNGGKMSDILLQASVQVIDSTRCNADDA YQGEVTEK
MMCAGIPEGGVDT CQGD SGGPLMYQSDQNHVVGIVSWG YCGGSPSTFGVYTKVSA YLNIWYNNVWKAE L.

FIG._36

429 / 454

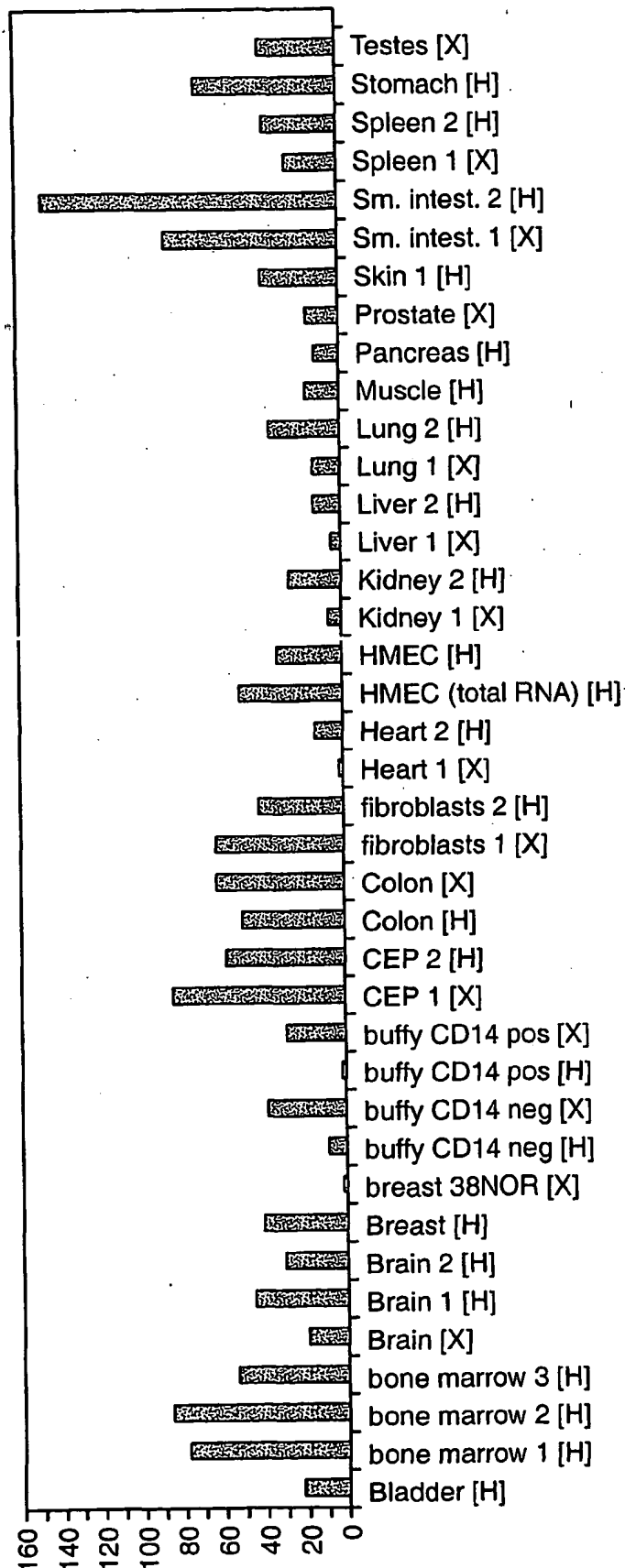


FIG. 30A

430 / 454

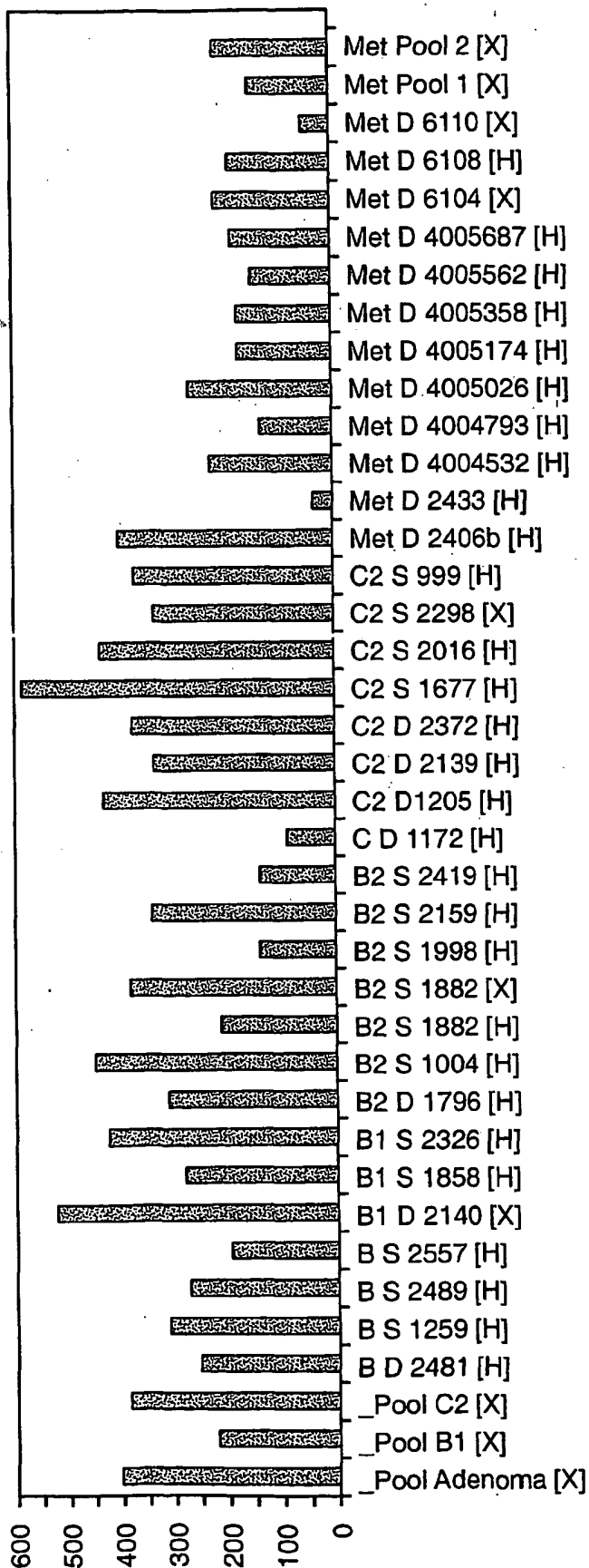


FIG.-30B

431 / 454

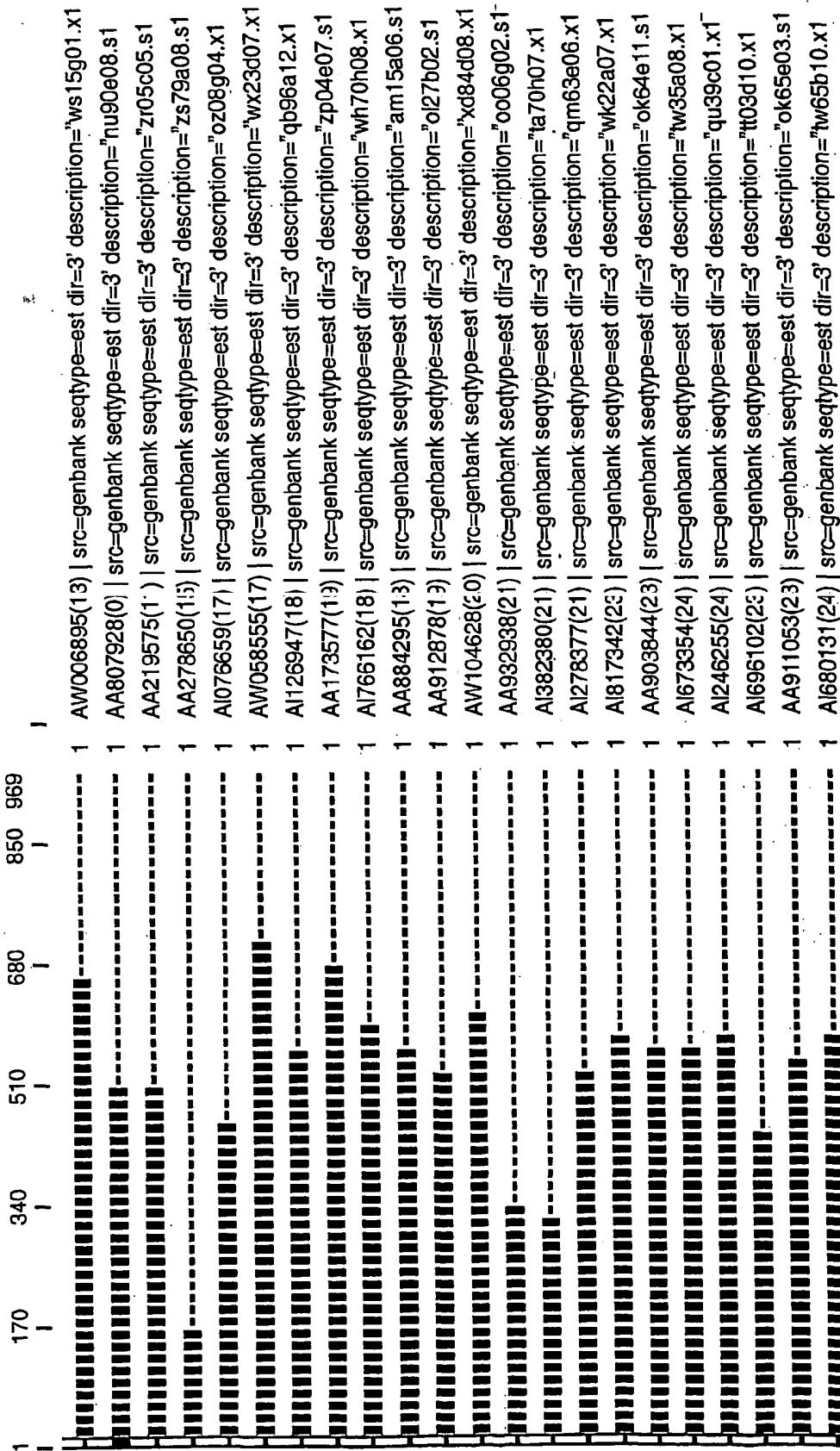
FIG.-31

ACTCACATATNGGGCGAATGGGCCCTCTNNATGCATGCTCGAGCGCTCGCCAGTGTGATGGATA
TCTGCAGAAATTCGCCCTTAAGCAGTGGTAACAACGCAGAGTACGCAGGGGAGACCGGAGGGC
AGAAGGCAGAGTCCAGGCTTAGACTGCAGTTCCTCGCTTACCTGTACCTGTACCTTAATTTGAGCT
GCCTCTTTGTAGTCTTAAAGGCAGGAGCTTCGTGTGTGGGTCTGTAAACCCGTAACGTTTCC
GTGGGCAAGTCTGTGTACTCTCTGCCCTGCTCAGCTCCAAACAACGCTTCTACACTGATAAC
AAGAAATATGCCGTAGATGATGTTCCCTTCTCAATCCCTGCTGCTCTGAAATTCGCCGACCTT
AGTAACATCATCAATAAATACTAAAGGACAAAATGAGTTCCACAAACATGTGGAGTTTGAT
TTCCTTATTAAGGCCAGTTTCTGCGAATGCCCTTGGACAAACACATGGAAATGGAGAACATC
TCATCAGAAAGAGTGTGGAATAGAAATACGTGGAGAAAGTATACGTGACCCAGCAGAGCAA
TGCAATGTTCCATGATGACTGGATCAGTTCAATTAAGGGGCGAGAGGAATGGATCTTGACTGGT
TCTTATGATAAGACTTCTCGGATCTGGTCCCTTGGAGGAAAGTACATAATGACAAATGTGGGA
CATACGGATGTTGTAAGAGATGTGGCCCTGGGTGAAAGAGTGTGAGAGAAAGTGTGAGAGAA
AGTGCTTCTATGGATCAGACTATCTCTTATGGGAGTGAATGTGAGAGAAACAAAGTGAA
GCCCTACACTGCTGTAGAGTCACTGTGGAAGTGTAGATTCTATAGCTGTGATGGCTCAGGA
ACTAAATTTTGCAGTGGCTCCTGGGATAAGATGCTAAAGATCTGCTTACAGTCCCTACAGAT
GAAGAAGATGAATGGAGGAGTCCACAAATCGACCAAGAAAGAAACAGAAAGACAGATTG
GGACTAAAGGACTCCCATAGTGACCCCTCTCTGGCCACATGGAGGCAGTTTCTCAGTCTCTG
TGGTCAGATGCTGAAGAAATCTGCAGTGCATCTTGGGACCATACATAGAGTGTGAGTGTGAGTGT
GAGTCTGGCAGTCTTAAGTCAACTTTGACAGGAAATAAAGTGTGAAATGTTTAAATGTTTCTTCT
CCACTTTGTAAACGTTTACATCTGGAAGCACAGATAGGCATATCAGACTGTGGGATCCCCGA
ACTAAAGATGGTCTTTTGGTGTGCTGTGCTCTCTATGATCTGGCTGCTCATGAAGACAAAGTCTG
AAATGGTCTCTACCCATGAACAGCAGCTGATTTTCAGGATCTTTGATAACATTTGTTAAGCTG
TGGGATACAAGAGTTGTAAAGGCTCCCTCTCTATGATCTGGCTGCTCATGAAGACAAAGTCTG
AGGTAGACTGGACAGACACAGGGCTACTTCTGAGTGGAGGAGCAAGTGTACATAAATGTATTC
TACAGATATTCACCTACCACTTCCCATGTTGGGCAAGTGTACATAAATTTGACTATAG
AGATTATTTCTGTAAATGAATGGAATGGTAGAGAACCATGAATACATAGATGCAGATGCAGAAA
GCAGCCCTTTTGAAGTTTATATAATGTTTTCACCCCTTCATAACAGCTAACGTATCACTTTTCT
TATTTTGTATTTATAAATAGATAGGTTGTGTTTATAAATAACAATCTGTGGCATACATCTCT
ATACAAACTTGAAATTAAGTGAAGTTTACATTTCTCTTTAAAGGTAAAGGAAAAA

432 / 454

FIG. 32A-1

One position equals 17 bases. ■ if more than 1 bases disagree with consensus sequence.
□ if more than 8 positions are unknown.
- if more than 8 positions are gap characters.



+

1 A1951347(24) | src=genbank seqtype=est dir=3' description="wx67g10.x1
1 A1952510(24) | src=genbank seqtype=est dir=3' description="wx74g05.x1
1 A1417099(24) | src=genbank seqtype=est dir=3' description="lg78g12.x1
1 AA502337(26) | src=genbank seqtype=est dir=3' description="ne26a03.s1
1 AA907840(22) | src=genbank seqtype=est dir=3' description="om16c08.s1
1 AA528399(102) | src=genbank seqtype=est dir=?' description="ne83g12.s1
1 cons for 1

433 / 454

FIG._32A-2

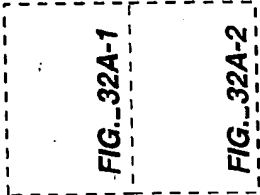


FIG._32A

+

FIG. 32B-1

NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2497296 3' simil" srcf=gbest377/306	1	6
NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1217990 3', mRNA " srcf=gbest19/76988	1	1
Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA c" srcf=gbest11/22843		
NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703670 3', mRNA s" srcf=gbest12/4143		
Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IM" srcf=gbest23/4980		
NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544493 3', simil" srcf=gbest38/51329		
Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1707" srcf=gbest23/53375		
Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 1" srcf=gbest10/48663		
NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2386143 3' simil" srcf=gbest33/2816		
Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1466866 3'" srcf=gbest20/65489		
Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524651 3'" srcf=gbest21/9292		
Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2604303 3'" srcf=gbcu/86072		
Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1565426 3", srcf=gbest21/26801		
Soares_totAL_fetal_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:20" srcf=gbest26/8381		
Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone " srcf=gbest25/38348		
NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2431044 3' simil" srcf=gbest35/12498		
NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1518764 3' similar" srcf=gbest21/161		
NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2261654 3' similar" srcf=gbest31/7180		
NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:1967136 3' simila" srcf=gbest25/1231		
NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2239699 3', mRNA s" srcf=gbest31/30525		
NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1518844 3' similar" srcf=gbest21/1467		
NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2264539 3' similar" srcf=gbest31/11554		

T T T T T T T

435 / 454

FIG.-32B

FIG._32B-1

FIG.-32B-2

436 / 454

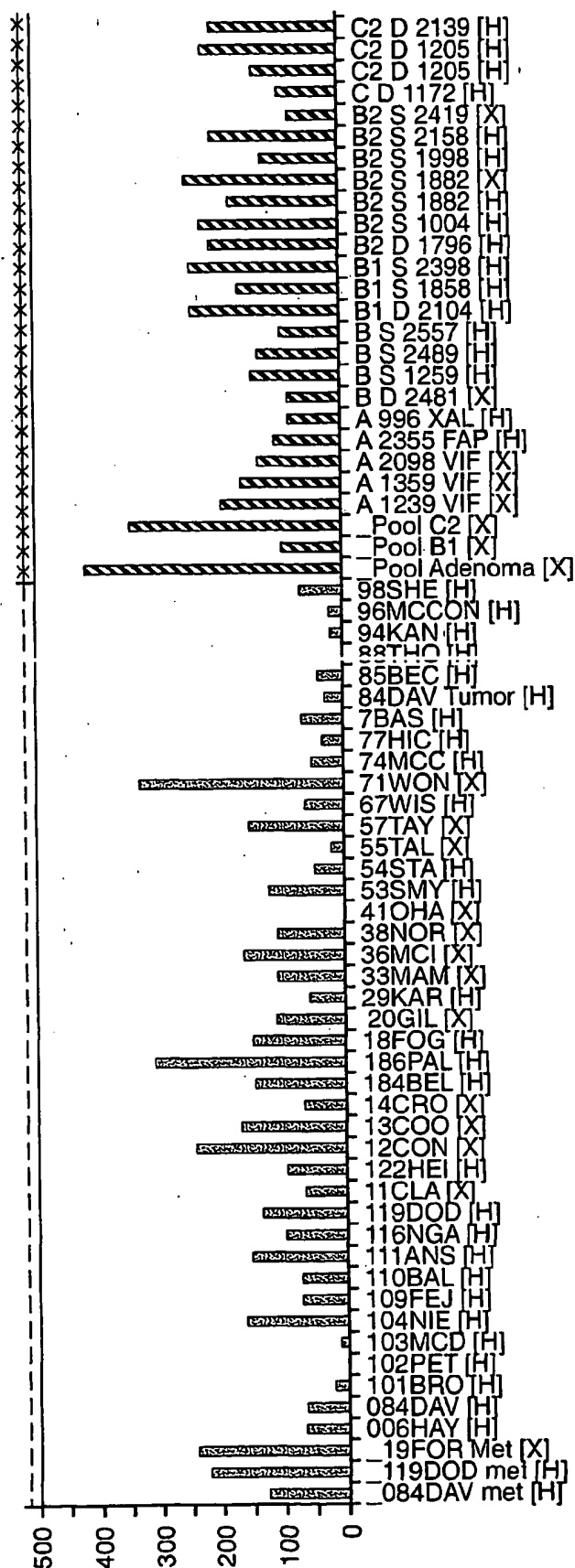


FIG.-34A

FIG.-34B

FIG.-34

437 / 454

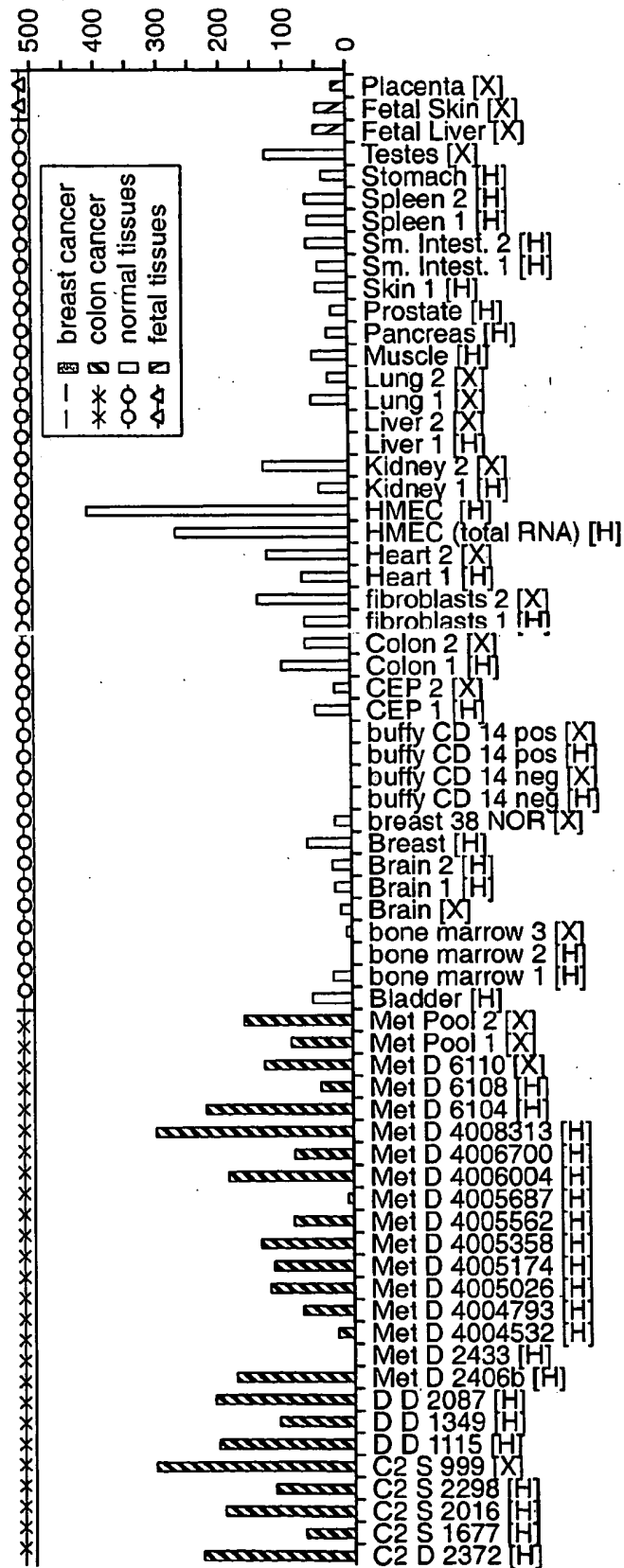


FIG..34B

438 / 454

FIG. 35

GAGAGGCAGCAGCTTGTTCAGCGGACAAAGGATGCTGGGCGTGAGGGACCAAGGCCCTGCCCTGCACCTCGGG
CCTCCTCCAGCCAGTGTGACCCAGGGACTTCTGACCTGCTGGCCAGCCCAAGACCTGTGTGGGAGGCCCT
CCTGTGCCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACCCGGAGGATCACAGAGCCAGCATG
GTACAGGATCCTGACAGTGATCAACCTCTGAACAGCCCTCGTGTCAAAACCCCTGCGCAAAACCCCGTATCC
CCATGGAGACCTTCAGAAAGTGTGGGATCCCATCATCATAGCACTACAGCCCTGGCGAGTATCATCA
TTGTGGTTGTCTCATCAAGGTGATTTCTGGATAAATACTACTTCTCTGCGGGCAGCCCTCTCCACTTCAT
CCCGAGGAAGCAGCTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGHACGAGGAGCACTGTGTCAAG
AGCTTCCCGAAAGGCCCTGCAGTGGCAGTCCGCCCTCTCAAGACCGATCCACACTGCAGGTGCTGGACT
CGGCCACAGGGAACCTGGTTCTCTGCCCTGTTTCGACAACTTCACAGAACTCTCGCTGAGACAGCCTGTAG
GCAGATGGGCTACAGCAGCAAAACCCACTTTCAGAGCTGTGGAGATTGGCCAGACCCAGGATCTGGATGTT
GTTGAAATCACAGAAAAAGCAGGCTTCGCCATGCGGAACCTCAAGTGGCCCTGTCTCTCAGGCTCCC
TGGTCTCCCTGCACCTGTTGCCCTGTGGGAAGAGCCTGAAGACCCCGGCTGGTGGTGGGAGGAGGC
CTCTGTGGATTCTTGGCCCTTGGCAGGTCAGCATCCAGTACGACAAACAGACGTCGTGTGGAGGAGCATC
CTGGAACCCCACTGGTCTCAACGGCAGCCCACTGTCTTCAGGAACATAACGATGTGTTCACCTGGAAGG
TGGGGCAGGCTCAGACAAACTGGGCAGCTTCCCATCCCTGGCTGTGGC(AAGATCATCATCATTTGAATT
CAACCCCATGTACCCCAAGACAATGACATCGCCCTCATGAAGCTGCAGTCCCACTCACTTCTCAGGC
ACAGTCAGGCCCATCTGTCTGCCCTTCTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTG
GATGGGCTTTACGAAGCAGAAATGGAGGGAAGATGTCTGACATACTGTCT(CAGGCGTCAGTCCAGGTCAT
TGACAGCACACGGTGAATGCAGACGATGCGTACCAGGGGGAAGTCAACCAGAAAGATGATGTGTGCAGGC
ATCCCGGAAGGGGTGTGGACACCTGCCAGGTGACAGTGGTGGGCCCCGATGTACCAATCTGACCAGT
GGCATGTGGTGCGCATCGTTAGCTGGGCTATGGCTGCGGGGGCCCCGAGTACCCAGGAGTATACACCAA
GGTCTCAGCCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTGTTGCTGTGCTGCCCTTTGCA
GTGCTGGGAGCCGCTTCTTCCCTGCCCTGCCCATCTGGGGATCCCCCAAGTCAAGACACAGAGCAAGAGT
CCCCCTGGGTACACCCCTCTGCCCAAGCTCAGCATTTCTTGGAGCAGCAAGGGCCCTCAATTCCTGTA
AGAGACCCCTCGCAGCCAGAGGGGCCAGAGGAAGTCAAGCCCTAGCTAGCTGGCCACACTTGGTGTCTCC
AGCATCCCAAGGAGAGACACAGCCCACTGAACAAGGTCTCAGGGGTATTCTAAGCCAAAGAGGAACCTTT
CCCACTACTAATGGAAGCAGGCTGTCTTGTAAAGCCAGATCACTGTGGCTGGAGAGGAGAAAGGA
AAGGCTGTGCGCAGCCCTGTCCGTCTTACCCATCCCCAAGCCTACTAGCAAGAAACCCAGTTGTAAT
ATAAATGCACCTGCTTGTGGTATGACTACCGTTACCTACTGTGTGCTCATTTGTTATTACAGCTATGG
CCACTATTATTAAAGAGCTGTGTACATCAAAAAAATAAAAAA

439 / 454

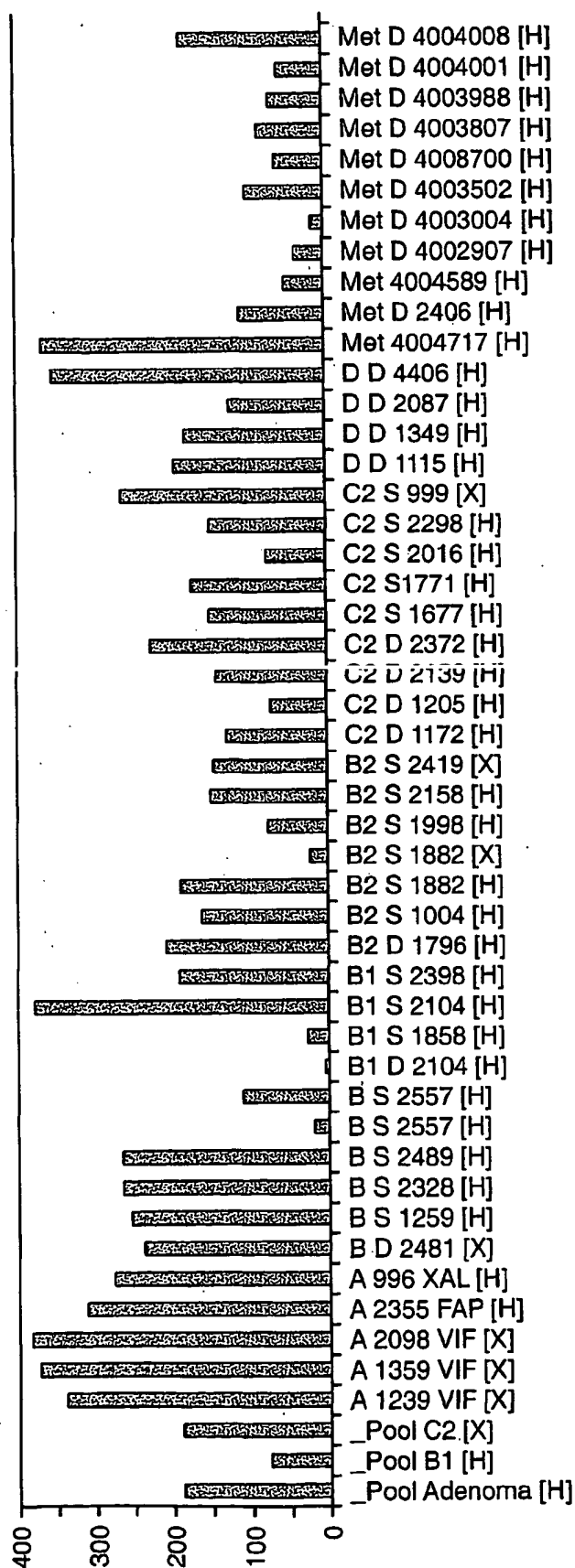


FIG.-37A

FIG.-37A FIG.-37B

FIG.-37

440 / 454

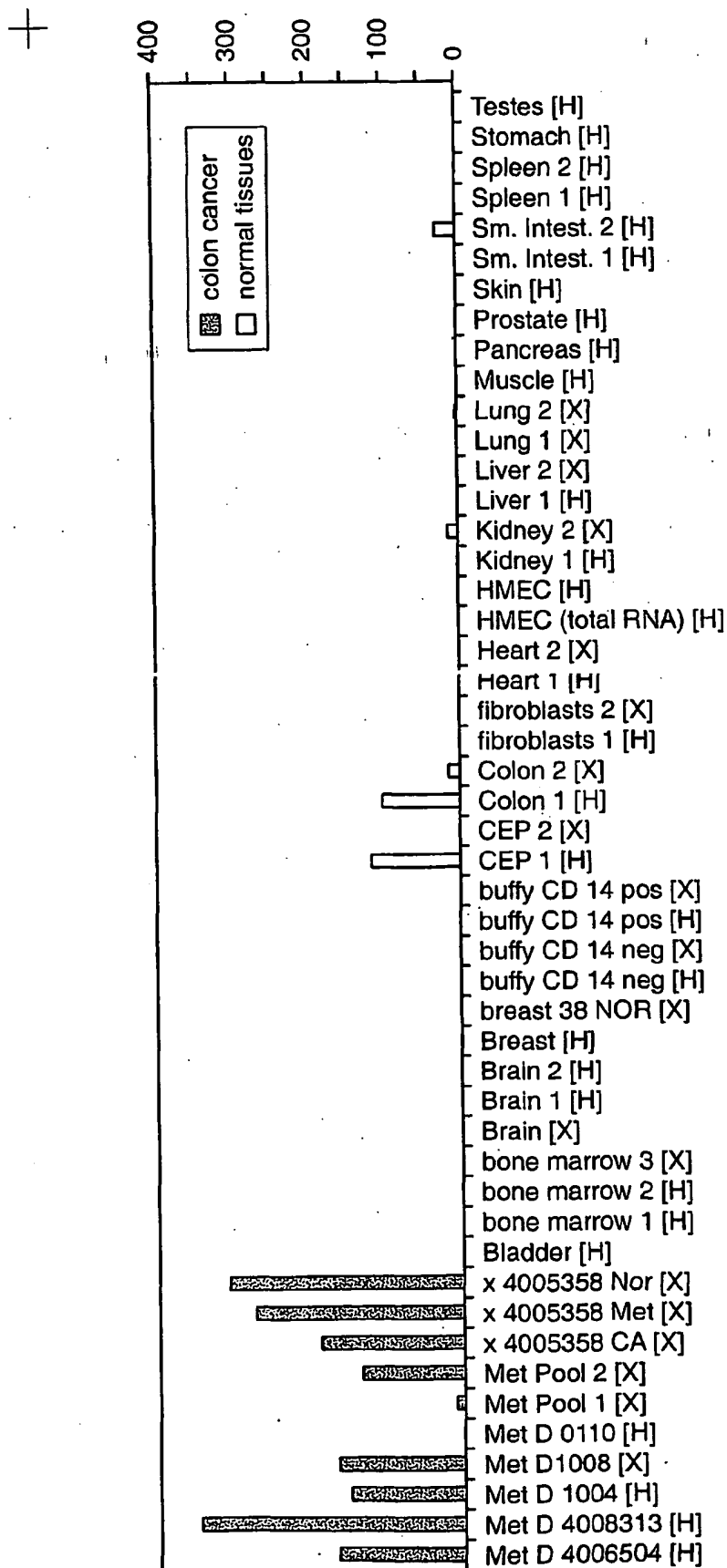


FIG. 37B

441 / 454

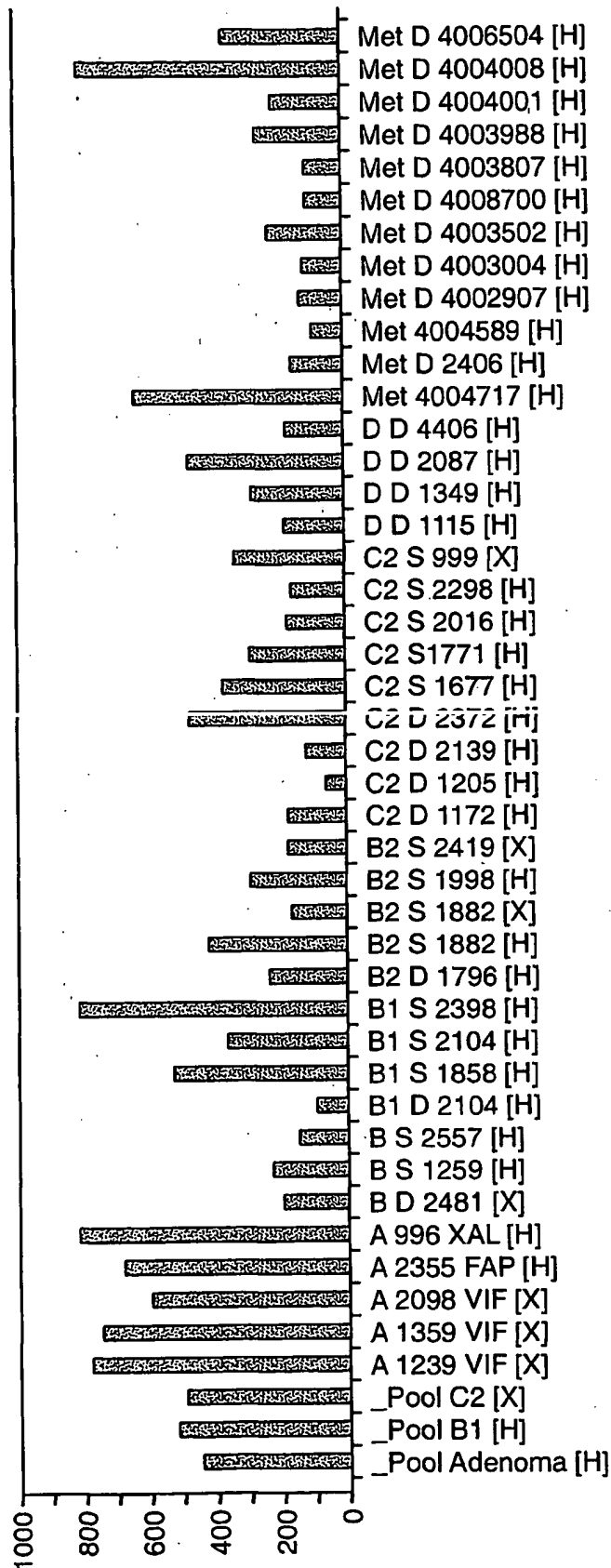


FIG.-38A

FIG.-38A FIG.-38B

FIG.-38

442 / 454

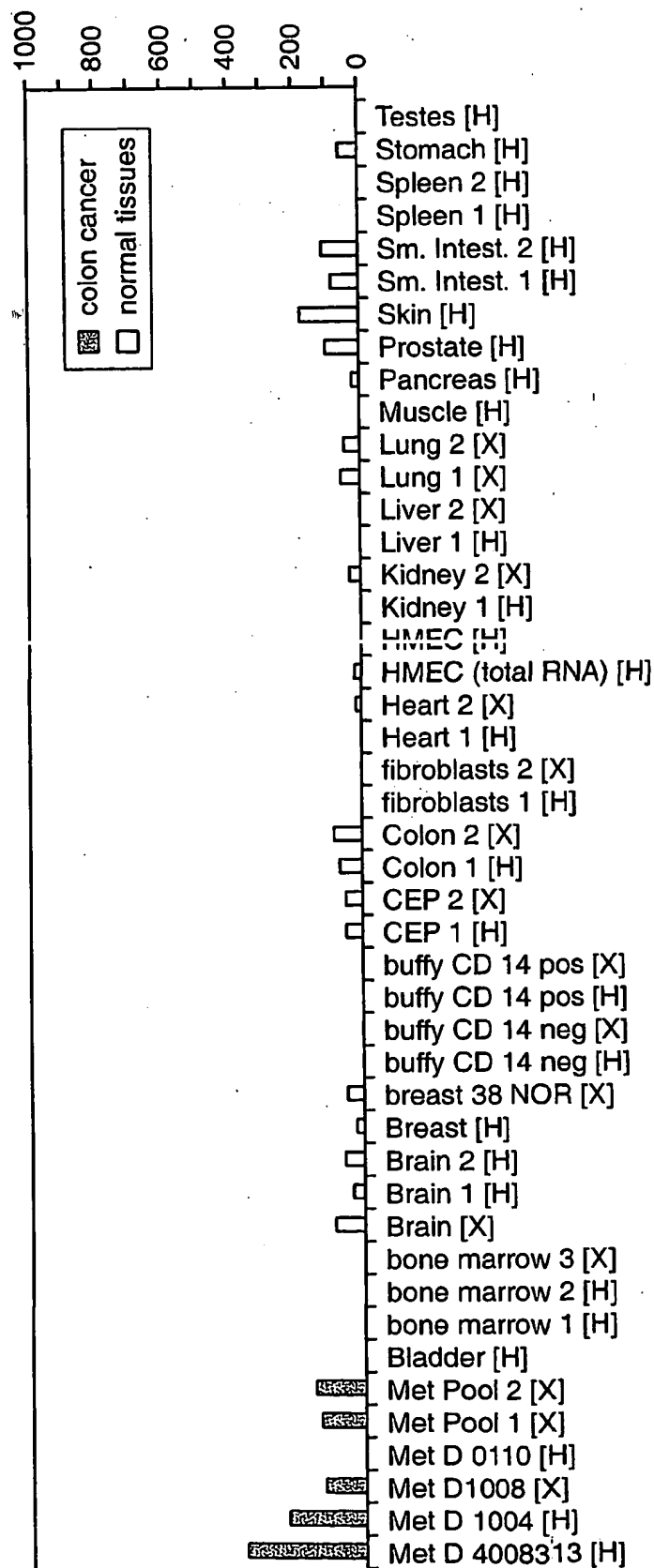


FIG. 38B

SUBSTITUTE SHEET (RULE 26)

AGAAATGGCTTCGGCTCCCTTCGCCGCCGGTATTCTGGTGATATGATCCCACTCTCACTCTCATAGGAGAC
GATCTCGAAGTAGATCATATACACCAAGATACCGGGCGGGAAGGACCGAAGCTCAAGGGTAAAGACAGTA
GAAATATATTTCAGTAAACAAATAATGTGTGAACCTTTTAAAGATGGTAATAGGGCATGGACTGAGTGTCTGCT
ATCTTGAAATGTGCACAGGTACACTTACCCTTTTTTTTTTTTTTTTTTTTTTTTAAAGTTTTTCCCATTCAGGATAACA
ACATTTGTGATCTGTACTACAGGAACCAATAATGTCTATCGCTCATACATGTGGCTATAAAGTACATAAAATATA
CTTAACCTATTCTAAATGTGGGTGGTAATACTGTCTGTGAAATTAATGTAAAGAAAGCTTTTTCACCTTAAAAAA
AATGCATTACTTTCACTTAAACACTAGACACCAAGTCGAAATAATTTTCAAGTTATAGTACTTATTTCAACAA
TTCTTAGAGATGCTAGCTAGTGTGAAAGCTAAAAAATAGCTTTTATTTATGCTGAATTGTGATTTTTTTTATGTC
CAAAATTTTTTTAGTTCTAATCATTTGATGATAGCTTTGGAAAAATAATAATATAGCCATGGCATTTTGACAGTT
CATTATTCCTATAAGAAATTAATAATTGAGTTTAGAGAGAAATGGTGGTGTGAGCTGATATATAACAGTTTACTG
AAATCAAAATATTATTTTGTTCATTAATCCCATTTGTATTTTAGGTTTCCTTTTACATCTCTTTTATATATGCA
TTCTGACATTACATAATTTTTTTTAAAGCTATGGAATAATAATTAAGAATTTAAAGCTCTGGTGGATGATTATCTG
CTAAGTAAGTCTGAATAATGTAAATATTTTGAATAATACTGTAAATATCTGTTCACACAAATGCTTTTCTTAATG
TTTTAAACCTTGAGTATTGCAGTTGCTGCTTTGTACAGAGGTTACTGCAATAAAGGAAGTGGATTTCATTATAA
CCTTAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA

FIG. 39

GGAAATATAGATCTTGATATTGAATCCATCAGTGATCAAGAGATACACCTATTGTGCTAAACAACCTTA
AGATGTATTGGTTATGGAATCATGTGTTGGATAGGTTCTTTAAGACCTGTTCCTCAAAATCTTGACACAGTT
TTCAAGGGTGGCTTATTGACTTGACCGTTGGGCAGATAAATCCAGATTTACCTTAAGATTGGGTAAAAAAGT
CATCTGTGACTTTGCTGGCAGGGCATTTGCTAAGTGGAGTACAGCATCTAAAAAGGGTTTCTTTAGAAAAGG
CAATATTGTCCAATGAAGTAAGCAGAAAGGACTCTGGGTTAGAGCATCTGCACAAAAAACTGGTGAGACCTTA
CTCTCCACTGCTCTGCAGCTGGATGGCTGATGGCAGGCTGAGCAGTGGGGAAGCAGGTTTTAAACAACAGGG
AGTCCTTCCAGGTCACCTGTATATTGAAGAAGAAACATAAAACTATTGTCTGTTACATTTCCGAGGTGAGCCTT
CTCTTAAAGTTTATAATATGCAAAATGCCAGCTTCTGGAAAGCAAGTATCATCATGTACCAAATGCTTTTA
TACACCATCACATTCATGAATTTTATTAGCATGGTCAGAACTTGTGTAAATATGTCTCTTAGATGATTTTGG
GGAGATGTGATTTATTTTTCATATTTTCAAAATGTCATTTTCATTTCAATAAAAGTTATCTATTGAGACAACC
GAAAAAATAAAAAAAAAAAAAA

FIG.-47

444 / 454

FIG.-40A

CCAAGTTCTACCTCATGTTTGGAGGATCTTGTCTAGCTATGGCCCTCGTACTCGGCTCCCTGTTGCTGCTGG
GGCTGTGCGGGAACCTCTTTTTCAGGAGGGCAGCCCTTCATCCACAGATGCTCCTAAGGCTTGGAATTATGAA
TTGCCCTGCAACAAATTATGAGACCCCAAGACTCCCATAAAGCTGGACCCATTTGGCATTTCTTTTGAACATAGT
GCATATCTTTCTCTATGTGGTACAGCCCGCTGATTTCCCAAGAGATATCTTTGAGAAATTTCTTACAGAAAGG
CATATGAATCCAAAATTTGATATGACAAAGCCAGAAACTGTAATCTTAAAGTCTAAAGATTTGTCTACTATGAA
GCAGGATTTATCTATGCTGTGCTCTGGGGCTGCTGTTTATTTATCTTGATGCCCTCTGGTGGGTATTTCTTT
TTGTATGTGCTGCTGCTGTAAACAAATGTGGTGGAGAAATGCCACAGCGACAGAAAGGAAATGGGCCCTTCC
TGAGGAAATAGCTTTTGCAATCTCCCTGTGTTGGTGATTTGTATAATAATAAGCATTTGGCATCTTTCTATGGTTTT
GTGGCAATATCACAGGTAAGAACCCGGATCAAAAAGGAGTGGGAAACTGGCAGATAGCAATTTCAAGGACTT
GCGAACTCTCTTGAATGAACTCCAGAGCAAAATCAAAATATATATTTGGCCCAAGTACAACACTACCAAGGACA
AGCGTTTCACAGATCTGAACAGTATCAATTCAGTGTCTAGGAGCGGGAATTTCTTTGACCGACTGAGACCCCAAC
ATCATCCCTGTTCTTGATGAGATTAAGTCCATGGCAACACAGCGATCAAGGAGACCAAGAGGCGTTGGAGAA
CATGAACAGCACCTTTGAAGAGCTTGCAACCAACAAAGTACACAGCTTAGCAGCAGTCTTGACAGCGTGAATA
CTAGCCTGCGGTCACTCTCAATGACCCCTCTGTGCTTGGTGCAATCCAATCAAGTGAAACCTGCAACACAGCATC
AGATTGCTCTAAGCCAGCTGAATAGCAACCCCTGAACCTGAGGAGCTTCCACCCGTGATGCAGAACTTGA
CAACGTTAATAACGTTCTTAGGACAGATTTGGATGGCTGTGTCACAGGCTATCAATCCCTTAATGATA
TACCTGACAGAGTACAAACGCCAAACACGACTGTCTGTCAGCAGGTATCAAAAGGCTTTGAATTCATTTGGT
TCAGATATCGACAAATGTAACCTCAGCGTCTTCCATTCAGGATATACITCTCAGCATCTCTGTTTATGTTAA
TAACACTGAAAGTTACATCCACAGAAATTTACCTACATTTGGAAGAGTATGATTCATACCTGCTGGCTGGGTG
GCCGTGTCATCTGCTCTGCTGACCCCTCATCGTGATTTTTTTTACTACCTGGGCTTACTGTGTGGCGTGTGC
GGCTATGACAGGCAATGCCACCCGACACCCGAGGCTGTCTCCAAACCCGAGGCGTCTTCCCTCATGGT
TGGAGTTGGATTAAGTTTCTCTTTTGTGATATTTGATGATCATTTGTTGTTCTTACCTTTGTCTTTTGGTG
CAAAATGTGGAAAAAATGATCTGTGAACCTTACACAGCAAGGAATTAATTCGGGTTTGTGATACACCCCTAC
TTACTAAATGAAGACTGGGAATACTATCTCTCTGGGAAGCTATTTAAATAATCAAAAATGAAGCTCACTTT
TGAACAAGTTTACAGTGACTGCAAAAAAATAAGAGGCACCTTACGGCACTCTTCCACTGCAGAACAGCTTCA
ATATCAGTGAACATCTCAACATTAATGAGCATACTGGAAGCATAAAGCAGTGAATTTGGAAGTCTGAAAGGTA
AATCTTAATATCTTCTGTGTTGGTGCAGCAGGAAGAAAAACCTTCAGGATTTTGTGCTGTGTTGGAATAGA
CAGAAATGAATATGACAGCTACTTTGGCTCAGACTGGTAAATCCCCCGCAGGAGTGAATCTTTTATCATTTG
CATATGATCTAGAAAGCAAAAGCAAAACAGTTTGTCCCTCCAGGAAATTTGAGGAACCTCCCTGAAAGAGATGCA

445 / 454

FIG.-40B

CAAACTATTAAACAATTCCACCAGCAACGAGTCCTTCTATAGAAACAATCACTGAGCACTCTATACC⁺AAAG
CGTCAAGATACTTCAACGCACAGGGAATGGATTGTTGGAGAGAGTAAC⁺TAGGATTCTAGCTTCTCTGGATT
TTGCTCAGAACTTCATCACAACAATACTTCCCTCTGTTATTATTAGGAAACTAAGAAGTATGGGAGAAC⁺A
ATAATAGGATATTTGAACATTTATCTGAGTGGATCGAGTTCTCTATCAGTGAGAAAGTGGCATCGTGCAA
ACCTGTGGCCACCGCTCTAGATACTGCTGTTGATGCTTTCTCTGTGTAGCTACATATATCGACCCCTTGAATT
TGTTTGTGGTTTGGCATAGGAAAAGCTACTGTATTTTACTTCCGGCTCTAATTTTTCGGGTAA⁺AACTGGCT
AAGTACTATCGTCGAATGGATTCGGAGGACGTGTACGATGTTGAAACTATA⁺CCCCATGCCATGAAAAATATGGA
AAATGGTAATAATGGTTATCATAAAGATCATGTATATGGTATTCACAATCCTGTGTATGACAAGCCCATCAC
AACAT⁺TGATAGCTGATGTTGAAACTGCTTGAGCATCAGGATAC⁺CTCAAAGTGGAAAGGATCACAGATTTTGG
GTAGTTTCTGGGTCTACAAGGACTTTCCAAATCCAGGAGCAACGCCAGTGGCAACG⁺TAGTGA⁺CTCAGGCGG
GCACCAAGGCAACGGCACCATTTGGTCTCTCTGGGTAGTGCTTTAAGAAATGAACACAATCACGTTATAGTCCAT
GGTCCATCACTATTCAAGGATGACTCCCTCCCTTCCCTGTCTATTTTGTGTTTCTACTTTT⁺TACACTGAGT
TTCTATTTAGACACTACAACATATGGGGTGTGTTCCCATGTTGGAGTGTGTAACACACACACCAGTTTACAGGAAAGAT
TGTGATGGCTAGATTCTAACATATTTGCCATGTTGGAGTGTGTAACACACAGAGTTT⁺TAAACA⁺AAATGAGTATTAT
GCATTTTGTGTACAGTAAACGGTGTATATACCTTTTGT⁺TACCACAGAGTTT⁺TAAACA⁺AAATGAGTATTAT
AGGACTTTCTCTAAATGAGCTAAATAAGTCA⁺CCATTTGACTTCTTGGTGTGTTGAA⁺AAATATCCATTTTC
ACTAAAAGTGTGTAAACCTACAGCATATTTCTTCACGCAGAGATTTTCACTATATATACTTTATCAAAGAT
TGGCCATGTTCCACTTGGAAATGGCATGCAAAAGCCATCATAGAGAAACCTGCGTAACTCCCATCTGACAAA
TTCAAAAAGAGAGAGAGAGATCTTGAGAGAGAAATGCTGTTCCGTTCAA⁺AAAGTGGAGTTGTTTAAACAGATGC
CAATTACGGGTACAGTTTAAACAGAGTTTCTGTGTCATTAGGATAAACATTAATTGGAGTGCAGCTAAC⁺A
TGAGTATCATCAGACTAGTATCAAGTGTCTAA⁺AAATGA⁺AAATATGAGAAAGATCCTGTCA⁺CAATTTCTTAGATC
TGGTGTCCAGCATGGATGA⁺AAACCTTTGAGTTTGGTCCCTAAATTTGCA⁺TGAAAGCACAAAGGTA⁺AAATATCA
TTTGCTTCCAGGAGTTTTCATGTGTGATCTGTCA⁺TATCA⁺AAAGTGTATCA⁺AAAGTGTGTCGGACAA
AATTTAACGTTGATGTAATGGAATTCAGATGTAGGCATTTCCCCCAGGTC⁺TTTTCATGTGCAGATTG⁺CAG
TTCTGATTCATTTGAATA⁺AAAAGGA⁺ACTTGG

446 / 454

FIG. 41

CAGCGGCGGTGAATCTAGGGCGGGTTCCGCGCCCGCCGAGGCTGAGAJCTGGGGCTGCTCGTGCCCTGTG
TGCCAGACGGGAGCTCCGCGCGGACCCCGGGCCCGCTTTCCTGCGGCTGAGTTCGGGGGAG
AACTCTCTGCGCCAGAAAGATTCTTCTTCGCGGAGGACAGC3AAAGATGAGGTGCGAGGAAGA
GAAGGCGTTCTGTCTGCGGGTGCAGCGGAGAGGCGAGTGCCATGTTCTCTCCATCCTAGTGGC
GCTGTGCTGTGGCTGCACCTGGCGCTGGCGGTGCGGGCGCGCCCT3CGAGGCGGTGCGCATCCCTATG
TGCCGGCACATGCCCTGGAACATCACGCGGATGCCAACCTGCA3CACAGCAGGAGAACGCCA
TCCTGGCATCGAGCAGTACGAGGAGCTGGGTGAGCTGAACTGCA3CGTGTGCGCTTCTTCTCTG
TGCCATGTACCGGCCCCATTGCAACCTTGGAGTTCCTGCACGACCTA3CAAGCCGTGCAAGTCCGTGTGC
CAACGCGCGCGGACGACTGCGAGCCCTCATGAAGATGTACAACCA3AGCTGGCCCGAAAGCCTGGCCT
GCGACGAGCTGCCCTGTATGACCGTGGGTGTCATTCGCCCTGAA3CCATCGTCACGACCTCCCGGA
GGATGTTAAGTGGATAGACATCACACAGACATGATGTTACAGGAA3GCCCTCTGTGATGTTGACTGTAA
CGCTAAGCCCCGATCGGTGCAAGTGTAAAGGTGAAGCCAACTTT3GCAACGTATCTCAGCAAAACT
ACAGCTATGTTATTCATGCCAAATAAAAGCTGTGAGAGGAGTGGCTGCAATGAGGTCAACAACGTTGT
GGATGTAAGAGAGATCTTCAAGTCTCATCACCCATCCCTCGAACTAA3GTTCCGCTCATACAAATCT
TCTTGCCAGTGTCCACATCTCTGCCCCATCAAGATGTTCTCATCAT3TGTACGAGTGGCGTCAAGGA
TGATGCTTCTGAAATATGCTTAGTTGAAATATGGAGATGCTAGTAAAGATCCATACAGTGGGA
AGAGGCTGCAGGAACAGCGGAGAACAGTTCAGGACAAAGAGAAACAGCCGGCGCACAGTCTGTAGT
AATCCCCCAACCAAGGAAAGCCCTCTGCTCCCAACACGAGCTCCCAAGAAAGAACATTAACATA
GGAGTGCCAGAGAGAACAAACCGAAAGAGTGTAGCTAACTAGTTTCCAAAGCGGAGACTTCCGAC
TTCCTTACAGGATGAGGTGGGCATTGCCCTGGACAGCCTATGTAAG3CCATGTGCCCTTGGCCCTAAACA
ACTCACTGCAGTGTCTTTCATAGACACATCTTGACGATTTTCTTAAGGCTATGCTTCACTTTTCTT
GTAAGCCATCACAGCCATAGTGGTAGGTTGGCTTGGTACAGAA3GTTGAGTTAAAGTGGTGGAA
GGCTTATGCTATGCTATGAGTAACTGATGCTATCTTAGAAGATCTTTA3GTTTATGTTGCTGCAAG
CAATCGACCTAATATGTGCATTGTAATAATGCCATATTTCAACAAACACGTAATTTTCTTACAG
TATGTTTATTAACCTTTTGTATCTGTTGTTGCAATGTTAGTATGTTTAAATGTTGATGAAATATA
TGTTTAAAGAGAACAGTAGTGGAAATGTTAAAGATCTTTA3TGTGTTTATGTTGCTGCAAGGA
TTTTTGTGATGAAAGGGATTTTGTGAAATATGAGAAATGAGAAATTAATAATGTTT
TACCAATGACTTCAGTTTCTGTTTGTAGCTAGAACTTAAACAAATAATAATAAGAAATAAAT
AAAAGGAGAGGACAAATGCTGGATTCCTGTTTGGTTACCTGATTTCCATGATCATGATGCTTC
TTGTCAACACCTCTTAAGCAGCACAGAACAGTGGTGTGCTGTACCTAGGAGTTAGGACTAGTAAT
TAGTTGGCTAATGCTCAAGTATTTATACCCACAAAGAGAGGTATGTCACCTCATCTTACTTCCAGACAT
CCACCTGAGAAATAATTTGACAAAGCTTAAATAATGGCTTTCATGTGAGTGCCAAATTTTGTCTTCAT
TTAAATAATTTTCTTAAATACATGTGAGAGGAGTTAAATAATAATGATACAGAGAGGAAAGTTGAGT
TCCACCTCTGAAATGAGAAATTAATGACAGTGGGATCTTAATCAGAAATAAGAACTTATTTGACG
ATTTATCAACAAATTTTCATAATGTGGACAAATGGAGGCAATTTATTTAAATAACAAATTTATGSCCT
TTTGTCAACACAGTAAAGTATTTTATAGGCAATCAATAATGCAACACGCCCAAGGAAATAAAT
CCTATCTAATCTTACTCTCCACTACACAGAGGTAATCACTATTAGTATTTTGGCATATTTCTCCAGGT
GTTTGTCTTATGCACTTATAAATGATTTTGAACAAATAAACTAGGAACCTGTATACATGTGTTTCAAC
CTGCCCTCTTGTCTGGCCCTTATTTGAGATAAGTTTCTGTCAGAAAGCAGAAACCATCTCATTTCT
AACAGCTGTGTTATATTCATAGTATGCTATTAACAACTGTTGTGCTATTTGGATACCTTAGGTGTT
TCTTCACTGACAACTACTGAATAAACAATCTCACCGGAATTC

447 / 454

FIG. 42

GATTAAATCCTATGACAAACTAAAGTTGGTTCTGTCTTCACCTGTTTTT3GTGAGGTTGTGTAAAGATTGGT
GTTTGTCTAGGAAGAGATTTAAGCATGCTTGTCTTACCCAGACTCAGA3AAGTCTCCCTGTTCTGTCTCCTAG
CTATGTTCCCTGTGTGTGTCATTCGTCTTTTCCAGAGCAAAACCGCC2AGAGTAGAAGTTGAGATTGGGGC
ACGCTGCAGACGATCCTGGGGGTGTGAACAAACACTCCACAGCATTGGAAAGATCTGGCTCACCGTCC
TCTTCATTTTTTCGCATTTATGATCCTCGTTGTGGCTGCAAGAGAGGTG1GGGGAGATGAGCAGCCGACTT
TGCTGCAACACCCCTGCAGCCAGGCTGCAAGAAGCTGTGCTACGATCACTACTTCCCCATCTCCCCACATC
CGGCTATGGGCCCCTGCAGCTGATCTTCGTGTCCAGCCCAGCGCTCCTAGTGGCCATGCACGTGGCCCTACC
GGAGACATGAGAAGAAGAGGAAGTTTCATCAAGGGGGAGATAAAGAGT3AATTTAAGGACATCGAGGAGAT
CAAAACCCAGAGGTTCCGCATCGAAGGCTCCCTGTGGTGACCTACACAAGCAGCATCTTCTTCCGGGTC
ATCTTCGAAGCCGCCCTTCATGTACGTCTTCTATGTCACTACGACGGCTTCTCCATGCAGCGCTGGTGA
AGTGCAACGCCCTGGCCCTTGTCCCAACACTGTGGACTGCTTTGTGTCTCCGGCCACGGAGAAGACTGTCTT
CACAGTGTTCATGATGTCAGTGTCTGGAATTTGCATCCTGTCTGAATGTCACCTGAATTGTGTTATTTGCTA
ATTAGATATTGTTCTGGGAAGTCAAAAAGCCAGTTTAAACGCAATTGCCAGTTGTGTAGATTAAAGAAATAG
ACAGCATGAGAGGGATGAGGCAACCCGTGCTCAGCTGTCAAGGCTCAGTGGCCCTCAGGTGAAACTCCAGATGCCACAA
AGATTCGACCTTAAATGCAACCATTTTGAACCCCTGTAGGCCCTCAGGTGAAACTCCAGATGCCACAAATG
AGCTCTGCTCCCTTAAAGCCTCAAAAAGCCCTAAATCTATGCTCTGTCTTAAATTTCTTTTACCTTAAG
TTAGTTCACCTGAGACCCCGGCTGTAGGGGTATTTGGTGAAGTACTTTTCATATTTTAAACAGAGGA
TATCGGCATTTGTTCTTTCTCTGAGGACAAGAAAAAGCCAGGTTCCACAGAGGACACAGAGAAAGGT
TTGGGTGTCCTCCTGGGGTTCTTTTGGCCAACTTTCCCACTTAAAGGTGAACATTTGGTCTTTTCATTT
GCTTTGGGAAGTTTAAATCTCTAACAGTGGACAAAGTTACCAGTGCCTTAAACTCTGTACACTTTTGGGA
AGTGAAAACTTTGTAGTATGATAGGTTATTTGTATGTAAGATGTTCTGGATACCATTAATATGTTCCCCC
TGTTCAGAGGCTCAGATTGTAATATGTAATGGTAATGTCATTCGCTACTATGATTTAAATTTGAAATATG
GTCCTTTTGGTTATGAATACCTTGCAGCACAGCTGAGAGGCTGTCTGTGTATTCATTTGTGGTTCATAGC
ACCTAAACAACATGTCAGCTCAATCGAGTGAGACAGACTAGAAAGTTCCTAGTTGGCTTATGATAGCAAAAT
GGCCTCATGTCAATATTAGATGTAATTTTGTGTAAGAAATACAGACTGGATGTACCACCAACTACTACC
TGTAATGACAGGCCCTGTCCCAACACATCTCCCTTTTCCATGCTGTGGTAGCCAGCATCGGAAAGAACGCTG
ATTTAAAGAGGTGAGCTTGGGAATTTTATGTACACAGTACCATTTAA1GGGGAGACAAAAATGGGGCCA
GGGAGGGAGAAGTTTCTGTCGTTAAAAACGAGTTTGGAAAGACTGGACTCTAAATTCCTGTGATTAAAG
ATGAGCTTTGTCTACCTTCAAAAGTTTGTGTTGGCTTACCCCTTCAGCTCCCAATTTTAAAGTGAAAT
ATAACTAATAACATGTGAAAGAATAAGAACTAAGTTTAGATAAATTTAGCAGCATCTATAGGAAGAT
TGAACCTGAATATTGCCATTATGCTTGACATGGTTTCCAAAAAATGGTACTCCACATACCTTCAGTGAGGG
TAAGTATTTTCTGTTGTCAGAATAAGCATTTGTAAAGCATTTTGTATAAATAAAGAAATAGCTTTTAATGA
TATGCTTTGTAACATAAATAATTTTGTAAATGTATCAATAACATTTAAACATTAAAAATATAATCTCTATAA

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449 / 454

CTCTGAGTGTCCAGTGGTCAAGTGGCCCAAGGATGGGGACCAACAGCCAAGCAGCCTTGGTCTTGGACCTAT
TTGGCTGTGCTTCTGCTGCTCTGAGGGAGGCTTACGGGTACAGGACAGAGGCAGCTGAGGCCAGAGC
ACTTTCAAGAAGTTGGCTACGCAGTCCCCCTCCACCCCTATCCCGAAGCCTCCCCATGGATCAACCC
TGACTCCTCTCAGCATGGCCCTCCCTTTGAGGGACAGAGTCAAGTGCAGCCCTCCCTCTCTCAGGAGGCC
ACCCCTCTCCAAACAGGAAAAGCTGTACCTGCCCCAATCCCTGCTGAAAAGGAAGTGGGTCCCCCTCTCC
CTCAGGAAGCTGTCCCCCTCCAAAAGAGTGGCTCTCTCTCCAGCACCCCAATGAACAGAAAGGAAGAAC
GCCAGCTCCATTTGGGACCAAGAGCCATCCAGAACCTGAGTCTTGGAATGACAGCCAGCACTGCCAACAG
GACCGTCCCCAAGGGGCTGGGGCCACCGGCTGGATGGCTTCCCCCTGGGGGGCTTCTCCAGACAATC
TGAACCAATCTGCTTCTTAACCGTACAGCATGTGGTATATGGTCCCCTGGAAACCTACACAGTCCAGCTA
CTCCACCTCACTCGCCAGGGTGAGACCCCTCAATTTCTTGAGATTG3ATATTTCCCGCTGTGCTGCCACTGC
CGCAGCCACACAAACCGCTAGAGTGTGCCAAACTTGTGTGGGAGGAAGCAATGAGCCGATTTCTGTGAGG
CCGAGTTCTCGGTCAAGACCCGACCCACTGGTGTGTCACCGCGGCAG3GGGAGGCTCGGTCTCTCTGCTT
CCAGGAGGAAGCTCCCCAGCCACACTACAGCTCCGGGCTGCCCCA3CCATCAGCCTGATATTTCTCTCG
GGTCTTGAGTGCCTTTCCCTCTGGGTGCCACATGGACAATATCAAGAACATCTGCCACCTGAGGC
GCTTCCGCTCTGTGCCAAGCAACCTGCCAGCTACTGACCCCCCTACAAAGGGAGCTGCTGGCACTGATCCA
GCTGGAGAGGGAGTTCAGCGCTGCTGCCGCCAGGGGAACAATCACACCTGTACATGGAAAGGCCCTGGAG
GATACCCCTTGACAAATACTGTGACCGGGAGTATGCTGTGAAGACCCCAACCACTTGTGTGCCGCCACCT
CTCCAGCCCTACTCGGGATGAGTGTCTTGGCCGCTGGGCTCTTACCCCACTATGACCGGGACATCTT
GACCATTGACATCAGTCGAGTCAACCCCAACCTCATGGGCCACCTCTGTGGAACCAAGAGTCTCAACC
AAGCATAAACATATTCCTGGGCTGATCCACAACATGACTGCCCGCTGTGTGACCTGCCATTTCCAGAAC
AGGCTGTGTGCAGAGGAGGAGAAATTAACCTTCATCAATGATCTGTGTGGTCCCCGACGTAACATCTG
GCGAGACCTGCTGCTGTGTTACCTGAGTCTGGGATGAACAGGTCAACTGCTTCAACATCAATAT
CTGAGGAACGTGGCTCTAGTGTCTGGAGACACTGAGAACGCCAAGGGCCAGGGGAGCAGGGCTCAACTG
GAGGAACAATAATCAGCTCCACCTCTGAGCCCCAAGGAAGATGAGTCAACCCAGAGCCCCTAGAGGCTCAG
ATG

FIG. 44

450 / 454

FIG.-45A

ACTACTATAGGGCTCGAGCGGCCCGCCCGGCGAGGTGGCCACCCACCATCATCTAAAGAAATAAACTTGG
CAAAATGACATGCAAGGTTCTTCAAGGCAGCAATAATTCAGAAAAATCTTCAAGGACCCCTATCTGCAGATGTT
CTGAATACCTCTGAGATAGAGATTGATTATTCACACAGGATACCTAATTCAGAACTCCAGAAATCAGGA
GACGGAGACATTTTGTCTAGTTTGCACCATTTGACCAATATGACCAATGAGAGTATCTTGTCTGTCTGTGTT
TGGTGTCTCTGGGCACAGAAATGCTGGGAAGCCTCTGTTCGACTGTTCAGATCCCGAGGTTTCAGAGGACGG
ATACAGAGGAACGAAACAAATTCGACCCCAATTAATCTTGTCTTACCGATGATCAAGATGTGGAGCT
GGGTCCCTGCAAGTCAATGAACAAACGAGAAAGATTATGGAACATGGGGGGGCCACCTTCATCAATGCCT
TTGTGACTACACCCATGTGTCTGCGTCCCGTCCATGCTCACCGGGAAGTATGTGCACAATCACAAT
GTCTACACCAACGAGAACTGCTTCTCCCTCGTGGCAGGCCATGATGAGCCTCGGACTTTTGTCTGT
ATATCTTAACAACACTGGCTACAGAAACAGCCTTTTGGAAATACCTCAATGAATATAATGGCAGCTACA
TCCCCCTGGTGGCGAGATGGCTTGGATTAAATCAAGAAATCTCGCTTCTATAATTAACCTGTTGTCTGC
AATGGCATCAAGAAAGAAAGCATGGATTGATTATGCAAAAGGACTACTTCACAGACTTAATCACTAACGAGAG
CATTAATTACTTCAAAATGTCTAAGAGAAATGTATCCCCATAGGCCCGTATATGATGGTGATCAGCCACGCTG
CGCCCCACGGCCCCGAGGACTCAGCCCCACAGTTTCTAAACTGTACCCCAATGCTTCCCAACACATAACT
CCTAGTTATAACTATGCACCAATATATGATAAACACTGGATTATGAGTACACAGGACCAATGCTGCCCAT
CCACATGGAATTTACAAACATTTACAGCGCAAAAGGCTCCAGACTTTGATGTCACTGAGTATCTGTGG
AGAGGCTGTATAACATGCTCGTGGAGACGGGGAGCTGGAGAAATTAATTAATTAACCTGACCCCGACCAT
GGTTACCATATTTGGCAGTTTGGACTGGTCAAGGGAAATCCATGCCATATGACTTTGATATTCGTGTGCC
TTTTTTTATTCGTGGTCCAAAGTGTAGAACAGGATCAATAGTCCACAGATCGTTCTCAACATTTGACTTGG
CCCCACGATCCTGGATATTTGCTGGCTCGACACACTCTCTGATGTGGACGGCAAGTGTCTCTCAAACTT
CTGGACCCAGAAAGCCAGGTAACAGTTTTCGAACAAACAGAGGCCAAATTTGGCGTGATACATTCCT
AGTGGAAAGAGGCAAAATTTCTACGTAAGAAAGAAATCCAGCAAGAAATCCAAACAGTCAAAATCACTTGC
CCAAATATGAACGGGTCAAGAACTATGCCAGCAGGCCAGGTACAGACAGCTGTGAACAAACCCGGGGAG
AAGTGGCAATGCATGAGGATACATCTGGCAAGCTTCGAATTCACAAAGTGAAGGACCCAGTGACCTTGCT
CACAGTCCGGCAGAGCACGCGGAACCTCTACGCTCGCGCTTCCATGACAAAGACAAAGAGTGCAGTTGTA
GGGAGTCTGGTTACCGTGGCCAGAGAACCAAGAAAGTCAACGGCAATTTCTGAGAAACCCAGGGGACT
CCAAAGTACAAGCCAGATTTGTCTCATCTCGGACAGACAGTCTCTGTCGTCGAATTTGAGGGTGAAT
ATATGACATAAATCTGGAAGAAGAAGAAATTCAGAGTGTGCAACCAAGAAACATTTGCTAAGCGTCAATG
ATGAAGGCCACAAGGGCCAGAGATCTCCAGGCTTCCAGTGTGGCAACAGGGCAGGATGCTGGCAGAT
AGCAGCAACGCGTGGGCCACCTTACACTGTCTCGAGTGACACAAAGTGTGTTTATCTTCCCAATGACTC
TATCCATTGTGAGAGAGAACTGTACCAATCGGCCAGAGCGTGGAAAGGACCATTAAGGCATACATTGACAAAG
AGATTGAAGCTCTGCAAGATAAATTAAGAAATTAAGAGAACTGAGAGGACATCTGAAGAGAAAGGAAAGCT
GAGGAATGTAGCTGCAGTAAACAAAGCTATTAATAAGAGAAAGGTGTAAAGAAAGCAAGAGAAATTAAG
GAGCCATCTTCAACCAATTCAGAGGAGCTGCTCAGGAAGTAGTAGCAACTTCAACTTTTCAAGAGAGAA
ACCGTAGGAGGAAGAGGAGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
CTCAGTTGCTTACGCGATGACAAACACCACTGGCAGACCCCGTTCTGGAACCTGGGATCTTTCTGTGC
TTGACAGAGTTCTAAACAATACACCTACTGGTGTGTCGCTACAGTTAATGAGACGCATTAATTTTCTTCT
GTGAGTTTGCTACTGGCTTTTGGAGTATTTTGATATGAATACAGATCCTTATCAGCTCACAAATACAGTG

452 / 454

CAAGAATTCCGGCACGAGGGCGGTGTTCCAGAAAGTGTCTGGATACTGTCAGTAGTTAATTCCTCAGCTGGCAGGT
TCCCTGAGTGCAGCTGGCTCGATAGTCGTAATGAAGAGTGTGTCGAAAGACCTTTGAATCCAGTATGAA
TGTAATACAGGAAATTAAATTTAAGCTAGGATCAGAGGGACTGTAAGACTGGGCTCCTTAGATTTCAAA
TCATAATTAAATATTCATCCACCACTCAAGAGGGACCTTGTGTGTCAGCCCAAGAAATTTTCTGTGCGCGGC
TGTGGAACCTCCAGTAGAGCCTAAGTTTGTGAAGCGGCTCCGTAATGCGGAATACCTAGGGAAGTATTTCTG
TGACTGCTGCCACTCATATGCAGAGTCGTGCATCCCTGCCCGAAATCCTGATGATGTGGGACTTCAAGAAGT
ACTACGTACGAATTTCTCCAAACAGCTGCTCGACAGCATATGGTACCAGCCCAATTTTCAATTTGCTGAGC
ATCGGCCAAAGCCTGTATGCGAAAGCCAAAGAGCTGGACAGAGTAAGGAATTCAGGAGCAGCTCTTCCA
TATCAAGAAGCTGTTGAAGACCTGTAGGTTTGTCTAMCAGTGCATTAAGGAGTTTCGAGCAGGTGCCGGGA
CACTTGACTGATGACTCCACCTGTCTCCCTTAGGACCTGGTCAAGATCAAGAAAGGGCTGCTGGCACCTT
TACTCAAGGACATTTCTGAAAGCTTCCCTTGACATGTGGCTGGCTGCTCAAGGAAAGGGCTTT
ATTTGTGAATTTTGGCAGAAATACGACTGTCACTTCCCATTTCAAGCAACATGTAGAAGATGTTTCAGC
GTGCAGGGCTTGCTTTACAAACAGTGTCTCCAGTCTCCGAGTCCCGGAGTCCCGGCTGCGAGGATCACAGCGA
GGAGAAACCTTCTGGAAAGTGTGGCCTCTGCAGCAACATGATGCCCTGAGTACTGTGAAAAAGACTGTTTC
AACATGCCCTTATGATAAACACCGATTTGTGCTCTATTTATTGCATATACTTAATGTTTCAAAAGAAATGCTGTG
TTAAGGAAAAAGATGGTCTATATTTCTTTATTGCTATATACTTAATGTTTCAAAAGAAATGCTGTG
TTTAAGCACAGGGCTGATAGTTGTGGTTTGTGTTTACAAATGTTCTGTTTGGCTGCTATTTGGTTTAA
GAGGTTTTTATACCTTTTGTATTTGAATAGTTATGTTTCACTGAAGCTGAGCCAGTTTGTATGTGTGCA
TATATGTGAACCTGAACAGCAAGATGAATTAATCACTGTTCTCTCTCTAAAGCTTGTGTTGATGAAACTG
GTTGGTCCCTTTCAAGTGMAMAAAWATATGACCCCAAAAAAATAAGCAATGCGAAAGTG
CTAATCCCTGACGCTCGTGGTGGCCCTGCGGCTTCTCTCTGAGCAGCAATGGCGGACAAAGGAAGAA
CGAGGCCCTCGCCCCCACCCTGCTGGACGCCGAACCCCGG

FIG. 46

453 / 454

FIG. 48A

AATTTTGGCCCCCTCCGAAGGCCCAAAGAAATTTCCGGCCACCGANGGAATTTTGGTACCACCCAGGGG
GGAATGGAAATGCTGCTTTCAAACTTAGTTTCCCTTCCATTCTTCTTAGTCTGGCCCTTTGACACAAAA
CTGGTAGAAAGAGCTGATAAATTGAGGCACTTGTACCCCTCCCTGTGCCCCCAGAAGGTTCTTTGGAGAG
AAGTGCAAGAAATTTGTGAACACGGCGGTGGAGGGGGTGGATGGCCATGGGCTGGCCCTCCGTATCAGGC
CTGCTCACCTTGCTGGGAGCTTTATCTGATCTCATTTTGAATGTTCCAGAGGGAGCATCATAGAGCCCCA
GAGCTCCGATTTCCAAAGAGTGATATGACATTTATGGAGATTGGTGTGTAAACATATTTTGATAAATACT
AACTTATTTTGTGGGTTTGGTTGCTCTTTGCTCTTAGGACCTGGTAGTTATTTTGTGCTTGAATTTTTC
CGTTATTTCTACATAGGCAAGAGAAATTCGAGGGATAGACAGTCTCCAAAGAAAAGTGAAGTGGTGGGAGA
GAATGCTTTTCTTTTCTTTTCTTCTTAGTTTCTTCTTCTGGCTGAGATTTCCGTGCAAGACAGCAC
CCAATAGACTATTTAGAGTTGACATTTGACATTTTAAATGGCGCCATGGCTCATTTTGTAGATTGAGAAAG
TGCGTCTCCCTGCTCCAAGTCTCATCATGACAGCGTGTGACAGCTGGGAGTGGGACCCATGCCCCCTCCTTAGA
AGAGGCCTTAAAGCTGGACACAGAAAGCACGCCATAGGCTGGGAGGGATGGCATAAATAGTTTCACTGGTCA
GGACGGGCTTCCCTGTTAGGAAAGGACACAGTGGGGTGCTTCTCTGTGTGCGAGGGGAGTGATTTAAGCAATGG
TATGAGTAGTGTTTTGTGCACTTGGCAGGGGTTTCTCTCTGTGTGCGAGGGGAGTGATTTAAGCAATGG
TGCTGGAGTAAGCCTTACAAATTTAAATAGACTTTTCTTATCATCTCTTAGTTTCCCTTGCCCAAACAGAAATATCT
AAATACACACAAGCAAAAAAATGATAGTTTTCACATCTCTTAGTTTCCCTTGCCCAAACAGAAATATCT
TAGTTCCACTGGCCAGGATTTTCTTACATAGTCAGAACTTACACATTACTAGAGGCACACCCACCAAGGAG
TATTTGTCTACTTTTATCTGTGCACCAGCCACAAATACCCACATTTGGAAAGACCCATTTGTGATGGGTAA
ACATCCCTTCCCTGTCTCCCAACCCCTGTGACTGCCCTGCAATGTGTTCATGACCTCCGAAGGCCCTAAT
CATGAAGCAGCAACCCAGCAGATCTCCACCCCTGCTCAGGACCTCTGTGAAGAGGGGATGAAGTG
GGTCTCAGGGAGGAGTGGGGCTTGTGGCAGCTGGCTCGGAGCCGGCTTACAGGAGGCAGCTCTG
CAGTTGGGAGGGCACCGTCCGGAGGAGACCAGGCCCTCTACACACCCCTCTACTTATCATCTCCCTGCT
CACACACCTTGTCCAAGGCTTTATGATCGGATTTATTTTCCAAATCGAGAGGACAGTGATGATGCAT
TTTCCCCAGGCTGTCTCAGAAAGTCCGCTAAATGTATACTGTGTGAGAAATTTCTCTCAGGACGCCACCTGG
TTTGGTTTGTGAGCAGTAAATCTTTTCCACTGTGACTTATTTCTCTCTCAGGACGCCACCTGG
TCCCTTGTGCTGACTCTAGCACAGTGGCCAGGATCCAATACAGTCCAAGGTTGACCCGAGGATGGTGGG
GCAGCGGCTTCTCCACCTACCCAGCCACCAAGGCCCTGACGCACCTGCTCTCTGACCTTTCAGCACATCC
CTGTGCACAGTGAAGGTGCTAGCCCGCTCAGCTTGTGTTTTCAGATGCGTGAACGCTGATGATACAG
CTCCTCCCTGCGGTGCCCTGCCACGGAGCAGGCAATGTGAACCTGGCTGTGTGTTGAGTCCACCTGGCA
TGGCTCCAGCCCCAACCCACAGTGGAGACTGGAGACAGGCAATGAGTCTGGTGGGGGACGTTGGACATG
CCCCATAGGGGCCCCACCCAGACTTAACAGGCAAGGTCCTGGGCATTGTCGACGCAGGACTCAATGCTAA

AGCAAAGCCTGCCCTGGCTCTGTGCCAGGGCCCTCTTCTTGATTTACACATCCCAATTTTACACAGACCCTTC
 CTTCTTAATAAAGCTGACAGTTCTGTGGCAGCCCAAGAACCCACACCATGAAGACAGGGAGTGAGGGGCC
 TTTTGTGCCAACTCCAGCACAGCTGCTTCTGGGTGTGTGAGAGGCACTGTCGTGCTCTGTGCGCTGGTGG
 TCTCTGTGAGACAGTTCCGAGGACGGGAAATGACGGGTGGTGGGGCTGTGAGGCTTATATGTGGAACCTGA
 TGCAGAGTTCCCTGCAGACGGATCTGGATATACACTATGTATAAATCTTACGTGTAATTTAAATAATATATC
 TGTGTTGGCATCGTCATGAGAAGATATATGTAAGGCTCTGAAGGGAGAGGGAGATGTACATTTCTGCCAGGC
 TCTCTGGGGA CCTATCCGAGTCATGAATGTAGACTGTTGATCCAGTGGTGCAAGAAGCTACACTCCCATG
 TGTCAATCAGCTTATGACTCTTAATGTATTTTAAAGCAAAAAATGTGAGCCGACTCCATCTTCACCCCTC
 GATTCTCTGAGTCCAGCCTTCTGTGCCAGTGTCTCACTGAGCCACAACGCTCTCGCCATCGGGACCCCGGC
 TGGGCTGGAGTCTCGGGGCACAGTTGCCATGGAGCCCTCCTGGGTCTTTCTACAAATGTGCTGAGTGCCA
 GCGCTGAACCCACAGGAGATGGAGTACCTTGGCCAAAGCTTAAAGAGAGATTTTCTCAGGGTATTTATTA
 GTGTGTCCAGCAGGGTCAGGAAGCAGGATGGAAGATGCATTCAGACTGTTAATTTATTAACAAGGCAAAAT
 GATTTTGTGTTTCTTGATGACAGACTATTAAGTTTGGGACTTATTTTCCATTTGAGAAGTTATAATAATATAT
 AATTAAGATGATAAGTTTCTGCTTAAAGTTGTGCTTTCAGCTTCAAAGAGTTTAAAGGAGCACTAAGGGTA
 ATGATACCAATGAGGGTTGGTTATATATCAAACTGAATAGCTGTGGTTCCTCCAGTAAATATTTTCTTCT
 ACTGAACATGGAGCCATTAATAAGAGTTGTGTGTTTTTTTATTAATATGTACATTTTGTATATTTTGTGCTTGT
 TGAATGTTCTATTTTCTAAAGTTTCTTTTAGTTTCTTAAAGTTGTCTATACATAGATTTAGATTTCTGATGC
 TAACTGCAAAATCAGTTGGTCTCTGCTGGGTCTCTCTCTGCTTTTATTTTACTTTTAAAGGACAAAGTGTAGTTG
 TCGTCCACCACCTTTCAAAAAATGTGAAACTGCCCTGCCCTTTTGTCTGACAACACTGTGTACATTG
 ACCACTTCTACCATATCTTTATGTTGTAAAAATCAAACTCTTTTGTGGTACATTAATCTCATGCTTCTGCAAA
 TTTCGAATAAAATCTATGGCTTCCAAAAAATAAAAAAAAAAAAAAAAA

BB-48
FIG. 1

INTERNATIONAL SEARCH REPORT

national Application No

PCT/US 00/07044

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 G01N33/574 G01N33/50 G01N33/543 C07K16/18 C07K14/47

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 G01N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, BIOSIS, MEDLINE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	HÖRNER, S. ET AL.: "AC133-positive cells in the peripheral blood and bone marrow of patients with chronic myelogenous leukemia" BLOOD, vol. 92, no. 10, 15 November 1998 (1998-11-15), page 316b XP000937697 abstract	1-3,6,7, 16
A	WO 97 41224 A (AMCELL CORP) 6 November 1997 (1997-11-06) claims 28,35-41	1-3,6,7, 16
A	WO 92 15602 A (DANA FARBER CANCER INST INC) 17 September 1992 (1992-09-17) page 1, line 1 -page 3, line 13; claims 1-6	1-3,6,7, 16
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☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

* Special categories of cited documents:

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"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

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"&" document member of the same patent family

Date of the actual completion of the international search

8 September 2000

Date of mailing of the international search report

- 1. 12. 00

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3018

Authorized officer

Gundlach, B

INTERNATIONAL SEARCH REPORT

national Application No

PCT/US 00/07044

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 97 42209 A (ICRF CLARE HALL LAB ;ARIZA RAFAEL R (GB); WOOD RICHARD D (GB); HOE) 13 November 1997 (1997-11-13) abstract; claim 22 ---	1-3,6,7, 16
A	WO 99 04030 A (KINZLER KENNETH W ;CHAN TIMOTHY A (US); MORIN PATRICE J (US); VOGE) 28 January 1999 (1999-01-28) claims 1,6,7,12,13,18,19,24,25,30,31,36 -----	1-3,6,7, 16

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 00/07044

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
see FURTHER INFORMATION sheet PCT/ISA/210
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-3, 6, 7, 16 (partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.1

Although claims 6 and 7 are directed to a diagnostic method practised on the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.

Continuation of Box I.1

Rule 39.1(iv). PCT - Diagnostic method practised on the human or animal body

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-3,6,7,16 (partially)

Method for screening anti colorectal cancer drugs involving
CZA8 (AC133)

2. Claims: 1-3,6,7,16 (partially)

Method for screening anti colorectal cancer drugs involving
BCX2

3. Claims: 1-3,6,7,16 (partially)

Method for screening anti colorectal cancer drugs involving
CBC2

4. Claims: 1-3,6,7,16 (partially)

Method for screening anti colorectal cancer drugs involving
CBC1

5. Claims: 1-3,6,7,16 (partially)

Method for screening anti colorectal cancer drugs involving
CBC3

6. Claims: 1-3,6,7,16 (partially), 4,5,8-10,17-22,
25-38 (fully)

Method for screening anti colorectal cancer drugs involving
CJA8

7. Claims: 1-3,6,7,16 (partially)

Method for screening anti colorectal cancer drugs involving
CJA9

8. Claims: 1-3,6,7,16 (partially)

Method for screening anti colorectal cancer drugs involving
CGA7

9. Claims: 1-3,6,7,16 (partially)

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Method for screening anti colorectal cancer drugs involving
BCN5

10. Claims: 1-3,6,7,16 (partially)

Method for screening anti colorectal cancer drugs involving
CQA1

11. Claims: 1-3,6,7,16 (partially)

Method for screening anti colorectal cancer drugs involving
BCN7

12. Claims: 1-3,6,7,16 (partially)

Method for screening anti colorectal cancer drugs involving
CQA2

13. Claims: 6,7,16 (partially), 11-15,23,24 (fully)

Method for screening anti colorectal cancer drugs involving
CAA9

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No
PCT/US 00/07044

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